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Predictors and Trends in Cancer Genetics Clinic Attendance Rate After the Adaptation of Telemedicine During the COVID-19 Pandemic

THESIS

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for the degree of

MASTER OF SCIENCE

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by

Angelica Cecilia Smullin

Thesis Committee:
Professor Emeritus Moyra Smith, Chair
Adjunct Professor Pamela Flodman
Health Sciences Associate Clinical Professor Deepika Nathan

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DEDICATION

To those I love and laugh with – thank you.

"All that is really worth doing is what we do for others."
– Lewis Carol

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ABSTRACT OF THE THESIS

Predictors and Trends in Cancer Genetics Clinic Attendance Rate After the Adaptation of Telemedicine During the COVID-19 Pandemic

by

Angelica Cecilia Smullin

Master of Science in Genetic Counseling

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Professor Emeritus Moyra Smith, Chair

Despite the clear benefit of cancer genetic counseling, many eligible patients never meet with a cancer genetic counselor. Many elements contribute to this, including the growing demand for genetic services, lack of genetic professionals, and patient non-attendance. Prior research in cancer genetic counseling and other medical specialties has investigated the use and outcomes of alternate service delivery models, however, little is known about the specific impact of telemedicine on patient attendance over a substantial period of time. This study analyzed demographic and clinical data from 800 adult patients seen for cancer genetic counseling before and after the adaptation of telemedicine during the global COVID-19 pandemic. The purpose of this research was to investigate telemedicine's impact on attendance rate at follow-up appointments as well as explore patient predictors of attendance status. Logistic regression analyses identified that patients were 3.54 times more likely to attend their first scheduled follow-up visit if they were in the telemedicine cohort ($p < 0.001$). Additionally, patients who had more relatives with cancer and patients of Asian descent were more likely to attend their first follow-up visit. Patients were less likely to attend their first scheduled follow-up visit if there was a greater amount of time between their initial appointment and their genetic test results

report date. This research builds upon current literature on attendance status and contributes novel findings on the scope and impact of telemedicine's role in increasing attendance and access to cancer genetic counselors. Recognizing and understanding telemedicine's positive outcomes may lay the foundation for the adoption and permanence of this service delivery model in the cancer genetic counseling setting.

I. INTRODUCTION

1. Cancer genetics overview

Cancer is one of the leading causes of death in the United States; it is estimated that 1.9 million new cancer diagnoses and 609,360 cancer deaths will occur in 2022 (American Cancer Society, 2022). In males, the most common cancers include prostate (26%), lung (12%), and colorectal cancer (8%). Among females, the most common cancers include breast (30%), lung (13%), and colorectal cancer (8%). Other cancers, such as pancreatic and ovarian cancer, are not as frequent in the general population, yet are common referral indications in a cancer genetic counseling clinic due to their rarity and high suspicion for a genetic predisposition. Males have higher rates of cancer diagnoses than females, with an average lifetime risk of 40.5%, or 1 in 2. For females, the average lifetime risk is around 1 in 3 or 38.9%. From 2011 to 2017, the average five-year cancer survival rate was 67.7% (SEER, 2021).

While a typical cell has an orderly life cycle marked by routine cell division, replication, and programmed cell death, cancer cells are characterized by their uncontrollable division, replication, and dispersal to different body locations. Cancerous cells can accumulate and form tumors, which can be benign (typically not harmful) or malignant (harmful). Cancer is considered metastatic when the cancerous cells have invaded the surrounding tissue and spread to other parts of the body (National Cancer Institute, 2021).

Cancer is caused by variations in a gene's DNA sequence that alter or disrupt the normal function of the gene, also known as pathogenic mutations. The human genome includes specific genes that are responsible for maintaining orderly cell division and function, so mutations in these genes can cause disorderly division and growth that is characteristic of cancer. These genetic mutations are typically acquired over one's lifetime, either as the result of errors in the

cell division process or from harmful environmental factors, such as tobacco use, ultraviolet (UV) exposure, and radiation. When genetic mutations occur after conception, they are considered somatic changes. However, some genetic mutations can be inherited if the mutation is present in a parent's reproductive cells or germ cells (sperm and egg). Genetic mutations that occur prior to conception are called germline changes; these are present in every cell of the individual (National Cancer Institute, 2017). It is also possible for genetic mutations to occur *de novo*, meaning the genetic mutation is novel in that individual, and not inherited from a parent. *De novo* mutations can occur in the formation of the sperm or egg, or during the fertilization of the embryo (National Cancer Institute). While *de novo* mutations do not typically confer a hereditary cancer risk to the individual's parents or siblings, the mutation can be passed down to that individual's offspring. These genetic mutations typically occur in genes that have a key role in the development of cancer: proto-oncogenes and tumor suppressor genes. Proto-oncogenes function by assisting in the normal growth and development of new cells, thus genetic mutations can cause these genes to become overactive, resulting in uncontrollable cell proliferation. Once mutated, these genes are called oncogenes. Conversely, tumor suppressor genes normally function in the opposite manner by slowing cell growth, repairing DNA replication errors, and assisting in apoptosis, or programmed cell death. Genetic mutations in these genes inactivate this system, also leading to uncontrollable cell growth (American Cancer Society, 2014).

Although all cancer is genetic, not all cancer is hereditary. Cancer is typically classified into three categories: sporadic, familial, and hereditary. About 75% of cancer is considered sporadic, meaning cancer occurs due to random, acquired genetic changes over the course of a lifetime, which may be caused by harmful environmental exposures, such as radiation, tobacco, and ultraviolet rays. For these reasons, sporadic cancers are typically seen in older individuals

without a family history of cancer and are typically more common cancers, such as breast and prostate cancer. Approximately 15 to 20% of cancer is considered familial, which accounts for families in which a pattern of cancer exists and appears hereditary, however, a genetic cause is not identified. Familial cancer can occur due to a combination of shared genetic and environmental factors. It is also possible for familial cancer to result from the cumulative, additive effect of common variants in multiple genes, known as polygenic inheritance (Zhang et al., 2020). Only 5-10% of cancer is hereditary, meaning that an individual inherited a genetic mutation that makes them more susceptible to developing cancer over their lifetime. Hereditary cancers typically tend to follow specific, identifiable patterns that can be traced throughout a family's history, such as multiple individuals in the family with cancer, multiple primary cancers in the same individual, cancer diagnoses at younger ages, and rarer cancers, such as ovarian cancer, pancreatic cancer, or breast cancer in a male.

Individuals with a hereditary cancer syndrome are born with a harmful genetic mutation that predisposes them to a higher risk of developing cancer, often at an earlier age of onset. It is important to note that inheriting a harmful genetic mutation does not guarantee a 100% chance of developing cancer, as many individuals with harmful genetic mutations remain cancer-free throughout their lifetime. However, inheriting a harmful genetic mutation significantly increases the lifetime risk of developing certain cancers. There are many well-characterized genes associated with hereditary cancer predisposition syndromes, such as *BRCA1*, *BRCA2*, *MLH1*, *MSH6*, *MSH2*, *PMS2*, *TP53*, *PTEN*, *STK11*, and *CDH1*. Hereditary cancer syndromes associated with mutations in these cancer-predisposing genes include Hereditary Breast and Ovarian Cancer Syndrome (HBOC), Lynch Syndrome, Li-Fraumeni, Cowden, Peutz-Jeghers, and Hereditary Diffuse Gastric Cancer. In individuals with a hereditary cancer syndrome but without a family

history of cancer, it is also possible that the genetic mutation in the cancer susceptibility gene occurred *de novo*, meaning the mutation is novel in that individual, and not inherited from a parent. It has previously been reported that *de novo* mutations account for at least 7% and up to 20% of germline *TP53* mutations in those with Li-Fraumeni syndrome. However, the rate of *de novo* mutations in other cancer-predisposing genes, such as *BRCA1 and BRCA2*, have been reported to be much lower, around 0.1% and 0.7% respectively, with the majority of mutations in these genes inherited from a parent (Gonzalez et al., 2009; Goldmard et al., 2016; Acuna-Hidalgo et al., 2016). Additionally, certain ethnic populations are known to be at higher risk for carrying and/or inheriting a mutation in a cancer susceptibility gene. For example, in the Ashkenazi Jewish population, there is a high frequency of founder cancer-predisposing mutations in specific genes, approximately 2%, in *BRCA1* 185delAG, *BRCA1* 5382insC, and *BRCA2* 6174delT (Levy Lahad et al., 1999).

1.2 Cancer genetic counseling

If an individual's personal or family history of cancer is suggestive of a hereditary cancer syndrome, they may be referred for a personalized cancer risk assessment with a cancer genetic counselor. Cancer genetic counselors are medical professionals with specialized training in genetics and cancer. Referrals to genetic counselors for individuals suspected to be at risk of a hereditary cancer syndrome are strongly recommended to obtain a detailed family history, provide personalized cancer risk assessment, and provide education and counseling. This individualized risk assessment may lead to genetic testing and personalized cancer screening or risk reduction strategies (ACOG, 2019).

The traditional framework for a cancer genetic counseling visit includes an initial pre-test counseling appointment and a follow-up post-test counseling appointment, if applicable. In a pre-

test counseling visit, cancer genetic counselors explain the purpose of genetic counseling, educate the patient on the relationship between cancer and genetics, and collect extensive information from the patient regarding their personal and family history. With the information obtained, the genetic counselor assesses the patient's cancer risk to determine whether their risk is increased over the general population. This risk assessment may be ascertained from the individual's personal and family history and a specific risk figure can be calculated using population-based cancer risk models, such as Tyrer-Cuzick (Tyrer et al., 2004) or BRCAPRO (Parmigiani et al., 1998). Cancer genetic counselors will then discuss whether the individual meets criteria for genetic testing. Published guidelines for cancer genetic testing are available through professional expert societies, such as the National Comprehensive Cancer Network (NCCN), the American College of Medical Genetics (ACMG), and the National Society of Genetic Counselors (NSGC). For example, among the NCCN guidelines, key criteria for genetic testing include a personal history of female breast cancer diagnosed at or before 45 years of age, triple-negative breast cancer diagnosed at or before 60 years of age, breast cancer, and Ashkenazi Jewish ancestry at any age, or male breast cancer at any age (NCCN, 2021). In addition to professional guidelines, many public and private insurance payers have their own criteria for genetic testing coverage that may or may not follow national guidelines. For example, Medicare does not currently cover genetic testing for individuals without a personal history of cancer. As new data on the clinical utility of cancer genetic testing emerges, these guidelines and criteria are subject to change.

If genetic testing is indicated and the individual meets the criteria for testing, the next step will then be for the cancer genetic counselor to explain the three possible results of genetic testing. The first is a positive result, meaning a harmful (pathogenic) mutation was identified in a

gene that is known to be associated with an increased risk for cancer. Typically, positive results have specific medical management guidelines provided by professional societies and may have treatment recommendations as well. Positive results can also have implications for family members. For example, many mutations in cancer-predisposing genes are inherited in an autosomal dominant manner. The National Cancer Institute defines autosomal dominant inheritance as "a way a genetic trait or condition can be passed down from parent to child. One copy of a mutated (changed) gene from one parent can cause the genetic condition [and] a child who has a parent with the mutated gene has a 50% chance of inheriting that mutated gene". While positive results can greatly increase the chance of developing cancer, they do not confer a 100% chance of developing cancer, as many individuals with pathogenic mutations do not develop cancer. Again, it is worth noting that if a pathogenic mutation is identified in an individual, it is possible that the mutation is *de novo*. While *de novo* mutations do not typically confer a hereditary cancer risk to the individual's parents or siblings, the mutation can be passed down to that individual's offspring.

The second type of result one can receive with genetic testing is a negative result, which indicates that no pathogenic mutation was identified in the genes analyzed. A negative result is not always straightforward to interpret. A negative result may indicate that the cancer is sporadic or familial in nature, however, it is also possible that the cancer is hereditary, and the specific gene was not tested. Alternatively, the individual could have a harmful variant in a gene that was tested, however, the current testing methodology used by the genetic testing laboratory was unable to identify the variant. Negative results may or may not change medical management recommendations, depending on the patient's personal and family history.

The third type of result one can receive is an uninformative result, called a Variant of Uncertain Significance, or a VUS. This type of result means a variant in a gene was identified but it is unknown whether the DNA alteration is cancer-predisposing or normal variation. Due to their uncertain nature, VUS results are treated as negative results and medical recommendations are based solely on the individual's personal and family history. Over time as the genetic testing laboratory acquires new evidence and data, these results may be reclassified. Current literature estimates that approximately 91.2% of VUSs are later reclassified as benign alterations (Mersch et al., 2018).

If genetic testing is elected, the cancer genetic counselor will meet with the individual again to disclose the results in a post-test counseling appointment. In this setting, cancer genetic counselors will explain the meaning of the result in the context of the individual's personal and/or family history. If the result is positive, the cancer genetic counselor will discuss the cancer risks associated with the genetic mutation, inform the patient of recommended screenings or relevant medical management guidelines, and discuss implications for family members who may now be at risk of having the familial genetic mutation. Cancer genetic counselors may also make referrals to other providers as needed.

1.3 Barriers to genetic counseling appointment attendance

Despite the clear benefit of cancer genetic counseling, many eligible patients never meet with a genetic counselor (Delikurt et al., 2015; Swink et al., 2019; Muessig et al., 2022). There are many elements that contribute to this, including the growing demand for genetic services and the lack of genetic professionals. The field of genetics is exponentially expanding due to advancements in genetic research, scientific knowledge, and DNA sequencing technology. This

unparalleled growth has generated a surging demand for genetic services and professionals, however, there remains a shortage of genetic counselors and genetic professionals across the country, making access to genetic services few and far between. In 2020, approximately 4,813 genetic counselors were actively practicing in the United States, or 1.49 genetic counselors per 100,000 people (Bellaiche et al., 2021). Additionally, the 2021 National Society of Genetic Counselors (NSGC) Professional Status Survey reported that 66% of US genetic counselors reported working in a Metropolitan Statistical Area, defined by the Census Bureau as "a core area containing a substantial population nucleus, together with adjacent communities having a high degree of economic and social integration with that core". With most genetic counselors practicing in urban hubs, access to genetic services is particularly deficient in rural geographic locations. On a different note, these areas may lack support services or the downstream infrastructure that should ideally accompany genetic testing.

Awareness and ability of providers to identify patients at risk for a hereditary cancer syndrome are also lacking, despite clear referral guidelines from multiple professional societies, including the National Comprehensive Cancer Network (NCCN), American College of Medical Genetics (ACMG), and the American College of Obstetricians and Gynecologists (ACOG) (Delikurt et al, 2015; Koil et al., 2003; Sweet et al., 2002). In 2019, an analysis of 200 patients with breast or ovarian cancer at Baylor University Medical Center identified that 30% of patients who qualified for genetic counseling and/or genetic testing never received a referral from their oncologist, and that "the initial referral to genetic counseling [was] the most significant barrier for at-risk patients...and likely in this population at large" (Swink et al., 2019).

Appointment non-attendance is another common and pervasive barrier to medical care access. Across specialties, approximately 23% of patients fail to show to their scheduled

appointments (Dantas et al., 2018). Not surprisingly, clinic non-attendance adversely affects patients' health as it disrupts their continuity of medical care. It also adversely affects the stability, efficiency, and functionality of clinics. Additionally, no-shows have been reported to be a measure of health disparity, with minority, low-income, and Medicaid patients typically having the highest no-show rates (Dantas et al., 2018).

Numerous studies on non-attendance have been conducted and several factors have been reported to be associated with non-attendance in the literature. Among the most reported associations with missed appointments are younger adults, proximity to clinic, lack of private insurance, lower socioeconomic status, prior no-show history, competing commitments (such as childcare, family, and work), forgetting the appointment, being too ill to attend, and high lead times (Dantas et al., 2018; Bedford et al., 2020). Identifying and understanding the factors that contribute to non-attendance allows for the development of interventions that may mitigate those barriers, thus increasing attendance and access to quality medical care.

1.4 The COVID-19 pandemic and telemedicine

In early March of 2020, the emergence of SARS-CoV-2 (severe acute respiratory syndrome coronavirus 2), colloquially known as COVID-19, marked a rapid, global disruption in daily life. Within days, entire industries were forced to adapt to an unknown and ever-changing landscape, swiftly adopting new service practices that would eventually become the new norm. Healthcare, in particular, made a rapid conversion in its service delivery model, with many providers and clinics fully transitioning to telemedicine in order to continue providing patient care amid an infectious global crisis. The American Telemedicine Association (ATA) defines telemedicine as "the use of medical information exchanged from one site to another via

electronic communications to improve patients' health status". Telemedicine quickly emerged as the prominent healthcare service delivery model during the pandemic.

Many genetic counseling clinics, which had previously often been characterized by in-person appointments, also transitioned to telemedicine in March of 2020 and began offering telephone or video counseling. Prior to COVID-19, telemedicine was not the primary service delivery model in many cancer genetic counseling clinics, despite numerous published studies demonstrating its efficacy, provider and patient acceptance, improved access to services, high patient satisfaction, increased convenience, and equivalent patient knowledge and emotional outcomes (Brown et al., 2021; Gorrie et al., 2021; Bracke et al., 2020; Solomans et al., 2018; Vrecar et al., 2017; Buchanan et al., 2015; Kinney et al., 2014; Trepanier et al., 2013; Meropol et al., 2011). One study showed that patients at risk for a hereditary cancer syndrome ranked in-person and local counseling as the least important characteristics when deciding the acceptability of a genetic counseling service delivery model (McDonald et al., 2014). Furthermore, genetic counseling professionals who utilized telemedicine prior to the pandemic were highly satisfied with their positions, and those not utilizing telemedicine were interested in doing so (Zierhut et al., 2018).

Despite the well-described benefits of telemedicine in healthcare, including increased convenience and reduced costs, travel, and wait times (Gorrie et al., 2021; Buchanan et al., 2015; Brown et al., 2018; Cohen et al., 2016; Cohen et al., 2013; Greenberg et al., 2021; Weissman et al., 2018; Bradbury et al., 2016; Buchanan et al., 2016; Bussell et al., 2019; Fentol GL et al., 2018; Hilgart et al., 2012; Hopper et al., 2011), telemedicine continues to be an underutilized service delivery model in the genetic counseling profession. The NSGC PSS (National Society of Genetic Counselor's Professional Status Survey) reported that only 36% of genetic counselors

used telephone counseling and 28% used audiovisual (video) counseling in January and February of 2020, prior to the onset of the pandemic. It has previously been reported that issues with billing/reimbursement and licensure may be the main barriers to widespread telemedicine use (Boothe et al., 2021; Mills et al., 2021; Bussel et al., 2019; Bradbury et al., 2016; Cohen et al., 2016; Radford et al., 2014).

Numerous billing challenges exist for traditional, in-person genetic counseling visits, with many issues stemming from the Centers for Medicare and Medicaid (CMS) lack of recognition for genetic counselors (Boothe et al., 2021). Billing for telemedicine visits presents an additional layer of complexity, as many insurance payors limit or lack reimbursement for video or phone genetic counseling, likely preventing telemedicine from being a widespread, sustainable alternative to healthcare delivery. Furthermore, many genetic counselors may be uncertain about billing practices; in one study, over 50% of surveyed genetic counselors using telemedicine were not billing or were unsure of how they were billing (Ma et al., 2021). Overall, research has identified that up to 39% of genetic counselors reported billing/reimbursement as one of the main obstacles to telemedicine use (Zierhut et al., 2018; Mills et al., 2021).

Furthermore, while telemedicine creates the opportunity for genetic counselors to practice in more than one state, applying for and maintaining multi-state professional licensure has been reported to be a significant challenge for individuals and employers. Lack of standardized licensure across states leads to a costly, arduous application process, for genetic counselors and physicians alike. The extensive variation among state applications, required documentation, and verification processes are all resource and time-intensive (Tschirgi et al., 2021; Bradbury et al., 2017). Among a recent survey of genetic counselors, licensure was cited as one of the most common challenges and barriers to telemedicine (Terry et al., 2019).

Telemedicine has also been reported to be associated with lower genetic testing uptake, with fewer patients consenting to genetic testing via telephone or video appointments (Shannon et al., 2020). There are also trends of decreased sample return rates and increased sample failure rates associated with telemedicine, likely due to the lack of oversight by healthcare professionals in ensuring timely, and proper, sample collection (Kinney et al., 2014; Shannon et al., 2020; Bergstrom et al., 2020; Mann et al., 2021).

Aside from technical and logistical obstacles associated with virtual care, not all patients may have equitable access to telemedicine. Disparities with telemedicine access have been identified, both in genetic and non-genetic settings, with traditionally underserved patient populations being less likely to use or benefit from telemedicine (Eberly et al., 2020; Mills et al., 2021; Rodriguez et al., 2021). A study by Ma et al. (2021) also found that genetic counselors perceived poor internet connection and unequal access to devices and data plans as major challenges to patients seen remotely.

In 2019, the year prior to the pandemic, the NSGC PSS reported that 20% of direct patient care genetic counselors worked remotely. During the pandemic in 2020, that number increased to 85%. Importantly, a recent survey of 165 genetic counselors identified that 93.5% of respondents hope to continue using telemedicine after the pandemic resolves (Bergstrom et al., 2021). Although telemedicine was not a commonly used service delivery model in the genetic counseling setting prior to COVID-19, it seems highly probable that the continued use of this model over the last 18 months may prompt further policy and initiatives to better enable genetic counseling clinics to retain some, if not all, aspects of telemedicine.

1.5 Aims and hypotheses

This retrospective chart review aims to collect and analyze data on patients seen in a university medical cancer genetic counseling setting over a 40-month period to:

1. Identify the proportion of patients who attended their scheduled cancer genetic counseling follow-up visit/s before and after the adaptation of telemedicine during the COVID-19 pandemic.
2. Identify telemedicine's impact on patient attendance in the cancer genetic counseling clinic.
3. Identify factors that may influence or predict whether a patient is more or less likely to return for follow-up in the cancer genetic counseling clinic.

I hypothesize that the adaptation of telemedicine during the COVID-19 pandemic has increased the attendance rate for follow-up visits in the cancer genetic counseling clinic (i.e., patient attendance is higher with a telemedicine service delivery model). I hypothesize that patients with increased cancer morbidity, such as late-stage diagnoses and cancers with higher mortality rates (ovarian cancer, pancreatic cancer) will be more likely to attend their scheduled cancer genetic counseling visits if the appointment is via telemedicine. Lastly, I hypothesize that patient demographic factors, such as proximity to clinic, age, and number of children will predict the likelihood of follow-up appointment attendance.

1.6 Significance of research

The purpose of this study is to build upon previous research that examined predictors of patient attendance for follow-up cancer genetic counseling appointments, which ultimately identified that a significant proportion of cancer genetic counseling patients do not attend their scheduled follow-up appointments. This research suggested that an alternate service delivery model for these visit types, such as telemedicine, might be a reasonable and effective way to bypass barriers specific to in-person visits (Spiewak, 2019). Further research examined differences in cancer genetic counseling appointments following the shift to telemedicine in the COVID-19 pandemic, identifying an increase in attendance rate after the switch to telemedicine (Shannon et al., 2020). However, this study was limited in that it only analyzed 12-weeks of patient data and the data were collected during a highly turbulent time in the pandemic. Conversely, a randomized trial comparing telemedicine to in-person cancer genetic counseling identified a decrease in the attendance rate with telemedicine (Buchanan et al., 2015).

The sudden and complete conversion to telemedicine in the cancer genetic counseling clinic elucidated a unique opportunity to evaluate the impact and utility of this service delivery model. In particular, understanding telemedicine's influence on attendance rate, both for initial and follow-up appointments, will provide vital insights, as many of the barriers associated with non-attendance are specific to the traditional, in-person format and thus may be ameliorated with telemedicine. Proximity to the clinic, competing commitments (such as childcare, family, work), and current illness may not present as challenges and perhaps may dissipate with the implementation of this alternate delivery model. For example, many cancer genetic counseling patients do not have the physical ability to drive to the clinic and meet with their genetic counselor due to the tremendous burden of their disease and treatment. Understanding if these

patients are more likely to attend their appointment in a telemedicine format may help increase attendance and access to valuable care in this population. Additionally, since non-attendance has been reported to be a measure of health disparity, identifying individuals more likely to not show to scheduled appointments allows for the development of targeted interventions and the subsequent reduction of these health care disparities (Starnes et al., 2019).

Several publications highlight the need for an alternate service delivery model in genetic counseling, such as telemedicine, to meet the ever-increasing demand for genetic counseling services (Rahm et al., 2019; Bracke et al., 2020; Greenberg et al., 2020), and an abundance of literature has emphasized the need for further research on telemedicine's impact in a genetic counseling setting (Khan et al., 2021; Gorrie et al., 2021; Mann et al., 2021). Currently, there is little evidence in the literature on the outcomes and efficacy of telemedicine, especially as it relates to attendance rate, and there are no published studies that analyze predictors and trends in cancer genetics clinic attendance rate due to telemedicine for a substantial length of time. Insight into the outcomes of telemedicine during the pandemic may identify if this model improves the delivery of genetic services, bypasses barriers specific to in-person appointments, and ultimately expand access to care. Recognizing telemedicine's effect in the cancer genetic counseling setting could prompt genetic professionals to adopt a telemedicine/hybrid model, and thus increase access to genetic services in certain patient populations. In the post-pandemic world, it is highly plausible that telemedicine may become a standard framework for genetic counseling, so it is crucial that a deeper understanding of telemedicine's effect is pursued.

II. METHODS

2.1 IRB protocol

This research study qualified for expedited review by the University of California, Irvine, Institutional Review Board and was approved under HS # 2021-6826.

2.2 Retrospective chart review

2.2.1 Patient selection

The initial study population included all cancer genetic counseling patients with a new patient appointment scheduled between April 3, 2018, and September 23, 2021. This time frame resulted in 889 patients. Data were collected chronologically until a total sample size of 800 patients was met. Upon evaluation of this study sample, 16 patients were excluded from analysis, with 4 patients ineligible for study inclusion due to their age (these patients were younger than 18 at the time of their new patient appointment) and 12 patients ineligible due to the date of their new patient appointment being prior to April 3, 2018. Chronological data collection resumed to accrue an additional 16 patients and re-obtain a total study population of 800 patients. For these 800 patients, each variable of interest was identified and collected through a manual chart review in the UCI Cancer Genetics Clinic Database (CaGen) and the electronic medical record system (EPIC). The total study population of 800 patients was divided into two cohorts, pre-telemedicine or telemedicine, with cohort separation dependent on the date of the patient's initial new patient appointment. The pre-telemedicine cohort consisted of all patients seen for an initial new patient consult between April 3, 2018, and March 17, 2020, for a total of 496 patients seen over 24 months. The telemedicine cohort consisted of all patients who were seen for an initial new patient consult between March 18, 2020, and April 2, 2021, for a total of 304 patients seen

over 13 months. All patients were 18 years or older at the time of their new patient visit and were seen by a UCI Cancer Genetic Counselor at the University of California, Irvine Medical Center Chao Family Comprehensive Cancer in Orange, CA, or the Comprehensive Digestive Disease Center in Costa Mesa, CA. In total, 800 patients met the initial study population criterion and were eligible for analysis.

2.2.2 Data collected from the internal UCI cancer genetics clinic database (CaGen) and electronic medical record (EPIC)

Demographic information, personal and family cancer history, logistical aspects of the cancer genetic counseling consultation, and pedigree information were collected from the CaGen database and Electronic Medical Record (EPIC) for each eligible patient in this study. This information included:

Demographic information:

- Patient age
- Patient gender
- Patient's race or ethnicity, as documented by the cancer genetic counselor during the visit. Race or ethnicity was categorized according to the NIH "Racial and Ethnic Categories and Definitions for NIH Diversity Programs and for Other Reporting Purposes" and is as follows (Notice Number: NOT-OD-15-089, release date April 8, 2015):
    - **American Indian or Alaska Native** – A person having origins in any of the original peoples of North and South America (including Central America) and who maintains tribal affiliation or community attachment.

- **Asian** – A person having origins in any of the original peoples of the Far East, Southeast Asia, or the Indian subcontinent including, for example, Cambodia, China, India, Japan, Korea, Malaysia, Pakistan, the Philippine Islands, Thailand, and Vietnam.
- **Black or African American** – A person having origins in any of the Black racial groups of Africa.
- **Hispanic or Latino** – A person of Cuban, Mexican, Puerto Rican, South or Central American, or other Spanish culture or origin, regardless of race. The term, "Spanish origin," can be used in addition to "Hispanic or Latino."
- **Native Hawaiian or Other Pacific Islander** – A person having origins in any of the original peoples of Hawaii, Guam, Samoa, or other Pacific Islands.
- **White** – A person having origins in any of the original peoples of Europe, the Middle East, or North Africa.
- **Other** – A person having origins in two or more of the above race/ethnicities

- Patient's primary language.
- Patient's home zip code. Zip code was used to determine the approximate travel distance to the UCI cancer genetic counseling clinic.
- Primary insurance payor. Payors were further categorized to include private insurance (HMO/PPO/EPOs), government insurance (Medicare/Medi-Cal/Tricare), or other.
- Primary insurance plan.

Personal and family cancer history:

- Personal history of cancer. If a patient had a personal history of cancer, the type of cancer and stage of cancer were noted.

- Prior germline (blood/saliva/buccal) genetic testing.
- Prior somatic (tumor) genetic testing.
- Previously known germline pathogenic mutation in the family. If there was a previously known germline pathogenic mutation in the family, the gene name was noted.

Details of the cancer genetic counseling visit/s:

- Referral date.
- Self-referral or physician-referral.
- Primary referral indication. Categories included personal history of cancer, family history or cancer, or both personal and family history of cancer.
- Date of initial visit.
- Date of follow-up visit/s.
- Attendance status at all visits.
- Visit setting for all appointments. Categories included in-person or telemedicine. Telemedicine was further categorized into telephone and video.
- Type of genetic test ordered.
- Number of genetic tests ordered.
- Type of sample collected for genetic testing.
- Date of sample collection.
- Date of report generation.
- Number of test results received.
- Type of test results received.

Pedigrees:

- Number of living children.
- Number of relatives with cancer.

After initial data extraction from the internal CaGen database, each patient entry was reviewed during manual EPIC data collection to evaluate for data consistency errors and ensure accuracy prior to data analysis. Errors in the internal database included incorrect appointment dating (i.e., date of follow-up being earlier than the date of new patient appointment), incorrect test report dating (i.e., date of the test report entered as the date of follow-up), incorrect attendance status, as well as incorrect genetic test results/classification. Identified errors were corrected prior to analysis. For data analysis, a study ID number was given to each patient and a unique code linking the study ID number to the patient was stored in a separate location.

2.3 Data analysis

Data analysis was performed using IBM SPSS Software Version 28 for descriptive and inferential analyses. Descriptive analyses included frequencies and distributions of patient demographic data, personal and family cancer history information, and genetic counseling appointment details. Initial inferential analyses included a comparison of cohort 1 (pre-telemedicine) and cohort 2 (telemedicine) for the collected variables using Chi-square tests for association, T-test for independent samples, and Fisher's exact tests.

Additional inferential analyses included univariate and multivariate analyses to focus on differences in attendance at follow-up visits. Univariate analysis included a Chi-square test for association to compare the proportion of patients who did or did not attend their scheduled

follow-up appointments (for first follow-up or any follow-up) across the variables of interest. Tests for linear association were also utilized for ordered variables in the univariate analysis.

For multivariate analysis, all variables which were significantly associated in the univariate analyses with attendance at first follow-up visit and any follow-up visit were then included in logistic regression analysis to identify which variables contributed independently to predicting attendance at follow-up. Binary logistic regression was used to investigate a dichotomous outcome (attended follow-up vs did not attend follow-up), while multinomial logistic regression was used to investigate a polychotomous outcome (never returned for follow-up vs returned at first follow-up vs returned at later follow-up). The significance level for all statistical tests is reported as a nominal p-value of 0.05 with no correction for multiple comparisons.

III. RESULTS

3.1 Descriptive data

3.1.1 Demographics of study population

The demographic information for the cancer genetic counseling participants in this study, both for the overall study population as well as between cohorts, is detailed in Table 1. Overall, there were 496 patients in the pre-telemedicine cohort and 304 patients in the telemedicine cohort, for a total of 800 participants. 249 of these patients identified as male and 551 patients identified as female (Figure 1). At the time of the initial new-patient consultation, the average participant's age was 53 with a range from 18 to 93 years old (Figure 3). Regarding race and ethnicity, 54.2% of the study population identified as White, 17.4% Hispanic or Latino, 17.4% Asian, 2.7% Black or African American, 0.8% American Indian or Alaska Native, 0.1% Native Hawaiian or Pacific Islander, and 7.5% 'Other', meaning they identified as 2 or more of the above ethnicities (Figure 5). English-speaking patients comprised most of the study population (89.4%), while 5.8% of participants preferred Spanish, 1.9% Vietnamese, 1.3% Korean, and less than 0.5% Chinese, Mon-Khmer, Amharic, Farsi, Mandarin, Romanian, Russian, and Sign Language (Figure 6).

Table 1: Demographics of the total study population.

	Descriptive Statistics				
	COHORT 1: Pre-telemed. N = 496	**COHORT 2: Telemed. N = 304**	**Overall Total**		
Demographics (cat.) *N = 800 unless otherwise specified*	**N (%)**	**N (%)**	**N (%)**	**χ2 (d.f.)**	**p-value**
Gender					
Female	374 (75.4)	177 (58.2)	551 (68.9)	25.95 (1)	< 0.001
Male	122 (24.6)	127 (41.8)	249 (31.1)		
Race/Ethnicity *N = 789*					
White	264 (53.9)	164 (54.8)	428 (54.2)		0.006*
Hispanic or Latino	80 (16.3)	57 (19.1)	137 (17.4)		
Asian	84 (17.1)	53 (17.7)	137 (17.4)		
Black or African American	10 (2.0)	11 (3.7)	21 (2.7)		
American Indian or Alaska Native	3 (0.6)	3 (1.0)	6 (0.8)		
Native Hawaiian or Pacific Islander	0 (0.0)	1 (0.3)	1 (0.1)		
Other (2 or more)	49 (10.0)	10 (3.3)	59 (7.5)		
Race/Ethnicity *N = 789*					
White	264 (53.9)	164 (54.8)	428 (54.2)	0.23 (2)	0.893
Asian	84 (17.1)	53 (17.7)	137 (17.4)		
Other	142 (29.0)	82 (27.4)	224 (28.4)		
Race/Ethnicity *N = 789*					
White	264 (53.9)	164 (54.8)	428 (54.2)	0.07 (1)	0.790
Other	226 (46.1)	135 (45.2)	361 (45.8)		
Language					
English	442 (89.1)	273 (89.8)	715 (89.4)	0.39 (2)	0.821
Spanish	28 (5.6)	18 (5.9)	46 (5.8)		
Other	26 (5.2)	13 (4.3)	39 (4.9)		

Age (years) Q1: 18 – 41 Q2: 42 – 55 Q3: 56 – 65 Q4: 66 – 93	120 (24.2) 135 (27.2) 113 (22.8) 128 (25.8)	84 (27.6) 79 (26.0) 77 (25.3) 64 (21.1)	204 (25.5) 214 (26.8) 190 (23.8) 192 (24.0)	3.27 (3)	0.352
Demographics (cont.)				**t (d.f.)**	**p-value**
Age in years Mean S.D. Median Range	53.7 15.3 55.0 18-93	52.2 16.2 53.0 18-89	53.1 15.7 55.0 18-93	1.26 (798)	0.208

***** p-value based on Fisher's exact test.

3.1.2 Clinical characteristics of study population

Table 2 summarizes the clinical characteristics of the participants in the overall study population as well as between cohorts. 424 (54.1%) patients seen at the UCI cancer genetic counseling clinic had private insurance plans (HMO/PPO/EPO) while 292 (37.2%) patients had government insurance plans (Medicare/Medicaid/TriCare). Over half of the patients seen in the cancer genetic counseling clinic did not require authorization from their insurance prior to being seen (56.6%). Referral indications were primarily due to a personal and family history of cancer (59.9%) or a family history of cancer (35%). Only 5.2% were referred solely for the patient's history of cancer. If patients were seen due to their personal history of cancer, ovarian cancer, colorectal cancer, breast cancer, and individuals with multiple cancer types were the most frequently seen (14.8%, 14.3%, 11.8%, and 17%, respectively). In terms of referral source, patients were most often referred by a physician (86.5%) compared to self-referrals (13.5%).

Prior to being seen at the UCI cancer genetics clinic, 14.1% of patients had prior germline genetic testing, and 3.4% of patients had prior somatic (tumor) genetic testing. Of those

patients who had prior genetic testing, 5.4% had an already identified pathogenic mutation. Sample types used for genetic testing included blood (56.6%) and saliva (43.4%). Most of the genetic testing was ordered through Lab A (72.7%), Lab B (14.5%), or Lab C (10%), and most of this testing were multi-gene panels (94.3%) Over half of the patients who had genetic testing received a negative result back (52.6%), while roughly a quarter received a VUS result (24.1%) or a positive (pathogenic or likely pathogenic) result (21%). Regarding patients' number of living children, the number of children documented on the pedigree ranged from 0 to 9, with a median of 2. For those patients with a family history of cancer, most patients had 4 relatives with a current or past cancer diagnosis.

It took an average of 69 days for a patient to be seen in the cancer genetic counseling clinic after their referral was placed. If genetic testing was ordered during the patient's visit, it took an average of 13 days for the patient to collect their sample. After sample collection, it took an average of 23 days until results were reported. While test results came back an average of 36 days after the patient was first seen, it took almost double the amount of time (62 days) until the patient's scheduled follow-up appointment.

Of the 800 patients seen for an initial new patient visit, 707 were scheduled to be seen for a subsequent follow-up visit. The 93 patients that were not scheduled for a follow-up visit likely had already had genetic testing prior to being seen at UCI, or patients who did not wish to proceed with further testing or counseling, and therefore only one visit was recommended. 553/707 successfully attended their first follow-up visit (78.2%), while 154/707 did not attend, either due to cancellations, no-shows, or needing to reschedule (21.8%). Overall, 658 patients attended at least one scheduled follow-up visit (93.1%) while only 49 patients (6.9%) never attended any of their scheduled follow-ups. Further combining these statistics, out of the 707

patients scheduled for a follow-up visit, 49 patients never returned to clinic (6.9%), 553 patients returned at their first scheduled follow-up (78.2%), and 105 patients returned at a later follow-up visit, meaning they did not attend their first scheduled follow-up visit but did attend a subsequent follow-up visit (14.9%).

In addition to descriptive statistics, cohorts were further compared in Tables 1 and 2 to identify whether there were significant differences present between those participants in the pre-telemedicine cohort versus the telemedicine cohort using Chi-square analysis. Significant differences were identified between cohort and patient gender ($p < 0.001$), insurance type ($p = 0.003$), referral indication (0.012), sample type ($p < 0.001$), genetic testing laboratory ($p < 0.001$), attendance at first follow-up visit ($p < 0.001$), and overall attendance at follow-up visits ($p < 0.001$). There were significantly more males in the telemedicine cohort (41.8% vs 24.6%), fewer patients with government insurance in the telemedicine cohort (39.3% vs 50%), more referral indications for personal history of cancer in the telemedicine cohort (8% vs 3.4%), more saliva samples in the telemedicine cohort (99.2% vs 11%), fewer tests ordered through Lab A in the telemedicine cohort (57.6% vs 80%), increased attendance at first follow-up visit in the telemedicine cohort (88.4% vs 72.4%), and fewer patients who never returned for follow-up in the telemedicine cohort (5.4% vs 7.3%). The t-test for independent samples was utilized to analyze continuous variables and identified significant cohort differences regarding number of living children ($p = 0.048$), number of relatives with cancer (0.010), days from referral to first visit ($p = 0.011$), days from first visit to sample collection ($p < 0.001$), and days from first visit to report date ($p < 0.001$). These variables were incorporated into a full logistic regression model for multivariate analysis to investigate their significance and will be further discussed in Section 3.3.

Table 2: Clinical characteristics of the study population.

	Descriptive Statistics				
	COHORT 1: Pre-telemed N = 496	**COHORT 2: Telemed N = 304**	**Overall Total**	**Statistical Analysis**	
Clinical characteristics (cat.) *N = 800 unless otherwise specified*	**N (%)**	**N (%)**	**N (%)**	**$\chi 2$ (d.f.)**	**p-value**
Insurance *N = 784*					
Private (HMO, PPO, EPO)	243 (50.0)	181 (60.7)	424 (54.1)	8.67 (2)	0.013
Government (Medicare, Medicaid)	196 (40.3)	96 (32.2)	292 (37.2)		
Other	47 (9.7)	21 (7.0)	68 (8.7)		
Insurance *N = 784*					
Private	243 (50)	181 (60.7)	424 (54.1)	8.58 (1)	0.003
Government/Other	243 (50)	117 (39.3)	360 (45.9)		
Insurance Authorization					
Auth Required	179 (36.1)	97 (31.9)	276 (34.5)	2.54 (2)	0.281
No Auth Required	278 (56.0)	175 (57.6)	453 (56.6)		
Unknown	39 (7.9)	32 (10.5)	71 (8.9)		
Referral Indication *N = 795*					
Personal history of cancer	17 (3.4)	24 (8.0)	41 (5.2)	8.76 (2)	0.012
Family history of cancer	182 (36.7)	96 (31.9)	278 (35.0)		
Both	295 (59.7)	181 (60.1)	476 (59.9)		
Personal History of Cancer					
Yes	312 (62.9)	205 (67.4)	517 (64.6)	1.69 (1)	0.193
No **Note: among those with no personal history of cancer, only 5 did not have a family history as well.*	184 (37.1)	99 (32.6)	283 (35.4)		

Cancer Type *N = 519* Breast Colorectal Ovarian Uterine Multiple Other	 42 (13.4) 43 (13.7) 52 (16.6) 24 (7.7) 52 (16.6) 100 (31.9)	 19 (9.2) 31 (15.0) 25 (12.1) 10 (4.9) 36 (17.5) 85 (41.3)	 61 (11.8) 74 (14.3) 77 (14.8) 34 (6.6) 88 (17.0) 185 (35.6)	8.27 (5)	0.142
Referral Source Provider Self	 432 (87.1) 64 (12.9)	 260 (85.5) 44 (14.5)	 692 (86.5) 108 (13.5)	0.39 (1)	0.528
Previous Germline Genetic Testing Yes No	 69 (13.9) 427 (86.1)	 44 (14.5) 260 (85.5)	 113 (14.1) 687 (85.9)	0.05 (1)	0.825
Previous Somatic Genetic Testing Yes No	 14 (2.8) 482 (97.2)	 13 (4.3) 291 (95.7)	 27 (3.4) 773 (96.6)	1.22 (1)	0.269
Prior Germline Mutation (Patient) Yes No	 26 (5.2) 470 (94.8)	 17 (5.6) 287 (94.4)	 43 (5.4) 757 (94.6)	0.05 (1)	0.831
Prior Germline Mutation (Relative) Yes No	 76 (15.3) 420 (84.7)	 36 (11.8) 268 (88.2)	 112 (14.0) 688 (86.0)	1.89 (1)	0.168
Sample Type *N = 691* Blood Saliva	 389 (89.0) 48 (11.0)	 2 (0.8) 252 (99.2)	 391 (56.6) 300 (43.4)	 508.9 (1)	< 0.001
Genetic Testing Laboratory *N = 799* Lab A Lab B Lab C Other	 406 (82.0) 33 (6.7) 38 (7.7) 18 (3.6)	 175 (57.6) 83 (27.3) 42 (13.8) 4 (1.3)	 581 (72.7) 116 (14.5) 80 (10.0) 22 (2.8)	 81.50 (3)	 < 0.001

Genetic Test Type					
Panel	467 (94.2)	287 (94.4)	754 (94.3)	0.29 (2)	0.866
Specific Site Analysis	26 (5.2)	16 (5.3)	42 (5.3)		
Both	3 (0.6)	1 (0.3)	4 (0.5)		
Genetic Testing Results					
Positive	102 (20.6)	66 (21.7)	168 (21.0)	0.79 (2)	0.674
Negative	272 (54.8)	149 (49.0)	421 (52.6)		
VUS	122 (24.6)	71 (23.4)	193 (24.1)		
No results (no sample)	0 (0.0)	18 (5.9)	18 (2.3)		
**Note: not included in Chi-square analysis*					
Attendance at 1st follow-up					
N = 707					
Attended	325 (72.4)	228 (88.4)	553 (78.2)	24.59	< 0.001
Did not attend	124 (27.6)	30 (11.6)	154 (21.8)	(1)	
Attendance at any follow-up					
N = 707					
Attended at least one	414 (92.2)	244 (94.6)	658 (93.1)	1.43 (1)	0.233
Did not attend any	35 (7.8)	14 (5.4)	49 (6.9)		
Overall attendance at follow-ups					
N = 707					
Never returned	35 (7.8)	14 (5.4)	49 (6.9)	27.15	< 0.001
Returned at 1st	325 (72.4)	228 (88.4)	553 (78.2)	(2)	
Returned later	89 (19.8)	16 (6.2)	105 (14.9)		
Clinical characteristics (cont.)				**t (d.f.)**	**p-value**
No. of living children					
Mean	1.77	1.57	1.69	1.98	0.048
S.D.	1.39	1.34	1.38	(796)	
Median	2.00	2.00	2.00		
Range	0 – 9	0 – 6	0 – 9		
No. of relatives with cancer					
Mean	4.68	4.06	4.44	2.58	0.010
S.D.	3.40	3.07	3.29	(792)	
Median	4.00	4.00	4.00		
Range	0 – 19	0 – 24	0 – 24		

Referral to initial visit (days)					
N = 705					
Mean	64.17	77.61	69.32	-2.56	0.011
S.D.	66.49	69.79	68.04	(703)	
Median	48.00	61.50	54.00		
Range	0 – 683	1 – 517	0 – 683		
Initial visit to sample collection (days)					
N = 686					
Mean	5.28	26.02	12.65	-8.51	< 0.001
S.D.	29.80	31.93	32.13	(684)	
Median	0.00	16.00	0.00		
Range	0 – 287	0 – 226	0 – 287		
Sample collection to report date (days)					
N = 680					
Mean	21.46	26.37	23.22	-1.14	0.253
S.D.	35.86	75.84	53.74	(678)	
Median	15.00	13.50	15.00		
Range	5 – 432	5 – 761	5 – 761		
Initial visit to report date (days)					
N = 701					
Mean	26.89	51.66	35.99	-5.14	< 0.001
S.D.	46.59	80.46	62.35	(692)	
Median	16.00	33.00	20.00		
Range	5 – 432	8 – 771	5 – 771		
Initial visit to 1st follow-up (days)					
N = 707					
Mean	59.63	65.17	61.65	-1.14	0.256
S.D.	70.59	44.65	62.41	(705)	
Median	42.00	56.00	43.00		
Range	7 – 735	3 – 367	3 – 735		

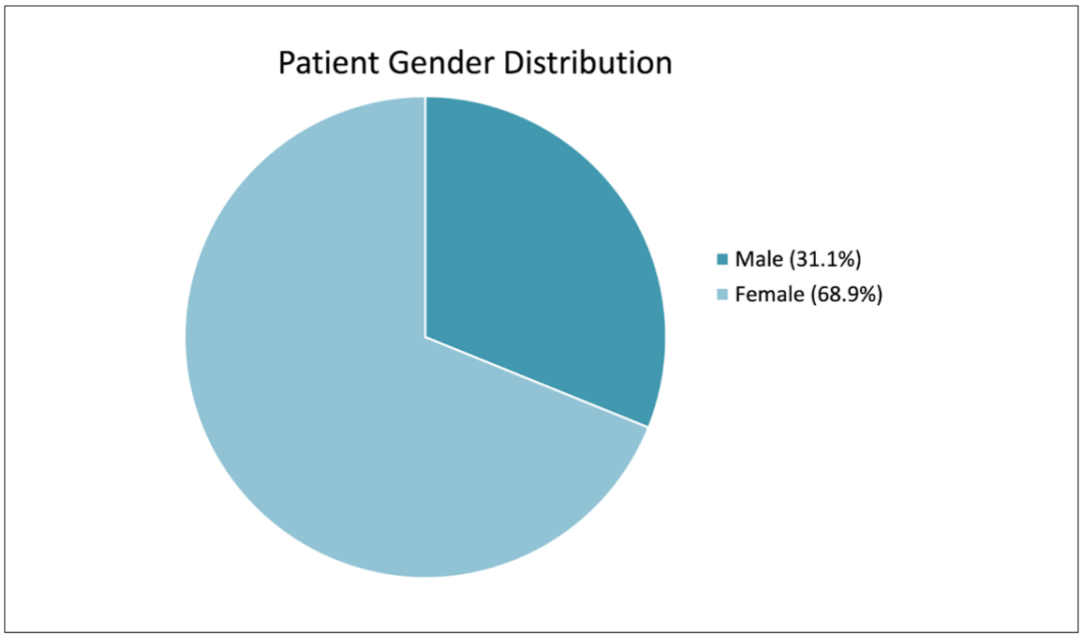

Figure 1: Distribution of patient gender. N = 800 adult patients scheduled for cancer genetic counseling. Females comprised 68.9% of the study population while males comprised 31.1%.

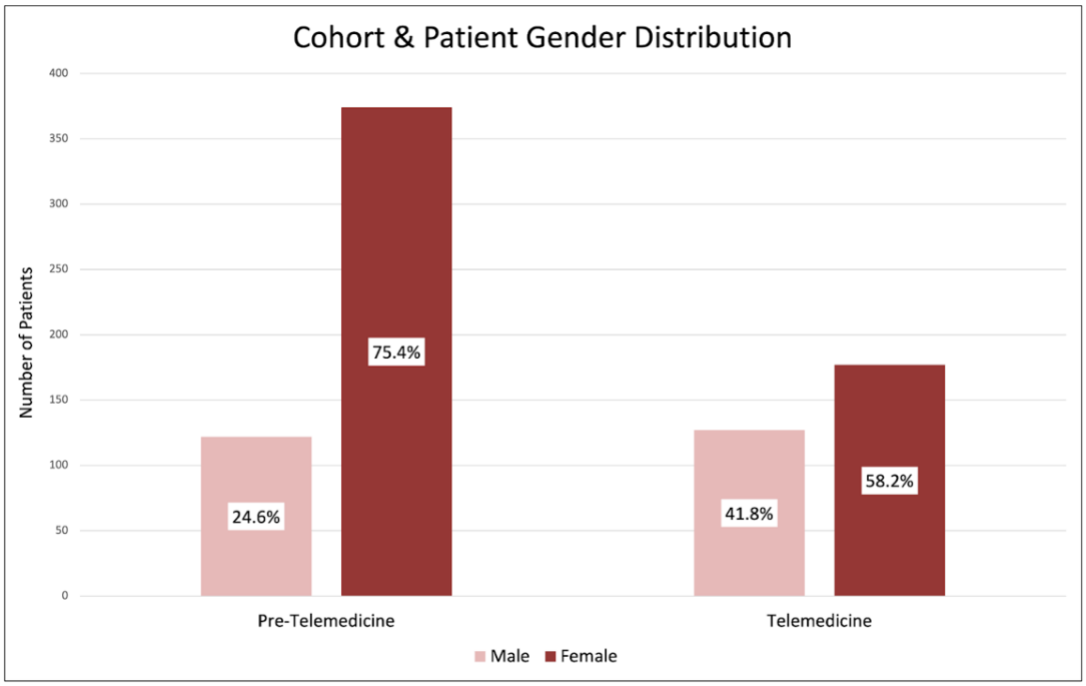

Figure 2: Distribution of patient gender between cohorts. N = 800 adult patients scheduled for cancer genetic counseling compared between the pre-telemedicine (N=496) and telemedicine (N=304) cohorts. There were significantly more males in the telemedicine cohort ($p < 0.001$)

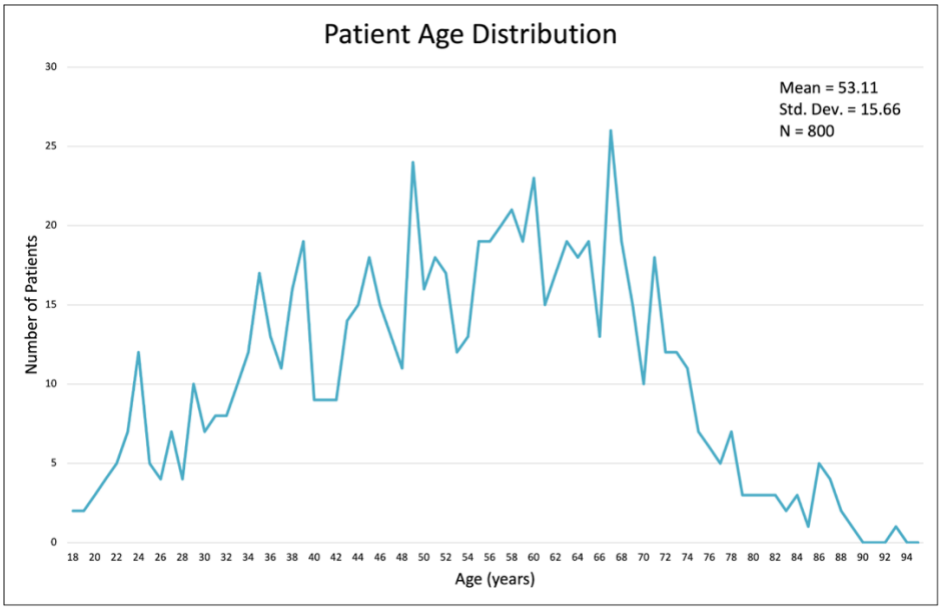

Figure 3: Distribution of patient age. N = 800 adult patients scheduled for cancer genetic counseling. The mean age of the 800 patients who attended an initial consultation is 53.11 years old.

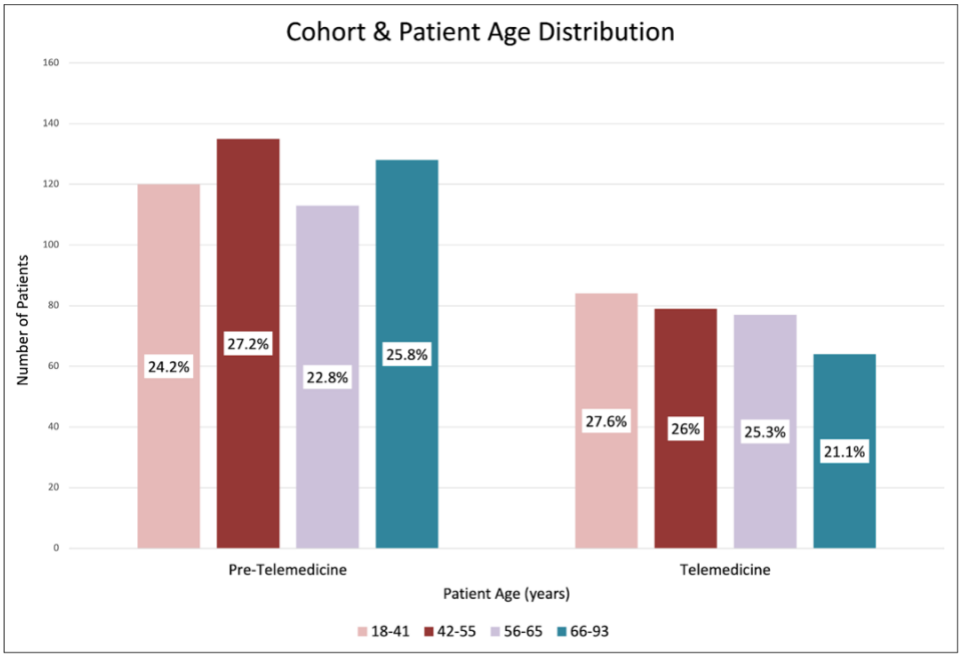

Figure 4: Distribution of patient age between cohorts. N = 800 adult patients scheduled for cancer genetic counseling compared between the pre-telemedicine (N=496) and telemedicine (N=304) cohorts. Age is categorized by quartile: 18-41, 42-55, 56-65, and 66-93. There was no significant association between cohort and quartile ages (p = 0.352).

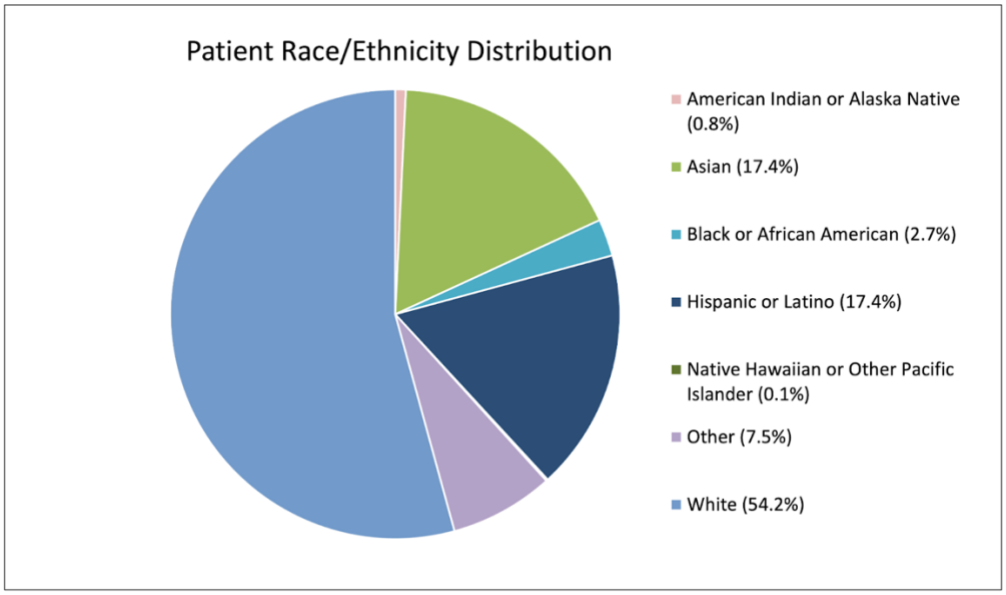

Figure 5: Distribution of patient race/ethnicity. N = 789 adult patients scheduled for cancer genetic counseling whose race/ethnicity was documented in the medical record. 11 records did not include information on the patient's race/ethnicity. Race/ethnicity was categorized per the NIH "Racial and Ethnic Categories and Definitions for NIH Diversity Programs and for Other Reporting Purposes" (NIH, 2015).

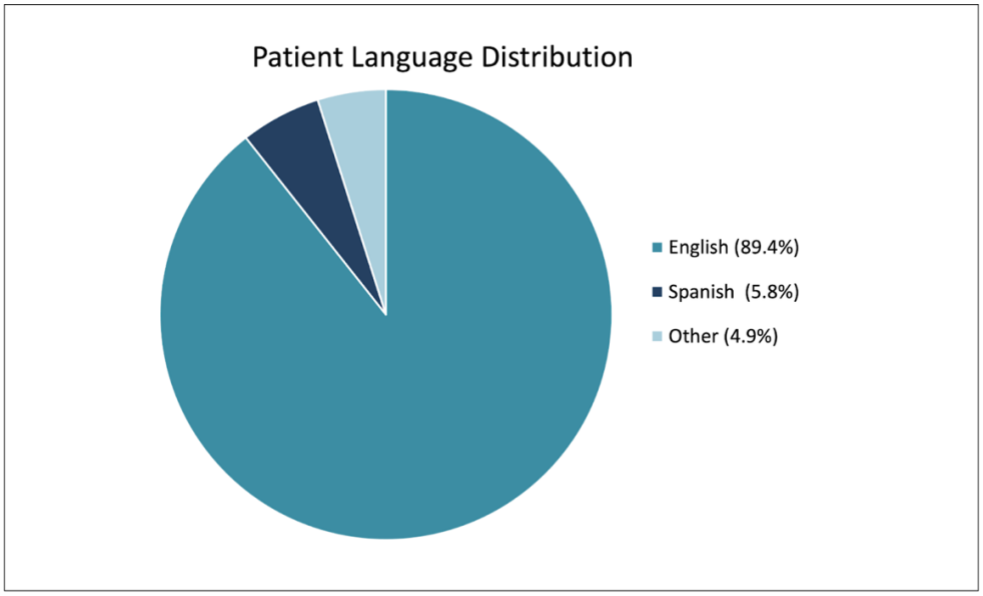

Figure 6: Distribution of patients' preferred language. N = 800 patients adult patients scheduled for cancer genetic counseling. "Other" indicates languages such as Vietnamese, Korean, Chinese, Mon-Khmer, Amharic, Farsi, Mandarin, Romanian, Russian, and Sign Language.

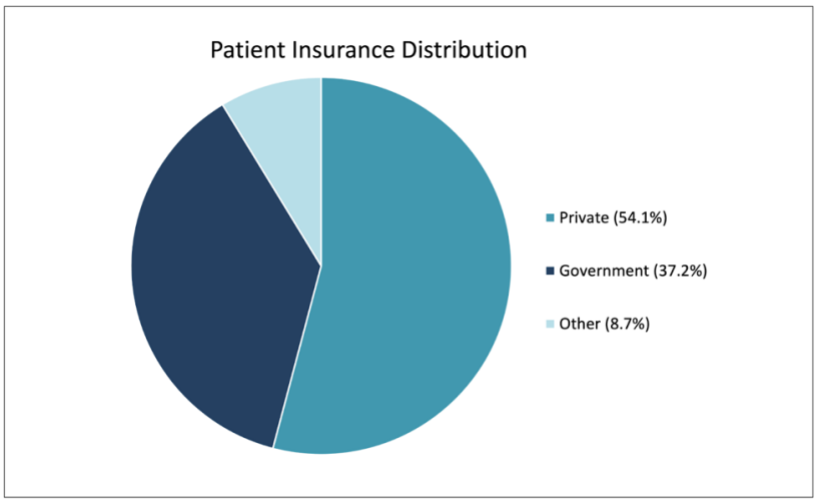

Figure 7: Distribution of patient insurance types. N = 784 adult patients scheduled for cancer genetic counseling. Insurance type was not documented for 16 patients in the medical record. Categories included private insurance (HMO, PPO, EPO, etc), government insurance (MediCal, Medicaid, TriCare), or "other" insurance, identifying payor/plans which did not fall cleanly into the private or government categories.

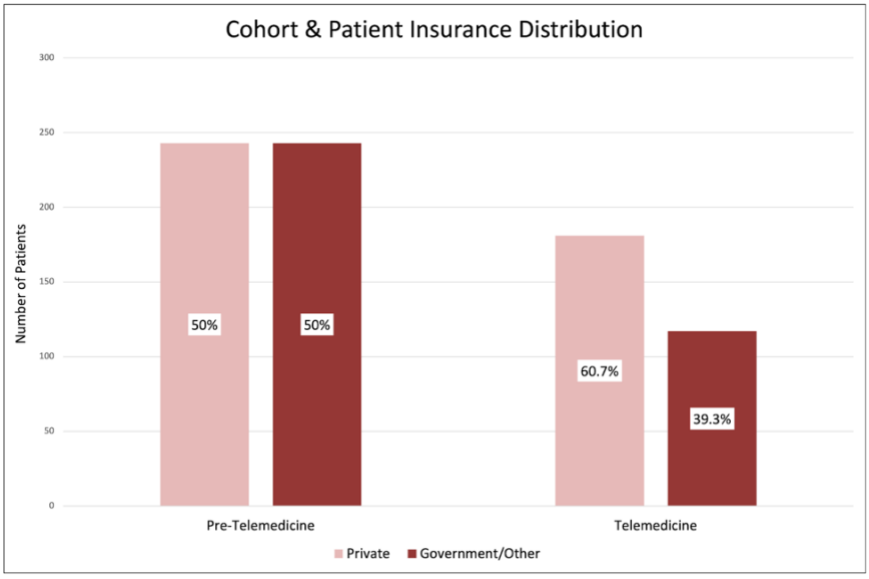

Figure 8: Distribution of patient insurance types between cohorts. N = 784 adult patients scheduled for cancer genetic counseling compared between the pre-telemedicine (N=486) and telemedicine (N=298) cohorts. Insurance type was not documented for 16 patients in the medical record. Categories included private insurance (HMO/PPO/EPO) or government insurance (MediCal/Medicaid/TriCare). The "Other" category was combined with the government category. There was significantly less government/other insurance in the telemedicine cohort (p = 0.003)

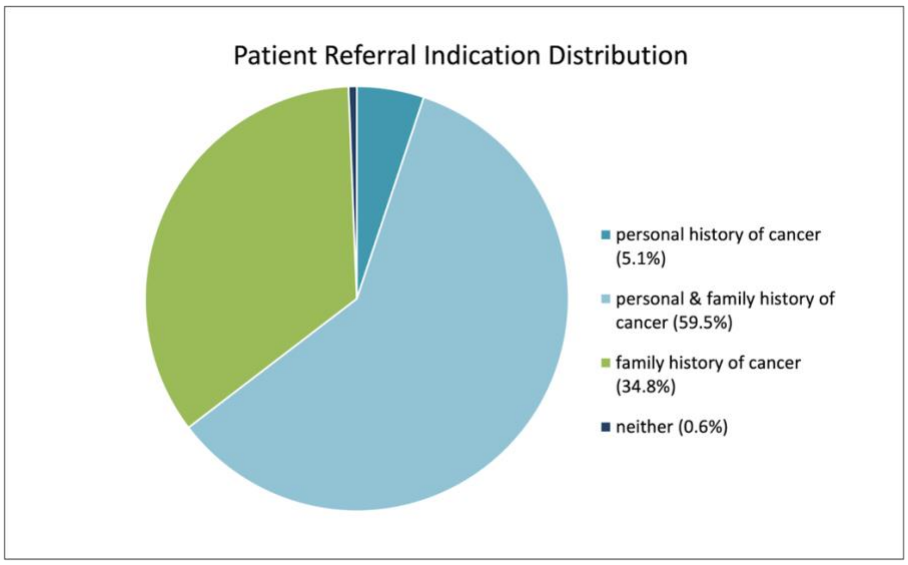

Figure 9: Distribution of patient primary referral indication. N = 800 adult patients scheduled for cancer genetic counseling. Most patients were referred due to their personal and family history of cancer (59.5%) or their family history of cancer (34.8%). Fewer patients were referred for just a personal history of cancer (5.1%) or neither a personal/family history of cancer (0.6%).

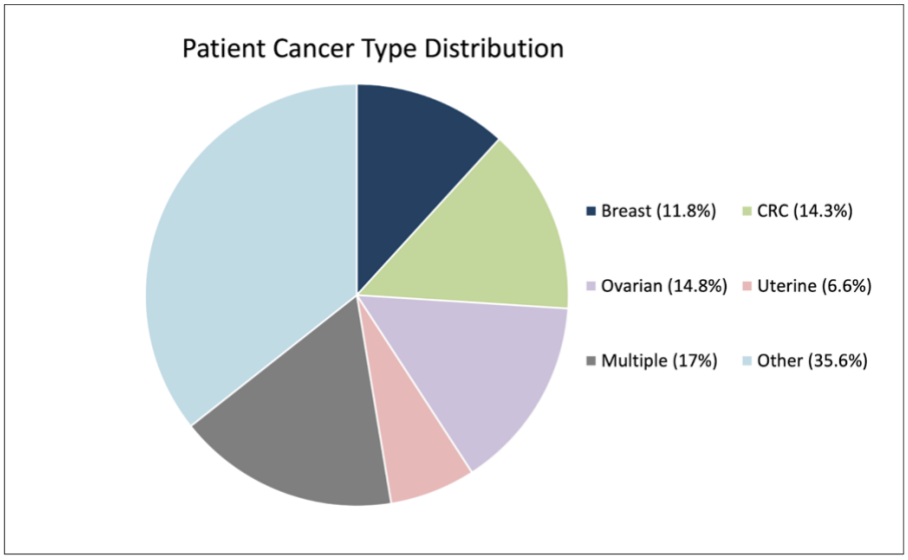

Figure 10: Distribution of patients' cancer types. N = 519 adult patients scheduled for cancer genetic counseling. Categories included breast, colorectal, ovarian, uterine, multiple, or other. "Multiple" included patients with 2 or more different cancer types as reported in the medical record. "Other" refers to additional cancers such as prostate, melanoma, pancreatic, renal, brain, neuroendocrine, gastric, lung, appendiceal, hematologic, thyroid, testicular, bladder, ocular, and cervical. Appendix A can be referenced for a more detailed distribution of cancer types.

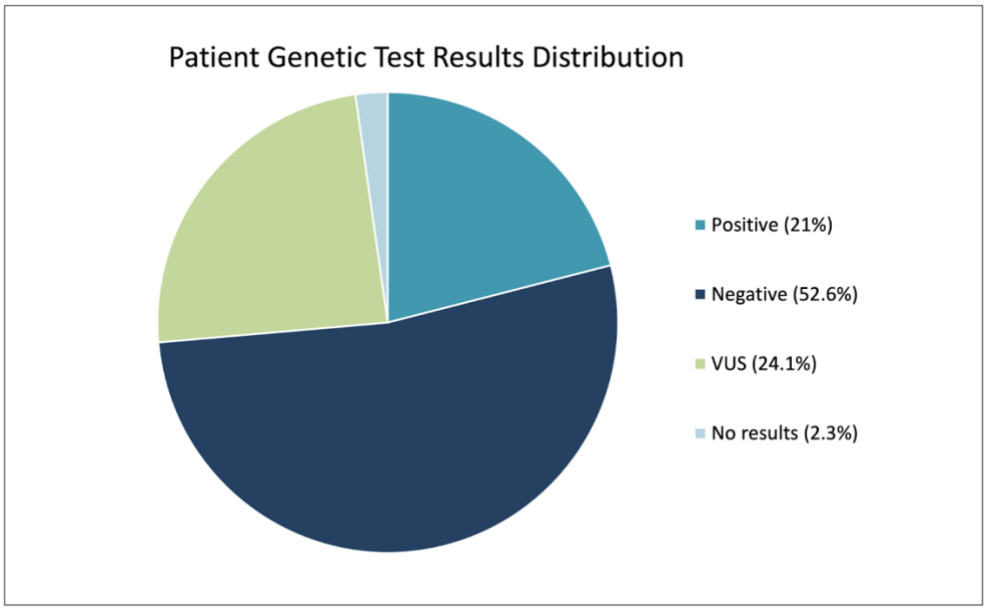

Figure 11: Distribution of patient genetic test results. N = 800 adult patients scheduled for cancer genetic counseling. "Positive" (21.8%) refers to patients who received a Pathogenic or Likely Pathogenic mutation on their test report. "No results" (2.3%) refers to those who did not submit a sample for genetic testing or whose testing was canceled (either due to patient preference or sample failure).

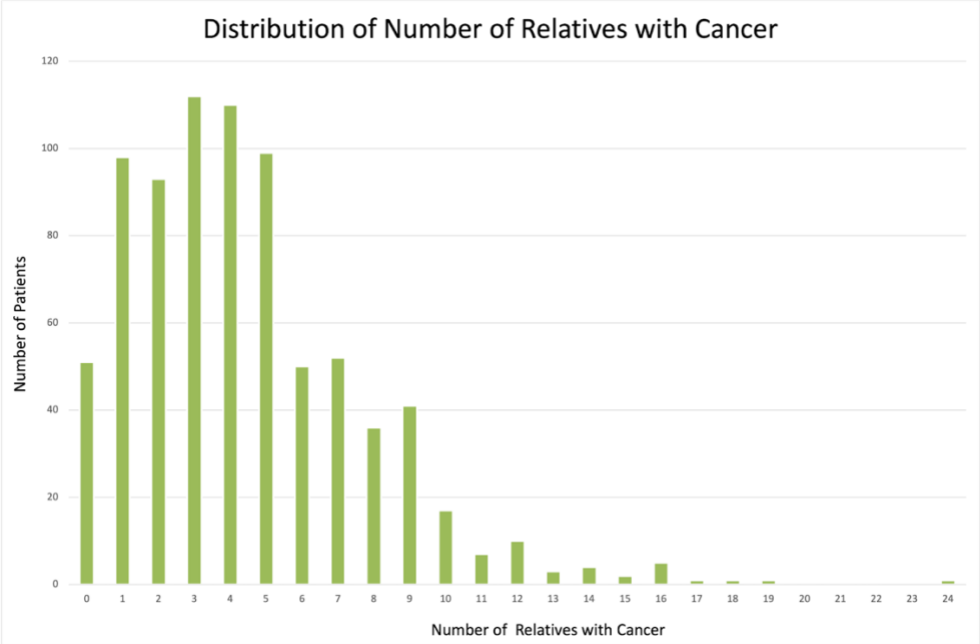

Figure 12: Distribution of patients' number of relatives with cancer. N = 800 adult patients scheduled for cancer genetic counseling.

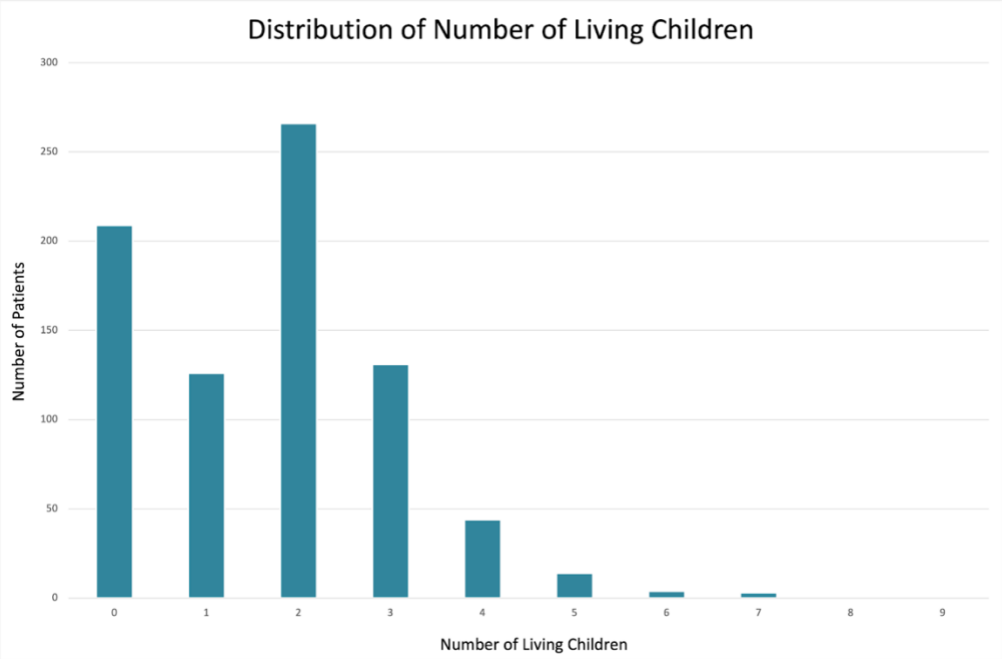

Figure 13: Distribution of patients' number of children. N = 800 adult patients scheduled for cancer genetic counseling.

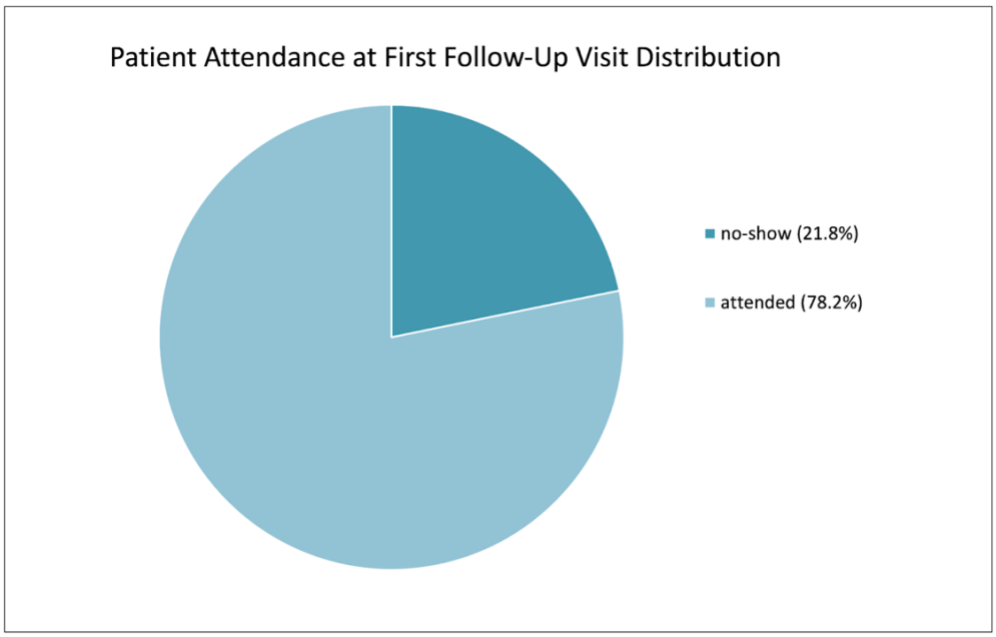

Figure 14: Distribution of patient attendance status at first follow-up visit. N = 707 adult patients scheduled for a follow-up cancer genetic counseling appointment.

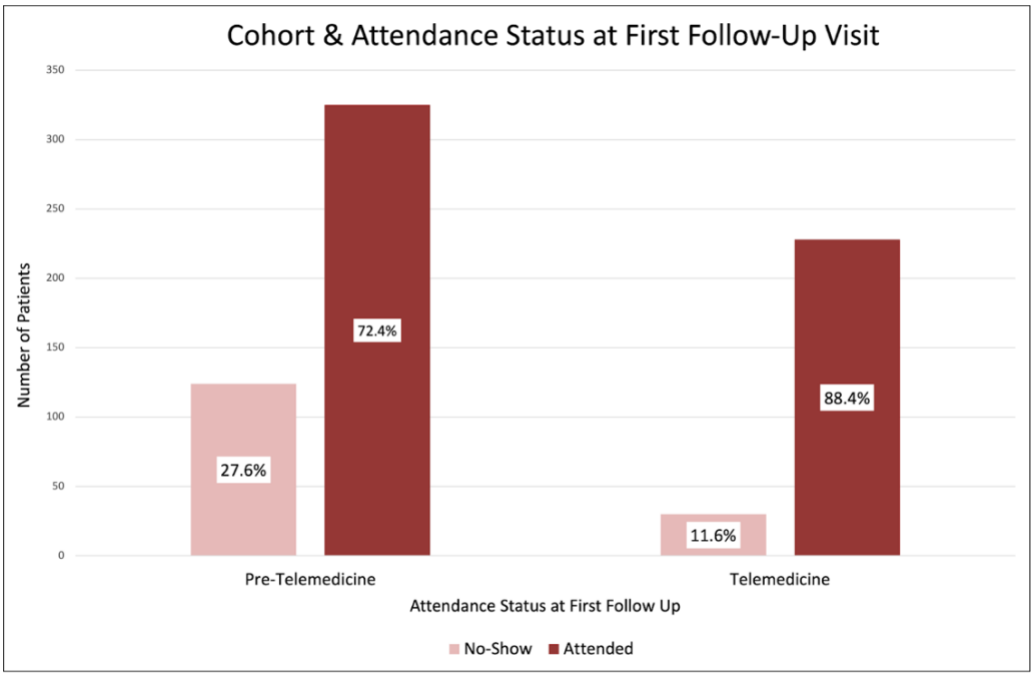

Figure 15: Distribution of patient attendance status at first follow-up visit between cohorts. N = 707 adult patients scheduled for a follow-up cancer genetic counseling appointment between the pre-telemedicine (N=449) and telemedicine (N=258) cohorts. Attendance at first follow-up visit significantly increased in the telemedicine cohort ($p < 0.001$).

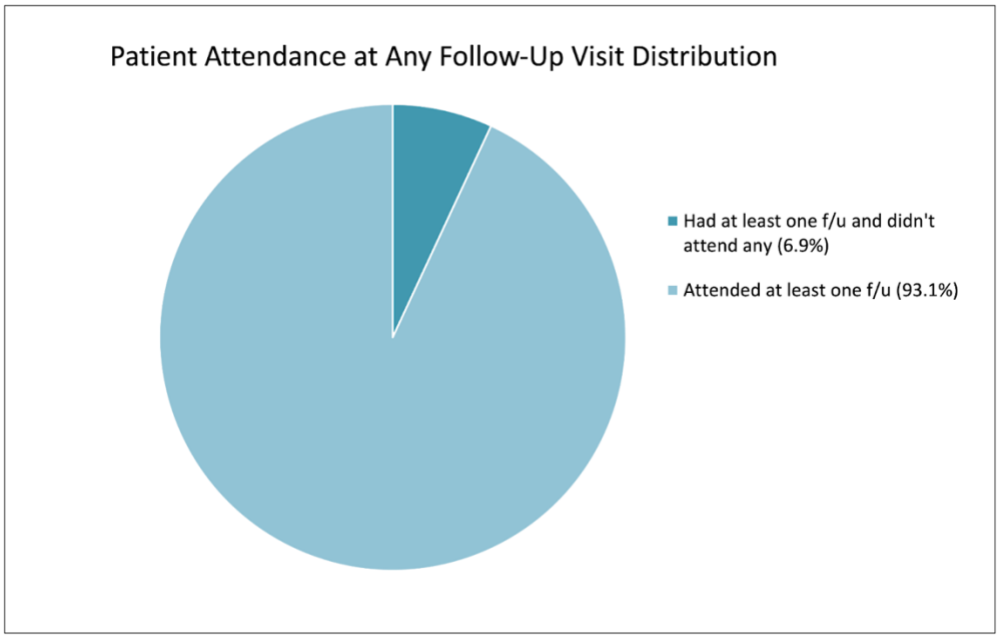

Figure 16: Distribution of patient attendance status at *any* follow-up visit. N = 707 adult patients scheduled for a follow-up cancer genetic counseling appointment.

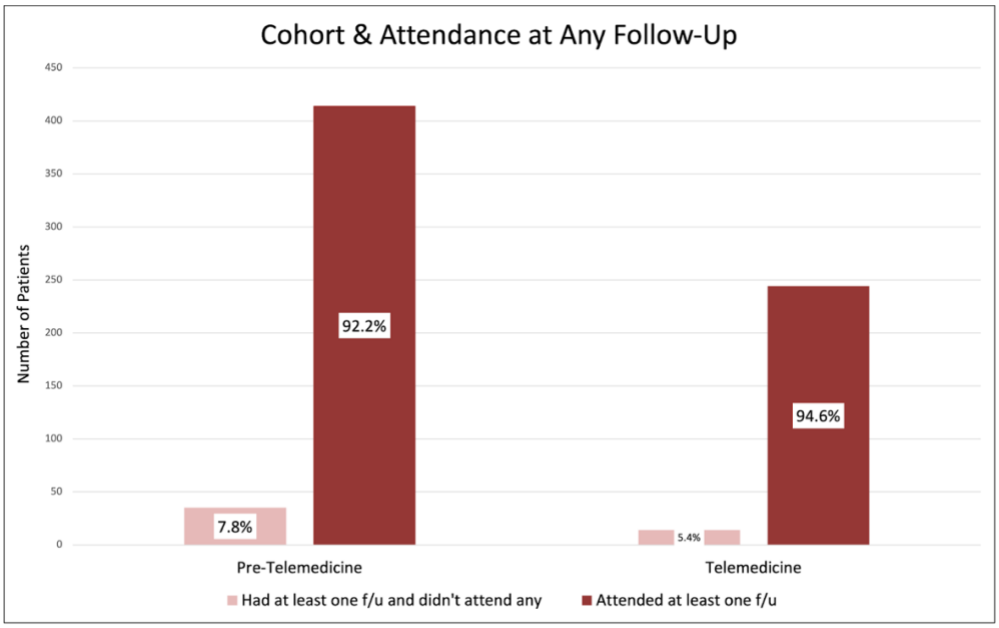

Figure 17: Distribution of patient attendance status at *any* follow-up visit between cohorts. N = 707 adult patients scheduled for a follow-up cancer genetic counseling appointment between the pre-telemedicine (N=449) and telemedicine (N=258) cohorts. Attendance at *any* follow-up visit increased in the telemedicine cohort, however, this increase was not statistically significant (p = 0.233).

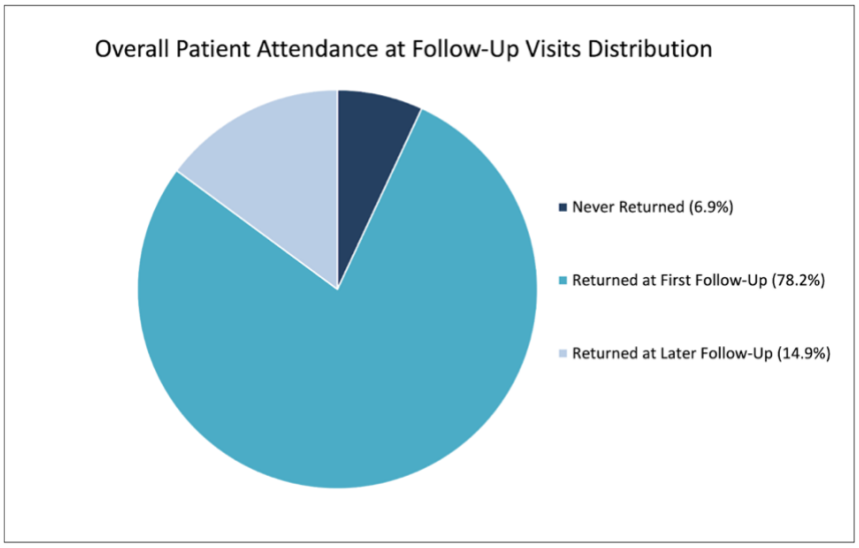

Figure 18: Distribution of *overall* patient attendance status at follow-up visits. N = 707 adult patients scheduled for cancer genetic counseling.

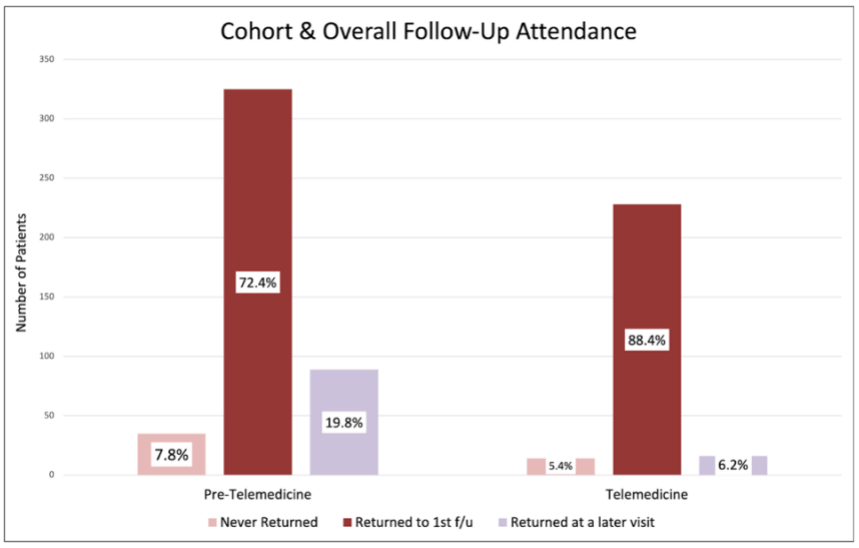

Figure 19: Distribution of *overall* patient attendance status at follow-up visits between cohorts. N = 707 adult patients scheduled for a follow-up cancer genetic counseling appointment between the pre-telemedicine (N=449) and telemedicine (N=258) cohorts. Patients who never returned to follow-up decreased in the telemedicine cohort, patients who returned at first follow-up increased in the telemedicine cohort, and patients who did not return at first follow-up but did return at a later visit decreased in the telemedicine cohort ($p < 0.001$). It is important to note that patients in the "Never Returned" for follow-up category may be censored for those who had their first visit at the latter end of the study time frame, and thus their attendance at follow-up was not accurately captured.

3.2 Univariate analysis of factors hypothesized to predict patient attendance at follow-up

3.2.1. First follow-up visit

To explore the impact of telemedicine on attendance rate and identify relationships between demographic/clinical characteristics and patient attendance in the cancer genetic counseling clinic, patients who successfully attended their first scheduled follow-up visit and patients who missed their first scheduled follow-up visit were statistically compared (Table 3 – 4). The same comparisons were employed for patients who attended at least one follow-up visit and those who had at least one follow-up visit scheduled but did not attend any (Table 5 – 6). Chi-square tests were utilized for statistical analysis.

Of the 800 patients seen for an initial new patient visit, 707 were scheduled for a subsequent follow-up visit. 553/707 patients successfully attended their first scheduled follow-up visit, for a follow-up attendance rate of 78.2%, while 154/707 patients missed their first scheduled follow-up visit, for a follow-up no-show rate of 21.8%. Regarding attendance for any follow-up visit, 658/707 patients attended at least one of their scheduled follow-up visits, for an overall follow-up attendance rate of 93.1%. Only 49/707 patients had at least one scheduled follow-up visit but didn't attend any (6.9%).

For attendance at first follow-up visit and attendance at any follow-up visit, demographic comparisons, including cohort, patient gender, age, race/ethnicity, and language, were statistically analyzed. Patient age was divided into four categories by quartiles (18-41, 42-55, 56-65, 66-93) and included as a dichotomous variable, categorized as less than 65 years old vs 65 years or older at the time of initial visit. Race and ethnicity categories were combined into four main categories due to small sample sizes: White, Hispanic or Latino, Asian, and Other. Clinical

comparisons included the place of service, insurance type, insurance authorization, referral indication, personal history of cancer, cancer type, cancer category, referral source, previous germline or somatic genetic testing, a previous known genetic mutation in the patient or their relative, sample type and time of collection, genetic testing laboratory, genetic test type, genetic test results, number of living children, parent status, number of relatives with cancer, and lead times. Lead times included the number of days from the referral date to the new patient appointment date, new patient appointment date to sample collection date, new patient appointment date to the results report date, and new patient appointment date to first follow-up visit date. Number of living children, number of relatives with cancer, and lead times were grouped by quartiles or based on group sizes.

For attendance at first follow-up visit (Tables 3 and 4), significant associations appeared between attendance status and cohort ($p < 0.001$), patient age (categorized as less than 65 years old vs 65 years or older at the time of initial visit, $p = 0.019$), place of service ($p = 0.002$), insurance type ($p = 0.023$), personal history of cancer ($p = 0.049$), previous germline testing ($p = 0.005$), previous known germline mutation ($p < 0.001$), sample type ($p < 0.001$), day of sample collection ($p = 0.002$), number of days to sample collection ($p < 0.001$), and number of days from the initial visit to the date results reported ($p = 0.050$). Race/ethnicity was further grouped into three categories due to small sample sizes (White, Asian, Other), and this grouping was significant ($p = 0.041$, see Appendix). Trends were identified between attendance status and age in quartiles and genetic testing laboratory; however, these associations did not meet statistical significance ($p = 0.055$ and 0.051 respectively).

Table 3: Comparisons of demographic characteristics between patients who attended their first follow-up visit and those who did not.

	Attendance at 1st Follow-Up Visit		**Statistical Analysis**	
	Attended N = 553	**No-Show N = 154**		
Demographic Comparisons ***N = 707 unless otherwise specified***	**N (%)**	**N (%)**	**$\chi 2$ (d.f.)**	**p-value**
Cohort				
Cohort 1 (pre-telemedicine)	325 (72.4)	124 (27.6)	24.59 (1)	< 0.001
Cohort 2 (telemedicine)	228 (88.4)	30 (11.6)		
Gender				
Female	383 (77.7)	110 (22.3)	0.27 (1)	0.604
Male	170 (79.4)	44 (20.6)		
Age (years)				
Q1: 18 – 41	152 (83.5)	30 (16.5)	7.61 (3)	0.055
Q2: 42 – 55	146 (77.2)	43 (22.8)		
Q3: 56 – 65	133 (80.1)	33 (19.9)		Test of linear association: $\chi 2$ (1) = 5.39, p = 0.02
Q4: 66 – 93	122 (71.8)	48 (28.2)		
65 Cutoff				
≤ 65 years old	431 (80.3)	106 (19.7)	5.47 (1)	0.019
> 65 years old	122 (71.8)	48 (28.2)		
Race/Ethnicity				
N = 698				
White	299 (78.1)	84 (21.9)	6.77 (3)	0.080
Hispanic or Latino	87 (75.7)	28 (24.3)		
Asian	105 (86.1)	17 (13.9)		
Other	56 (71.8)	22 (28.2)		
Race/Ethnicity				
N = 698				
White	299 (78.1)	84 (21.9)	6.37 (2)	0.041
Asian	105 (86.1)	17 (13.9)		
Other	143 (74.1)	50 (25.9)		

Language				
English	496 (78.7)	134 (21.3)	4.33 (2)	0.115
Spanish	27 (65.9)	14 (34.1)		
Other	30 (83.3)	6 (16.7)		

Table 4: Comparisons of clinical characteristics between patients who attended their first follow-up visit and those who did not.

	Attendance at 1st Follow-Up Visit		**Statistical Analysis**	
	Attended N = 553	**No-Show N = 154**		
Clinical Comparisons ***N = 707 unless otherwise specified***	**N (%)**	**N (%)**	**χ2 (d.f.)**	**p-value**
Place of Service				
CCC (Orange, CA)	258 (73.3)	94 (26.7)	9.97 (1)	0.002
CDDC (Costa Mesa, CA)	295 (83.1)	60 (16.9)		
Insurance				
Private	310 (82.0)	68 (18.0)	7.56 (2)	0.023
Government	189 (73.8)	69 (26.2)		
Other/Unknown	43 (71.7)	17 (28.3)		
Insurance Authorization				
Authorization required	180 (74.7)	61 (25.3)	2.78 (2)	0.249
No authorization required	322 (80.3)	79 (19.7)		
Unknown	51 (78.5)	14 (21.5)		
Referral Indication *N = 703*				
Personal history of cancer	21 (72.4)	8 (27.6)	4.20 (2)	0.122
Family history of cancer	210 (82.4)	45 (17.6)		
Both	319 (76.1)	100 (23.9)		
Personal History of Cancer				
Yes	340 (75.9)	108 (24.1)	3.88 (1)	0.049
No	213 (82.2)	46 (17.8)		

Cancer Type (top 5) *N = 450* Breast CRC Ovarian Uterine Multiple Other	 29 (67.4) 55 (78.6) 55 (78.6) 27 (81.8) 60 (75.9) 117 (75.5)	 14 (32.6) 15 (21.4) 15 (21.4) 6 (18.2) 19 (24.1) 38 (24.5)	 2.87 (5)	 0.719
Cancer Category *N = 450* Female Cancer Male Cancer GI Cancer Multiple Other	 127 (76.5) 21 (77.8) 76 (74.5) 35 (72.9) 84 (78.5)	 39 (23.5) 6 (22.2) 26 (25.5) 13 (27.1) 23 (21.5)	 0.81 (4)	 0.938
Referral Source Provider Self	 475 (77.9) 78 (80.4)	 135 (22.1) 19 (19.6)	 0.32 (1)	 0.573
Prior Germline Genetic Testing Yes No	 32 (62.7) 521 (79.4)	 19 (37.3) 135 (20.6)	 7.72 (1)	 0.005
Prior Somatic Genetic Testing Yes No	 16 (69.6) 537 (78.5)	 7 (30.4) 147 (21.5)	 1.05 (1)	 0.307
Prior Germline Mutation (Patient) Yes No	 11 (44.0) 542 (79.5)	 14 (56.0) 140 (20.5)	 17.81 (1)	 < 0.001
Prior Germline Mutation (Relative) Yes No	 79 (82.3) 474 (77.6)	 17 (17.7) 137 (22.4)	 1.08 (1)	 0.298
Sample Type *N = 673* Blood Saliva	 280 (74.3) 258 (87.2)	 97 (25.7) 38 (12.8)	 17.19 (1)	 < 0.001

Sample Collection Same day Not same day	 298 (73.9) 255 (83.9)	 105 (26.1) 49 (16.1)	 10.04 (1)	 0.002
Genetic Testing Laboratory Lab A Lab B Lab C Other	 418 (78.1) 88 (83.8) 38 (74.5) 8 (53.3)	 117 (21.9) 17 (16.2) 13 (25.5) 7 (46.7)	 7.78 (3)	 0.051
Genetic Test Type *N = 703* Panel Single Site	 516 (77.7) 33 (84.6)	 148 (22.3) 6 (15.4)	 1.03 (1)	 0.311
Genetic Testing Results Positive Negative VUS	 108 (78.3) 314 (78.5) 131 (78.9)	 30 (21.7) 86 (21.5) 35 (21.1)	 0.02 (2)	 0.990
Number of Living Children *N = 706* 0 1 2 3 or more	 142 (78.0) 86 (77.5) 191 (80.6) 134 (76.1)	 40 (22.0) 25 (22.5) 46 (19.4) 42 (23.9)	 1.27 (3)	 0.736 Test of linear association: $\chi2$ (1) = 0.02, p = 0.884
Parent Status No children Has children	 142 (78.0) 411 (78.3)	 40 (22.0) 114 (21.7)	 0.01 (1)	 0.941
Number of Relatives with Cancer *N = 702* Q1: 0 – 2 Q2: 3 – 4 Q3: 5 – 6 Q4: ≥ 7	 160 (76.6) 152 (76.4) 108 (81.8) 131 (80.9)	 49 (23.4) 47 (23.6) 24 (18.2) 31 (19.1)	 2.39 (3)	 0.495 Test of linear association: $\chi2$ (1) = 1.71, p = 0.192

Referral to initial visit (days) *N = 618* Q1: 0 – 30 Q2: 31 – 53 Q3: 54 – 91 Q4: ≥ 92	 124 (79.5) 120 (76.9) 121 (78.1) 115 (76.2)	 32 (20.5) 36 (23.1) 34 (21.9) 36 (23.8)	.56 (3)	0.906 Test of linear association: $\chi2$ (1) = 0.35, p = 0.557
Initial visit to sample collection (days) *N = 668* 0 1 – 14 15+	 298 (73.9) 99 (92.5) 135 (85.4)	 105 (26.1) 8 (7.5) 23 (14.6)	22.29 (2)	< 0.001 Test of linear association: $\chi2$ (1) = 13.5, p = < 0.001
Sample collection to report (days) *N = 663* Q1: 5 – 11 Q2: 12 – 15 Q3: 16 – 21 Q4: ≥ 22	 153 (81.0) 147 (80.8) 118 (77.1) 110 (79.1)	 36 (19.0) 35 (19.2) 35 (22.9) 29 (20.9)	0.96 (3)	0.810 Test of linear association: $\chi2$ (1) = 0.45, p = 0.501
Initial visit to report date (days) *N = 675* Q1: 5 – 14 Q2: 15 – 21 Q3: 22 – 35 Q4: ≥ 36	 144 (75.0) 131 (78.0) 131 (86.8) 133 (81.1)	 48 (25.0) 37 (22.0) 20 (13.2) 31 (18.9)	7.81 (3)	0.050 Test of linear association: $\chi2$ (1) = 4.02, p = 0.045
Initial visit to 1st follow-up (days) *N = 707* Q1: 3 – 35 Q2: 36 – 43 Q3: 44 – 63 Q4: ≥ 64	 173 (77.6) 102 (77.9) 147 (81.2) 131 (76.2)	 50 (22.4) 29 (22.1) 34 (18.8) 41 (23.8)	1.44 (3)	0.695 Test of linear association: $\chi2$ (1) = 0.00, p = 0.986

3.2.2. Any follow-up visit

The same demographic and clinical characteristics compared for first follow-up visit were then compared between patients who attended at least one of their scheduled follow-up visits (658/707 or 93.1%) and those who never attended their scheduled follow-up visits (49/707 or 6.9%).

Although attendance at any follow-up did increase in the telemedicine cohort, this difference was not statistically significant ($p = 0.233$). This is likely due to loss of power, as the sample size for no-show is increasingly small, with only 49/707 patients who missed their appointment. Significant associations were identified (Tables 5 and 6) between attendance status and referral indication ($p = 0.010$), previous germline genetic testing ($p < 0.001$), previous known germline genetic mutation in patient ($p < 0.001$), genetic testing laboratory ($p < 0.001$), genetic test results ($p < 0.001$), and number of days from initial new patient consultation to first scheduled follow-up visit ($p = 0.032$).

Table 5: Comparisons of demographic characteristics between patients who attended any follow-up visit and those who did not.

	Attendance at Any Follow-Up Visit		**Statistical Analysis**	
	Attended N = 658	**No-Show N = 49**		
Demographic Comparisons *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**$\chi 2$ (d.f.)**	**p-value**
Cohort				
Cohort 1 (pre-telemedicine)	414 (92.2)	35 (7.8)	1.43 (1)	0.233
Cohort 2 (telemedicine)	244 (94.6)	14 (5.4)		
Gender				
Male	201 (93.9)	13 (6.1)	0.35 (1)	0.555
Female	457 (92.7)	36 (7.3)		
Age (years)				
Q1: 18 – 41	174 (95.6)	8 (4.4)	3.82 (3)	0.281
Q2: 42 – 55	175 (92.6)	14 (7.4)		
Q3: 56 – 65	150 (90.4)	16 (9.6)		Test of linear association: $\chi 2$ (1) = 1.00, p = 0.317
Q4: 66 – 93	159 (93.5)	11 (6.5)		
65 Cutoff				
65 and younger	499 (92.9)	38 (7.1)	0.07 (1)	0.786
Over 65	159 (93.5)	11 (6.5)		
Race/Ethnicity *N = 698*				
White	357 (93.2)	26 (6.8)	2.63 (3)	0.452
Hispanic or Latino	109 (94.8)	6 (5.2)		
Asian	116 (95.1)	6 (4.9)		
Other	70 (89.7)	8 (10.3)		
Language				
English	588 (93.3)	42 (6.7)	0.69 (2)	0.710
Spanish	37 (90.2)	4 (9.8)		
Other	33 (91.7)	3 (8.3)		

Table 6: Comparisons of clinical characteristics between patients who attended any follow-up visit and those who did not.

	Attendance at Any Follow-Up Visit		**Statistical Analysis**	
	Attended N = 658	**No-Show N = 49**		
Clinical Comparisons *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**$\chi 2$ (d.f.)**	**p-value**
Place of Service				
CCC (Orange, CA)	323 (91.8)	29 (8.2)	1.86 (1)	0.173
CDDC (Costa Mesa, CA)	335 (94.4)	20 (5.6)		
Insurance *N = 694*				
Private	356 (94.2)	22 (5.8)	4.31 (2)	0.116
Government	232 (90.6)	24 (9.4)		
Other/Unknown	58 (96.7)	2 (3.3)		
Insurance Authorization				
Authorization required	223 (92.5)	18 (7.5)	0.94 (2)	0.624
No authorization required	376 (93.8)	25 (6.2)		
Unknown	59 (90.8)	6 (9.2)		
Referral Indication				
Personal history of cancer	23 (79.3)	6 (20.7)	9.28 (2)	0.010
Family history of cancer	241 (94.5)	14 (5.5)		
Both	390 (93.1)	29 (6.9)		
Personal History of Cancer				
Yes	413 (92.2)	35 (7.8)	1.47 (1)	0.225
No	245 (94.6)	14 (5.4)		
Cancer Type (top 5) *N = 450*				
Breast	37 (86.0)	6 (14.0)	5.25 (5)	0.387
CRC	66 (94.3)	4 (5.7)		
Ovarian	67 (95.7)	3 (4.3)		
Uterine	32 (97.0)	1 (3.0)		
Multiple	72 (91.1)	7 (8.9)		
Other	142 (91.6)	13 (8.4)		

Cancer Category *N = 450* Female Cancer Male Cancer GI Cancer Multiple Other	 154 (92.8) 24 (88.9) 92 (90.2) 43 (89.6) 103 (96.3)	 12 (7.2) 3 (11.1) 10 (9.8) 5 (10.4) 4 (3.7)	4.05 (4)	0.400
Referral Source Provider Self	 565 (92.6) 93 (95.9)	 45 (7.4) 4 (4.1)	1.37 (1)	0.241
Prior Germline Genetic Testing Yes No	 37 (72.5) 621 (94.7)	 14 (27.5) 35 (5.3)	35.88 (1)	< 0.001
Prior Somatic Genetic Testing Yes No	 20 (87.0) 638 (93.3)	 3 (13.0) 46 (6.7)	1.38 (1)	0.241
Prior Germline Mutation (Patient) Yes No	 14 (56.0) 644 (94.4)	 11 (44.0) 38 (5.6)	55.21 (1)	< 0.001
Prior Germline Mutation (Relative) Yes No	 90 (93.8) 568 (93.0)	 6 (6.3) 43 (7.0)	0.08 (1)	0.778
Sample Type *N = 673* Blood Saliva	 355 (94.2) 283 (95.6)	 22 (5.8) 13 (4.4)	0.701 (1)	0.402
Genetic Testing Laboratory *N = 706* Lab A Lab B Lab C Other	 504 (94.2) 98 (93.3) 47 (92.2) 8 (53.3)	 31 (5.8) 7 (6.7) 4 (7.8) 7 (46.7)		< 0.001*
Genetic Test Type Panel Single Site	 616 (92.8) 38 (97.4)	 48 (7.2) 1 (2.6)	1.24 (1)	0.266

Genetic Testing Results Positive Negative VUS	 120 (87.0) 381 (95.3) 157 (94.6)	 18 (13.0) 19 (4.8) 9 (5.4)	 11.99 (2)	 0.002
Number of Living Children *N = 706* 0 1 2 *3* or more	 172 (94.5) 103 (92.8) 221 (93.2) 162 (92.0)	 10 (5.5) 8 (7.2) 16 (6.8) 14 (8.0)	 0.89 (3)	 0.828 Test of linear association: $\chi 2$ (1) = 0.71, p = 0.399
Parent Status No children Has children	 172 (94.5) 486 (92.6)	 10 (5.5) 39 (7.4)	 0.78 (1)	 0.376
Number of Relatives with Cancer *N = 702* Q1: 0 – 2 Q2: 3 – 4 Q3: 5 – 6 Q4: ≥ 7	 194 (92.8) 184 (92.5) 125 (94.7) 152 (93.8)	 15 (7.2) 15 (7.5) 9 (5.3) 10 (6.2)	 0.78 (3)	 0.853 Test of linear association: $\chi 2$ (1) = 0.37, p = 0.546
Referral to initial visit (days) *N = 618* Q1: 0 – 30 Q2: 31 – 53 Q3: 54 – 91 Q4: ≥ 92	 147 (94.2) 145 (92.9) 143 (92.3) 140 (92.7)	 9 (5.8) 11 (7.1) 12 (7.7) 11 (7.3)	 0.52 (3)	 0.916 Test of linear association: $\chi 2$ (1) = 0.33, p = 0.565
Initial visit to sample collection (days) *N = 668* 0 1 –14 15+	 378 (93.8) 103 (96.3) 153 (96.8)	 25 (6.2) 4 (3.7) 5 (3.2)	 2.65 (2)	 0.266 Test of linear association: $\chi 2$ (1) = 2.49, p = 0.115

Sample Collection Same day Not same day	 378 (93.8) 280 (92.1)	 25 (6.2) 24 (7.9)	 0.77 (1)	 0.381
Sample collection to report date (days) *N = 663* Q1: 5 – 11 Q2: 12 – 15 Q3: 16 – 21 Q4: ≥ 22	 183 (96.8) 169 (92.9) 143 (93.5) 135 (97.1)	 6 (3.2) 13 (7.1) 10 (6.5) 4 (2.9)	 5.19 (3)	 0.159 Test of linear association: $\chi2$ (1) = 0.00, p = 0.994
Initial visit to report date (days) *N = 675* Q1: 5 – 14 Q2: 15 – 21 Q3: 22 – 35 Q4: ≥ 36	 182 (94.8) 155 (92.3) 147 (97.4) 157 (95.7)	 10 (5.2) 13 (7.7) 4 (2.6) 7 (4.3)	 4.58 (3)	 0.206 Test of linear association: $\chi2$ (1) = 0.99, p = 0.319
Initial visit to 1st follow-up (days) *N = 707* Q1: 3 – 35 Q2: 36 – 43 Q3: 44 – 63 Q4: ≥ 64	 209 (93.7) 123 (93.9) 174 (96.1) 152 (88.4)	 14 (6.3) 8 (6.1) 7 (3.9) 20 (11.6)	 8.80 (3)	 0.032 Test of linear association: $\chi2$ (1) = 2.34, p = 0.126

* p-value from Fisher's exact test

3.3 Multivariate analysis

3.3.1 Attendance at first follow-up visit

Using binary logistic regression, the demographic and clinical characteristics that were previously identified to be associated with attendance status in the univariate analysis were further analyzed to investigate which variables contributed independently to prediction of attendance status at first follow-up visit.

In the first binary logistic regression model for attendance at first follow-up visit, patients in the telemedicine cohort were 3.78 times more likely to attend their first follow-up visit than patients in the pre-telemedicine cohort (p=0.019, CI: 1.24, 11.49). Patients identifying as Asian were 2.51 times more likely to attend their first follow-up visit than White individuals. Patients with a family history of cancer were 1.08 times more likely to attend the first follow-up with every one additional relative affected with cancer (p=0.035, CI: 1.08, 1.01). Finally, with every 1-week increase between the patient's new patient appointment and their genetic test results report date, patients were 0.98 times less likely to attend their first follow up visit (p=0.034, CI: 0.99, 1.00. Note, this Odds Ratio was obtained by multiplying the coefficient for this variable by 7 and taking the exponent).

Variables that were non-significant and did not independently predict attendance at first follow-up visit included: insurance type, previous germline genetic testing, previously known germline mutation, sample type, sample collection, age (categorized as less than 65 years old vs 65 years or older at the time of initial visit), place of service, and personal history of cancer. Insurance type was removed from the multivariate model since it was not close to a significance level of 0.05. Due to increasingly small sample sizes, previous germline genetic testing and

previous known genetic mutation were also removed from the multivariate model. Furthermore, sample type and sample collection date were highly correlated with cohort (i.e., in the pre-telemedicine cohort, blood was collected on the same day as the patient's visit, however, after the switch to telemedicine, saliva kits were mailed to the patient for saliva sample collection and thus collected numerous days after the visit date) therefore these variables were also dropped from the multivariate model. Eliminating these variables from the model did not affect the fit of the model. Age, place of service, and personal history of cancer were kept in the model as these variables were close to significance.

Additionally, variables that were previously found to be significantly different between cohorts were also explored in the multivariate model (i.e., patient gender, referral indication, genetic testing laboratory, number of relatives with cancer, number of children, and days from referral to new patient visit). Although it was an interesting finding that the cohorts differed in genetic testing laboratory distribution, there was no reason that this variable in particular had an impact on attendance. Apart from number of relatives with cancer, the inclusion of these variables made no difference in the model coefficients and were themselves non-significant, therefore these variables were not included in the logistic regression model as they did not independently predict return for follow-up. Number of relatives with cancer was found to be a significant variable in the multivariate model and therefore was included for analysis.

Table 7: Binary logistic regression model of attendance status at **FIRST** follow-up visit

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort							
Pre-telemedicine *(reference)*							
Telemedicine	1.329	0.568	1	0.019	3.78	1.24	11.49
Age							
≤ 65 *(reference)*							
> 65	-0.297	0.273	1	0.277	0.74	0.44	1.27
Race/Ethnicity							
White *(reference)*			2	0.007			
Asian	0.918	0.347	1	0.008	2.51	1.27	4.95
Other	-0.239	0.232	1	0.302	0.79	0.50	1.24
Place of Service							
CCC (Orange, CA) *(reference)*							
CDDC (Costa Mesa, CA)	0.398	0.212	1	0.061	1.49	0.98	2.26
Insurance							
Private *(reference)*							
Government/Other	-0.011	0.247	1	0.966	0.99	0.61	1.61
Personal Cancer History							
Yes *(reference)*							
No	0.380	0.234	1	0.105	1.46	0.92	2.31
Previous Germline GT							
Yes *(reference)*							
No	-0.260	0.648	1	0.688	0.77	0.22	2.75
Previous Known Mutation							
Yes *(reference)*							
No	0.502	0.978	1	0.608	1.65	0.24	11.23
Sample Type							
Blood *(reference)*							
Saliva	-0.038	0.361	1	0.916	0.96	0.47	1.95
Sample Collection							
Same Day *(reference)*							
Not Same Day	-0.067	0.502	1	0.894	0.94	0.35	2.50
Number of Relatives with Cancer	0.075	0.036	1	0.035	1.08	1.01	1.16
Days from Initial Visit to Report	-0.003	0.001	1	0.034	0.99	0.99	1.00

Outcome: 0 = no-show
1 = attended

After removal of the non-significant variables, the final logistic regression model which best explains the data is shown in Table 8. In terms of attendance at first follow-up visit, patients in the telemedicine cohort were 3.54 times more likely to attend than those in the pre-telemedicine cohort ($p < 0.001$, 95% CI: 2.13, 5.89). Patients identifying as Asian were 2.59 times more likely to attend their first follow-up visit than White individuals. Patients with a family history of cancer were 1.08 times more likely to attend their first follow-up with every one additional relative affected with cancer ($p=0.037$, CI: 1.00, 1.15). Finally, with every 1-week increase between the patient's new patient appointment and their genetic test results report date, patients were 0.98 times less likely to attend their first follow-up visit ($p=0.029$, CI: 0.99, 1.00. Note, this Odds Ratio was obtained by multiplying the coefficient for this variable by 7 and taking the exponent). Patient age (categorized as less than 65 years old vs 65 years or older at the time of initial visit), personal history of cancer, and place of service were not found to independently predict attendance status at first follow-up visit, although these variables were still close to significant.

Table 8: Final binary logistic regression model of attendance status at **FIRST** follow-up visit

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort							
Pre-telemedicine *(reference)*							
Telemedicine	1.265	0.260	1	< 0.001	3.54	2.13	5.89
Age							
≤ 65 *(reference)*							
> 65	-0.369	0.228	1	0.105	0.69	0.44	1.08
Race/Ethnicity							
White *(reference)*			2	0.005			
Asian	0.953	0.345	1	0.006	2.59	1.32	5.09
Other	-0.234	0.226	1	0.300	0.79	0.51	1.23
Personal Cancer History							
Yes *(reference)*							
No	0.303	0.225	1	0.179	1.35	0.87	2.10
Number of Relatives with Cancer	0.072	0.035	1	0.037	1.08	1.00	1.15
Place of Service							
CCC (Orange, CA) *(reference)*							
CDDC (Costa Mesa, CA)	0.331	0.209	1	0.113	1.39	0.92	2.09
Days from Initial Visit to Report	-0.003	0.001	1	0.029	0.99	0.994	1.00

Outcome: 0 = no-show
1 = attended

3.3.2 Any follow-up visit

Additional analyses were explored to assess differences between patients who never attended a follow-up and those who attended at least one follow-up. The variables that were included in the final binary logistic regression model for attendance at first follow-up were included in the model for attendance at any follow-up (Table 9). In this initial model, the only variable that reached significance was number of relatives with cancer ($p = 0.048$, CI: 1.001, 1.35); with every one additional relative affected with cancer, patients were 1.16 times more likely to attend at least one follow-up visit compared to patients who never attended a follow-up visit. The remainder of the variables (cohort, patient age, race/ethnicity, personal history of cancer, place of service, and days from new patient visit to report date) were non-significant and thus were not found to independently predict attendance status at any follow-up visit. An additional two models were run with stepwise exclusion on the non-significant variables (see Appendix: Table 10, 11) and again, no variables reached significance. Non-significance is most likely explained by small sample sizes resulting in loss of power, as the reference category (patients who had at least one follow-up but didn't attend any) only had 49 total patients, while 658 patients attended at least one follow-up visit.

As a final analysis, a multinomial logistic regression model was run to compare patients who never returned, those who returned at their first follow-up visit, and those who returned at a later follow-up visit. Again, although the significance for many of these variables was likely not detected due to small sample sizes, the multinomial model did identify a difference in effect for the telemedicine variable, with those in the telemedicine cohort 2.31 times more likely to return at their first scheduled follow-up visit (see Appendix J, Model 2).

Table 9: Final binary logistic regression model of attendance status at **ANY** follow-up visit

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort							
Pre-telemedicine *(reference)*							
Telemedicine	0.637	0.443	1	0.151	1.899	0.793	4.508
Age							
≤ 65 *(reference)*							
> 65	0.459	0.470	1	0.328	1.583	0.630	3.976
Race/Ethnicity							
White *(reference)*			2	0.256			
Asian	1.059	0.642	1	0.099	0.288	0.820	10.140
Other	0.151	0.417	1	0.718	1.162	0.513	2.633
Personal Cancer History							
Yes *(reference)*							
No	0.264	0.425	1	0.535	1.302	0.566	2.996
Number of Relatives with Cancer	0.151	0.076	1	0.048	1.163	1.001	1.350
Place of Service							
CCC (Orange, CA) *(reference)*							
CDDC (Costa Mesa, CA)	0.158	0.380	1	0.678	1.171	0.556	2.468
Days from Initial Visit to Report	0.002	0.004	1	0.695	1.002	0.993	1.010

Outcome: 0 = had at least one follow-up visit but never attended
1 = attended at least one follow-up

IV. DISCUSSION

Cancer genetic counseling provides clear benefits to patients and their families, however, access to cancer genetic counselors is limited, likely due to the growing demand for genetic services and lack of genetic professionals. An additional obstacle to access is patient non-attendance, which is a common and pervasive barrier to healthcare across all medical specialties (Dantas et al., 2018). Reasons for patient non-attendance have long been studied in various specialties, yet there is little understanding of the impact of telemedicine as an alternate service delivery model on attendance and access in a cancer genetic counseling setting.

Previous research in the UCI cancer genetics clinic suggested that telemedicine might be an effective way to improve follow-up attendance after finding a significant increase in patient no-shows compared to the initial visit (Spiewak 2019). Several research studies have explored this possibility and suggest that remote medical care may be a feasible alternative to increase genetic counseling access and attendance, as well as attempt to meet the ever-increasing demand for genetic counseling services (Bracke et al., 2020; Greenberg et al., 2020; Rahm et al., 2019). Surprisingly, despite numerous publications demonstrating telemedicine's efficacy across various medical specialties, including provider and patient acceptance, increased access to services, high patient satisfaction, convenience, and equivalent patient knowledge and emotional outcomes, the majority of cancer genetic counselors remained in a traditional, in-person clinic setting prior to the COVID-19 pandemic (Bergstrom et al., 2021; Bracke et al., 2020; Brown et al., 2021; Buchanan et al., 2015; Cohen et al., 2016; Gorrie et al., 2021; Mauer et al., 2021; NSGC Professional Status Survey Executive Summary 2020; Solomans et al., 2018; Vrecar et al., 2017).

It was only with the rapid emergence of the global COVID-19 pandemic that telemedicine became the dominant service delivery model in the cancer genetics setting. The onset of the COVID-19 pandemic in March 2020 prompted a sudden and complete conversion to telemedicine for many medical professionals, including cancer genetic counselors. This rapid transition created a unique opportunity to investigate the impact of telemedicine on attendance and evaluate whether this service delivery model bypasses barriers and increases access to cancer genetic counselors. Recent studies published during the COVID-19 pandemic have assessed the experiences, preferences, challenges, and successes of telemedicine, demonstrating, and echoing the positive outcomes of this service delivery model in cancer genetic counseling (Binion et al., 2021; Breen et al., 2021; Mauer et al., 2021; Norman et al., 2022; Rezich et al., 2021; Shannon et al., 2021). However, there is little evidence in the literature on the outcomes and efficacy of telemedicine as it relates to attendance in the cancer genetic counseling setting, nor is there sufficient data on predictors and trends in attendance due to telemedicine over a substantial period. Further research into telemedicine's impact in a cancer genetic counseling setting is needed, as insight into the outcomes of telemedicine during the pandemic could help identify if this model improved the delivery of cancer genetic services, bypassed barriers specific to in-person appointments, and ultimately expanded attendance and access to care (Khan et al., 2021; Gorrie et al., 2021; Mann et al., 2021; Singh et al., 2021). In the post-pandemic world, it is highly plausible that telemedicine may become a standard framework for genetic counseling, so it is crucial that a deeper understanding of telemedicine is pursued.

The purpose of this study was to explore the comparison in attendance rate between a pre-telemedicine period and telemedicine period because of the previous hypotheses that it would be a useful model. Furthermore, it aimed to identify if certain patient populations in the

cancer genetic counseling clinic benefitted, or did not benefit, from telemedicine and evaluate factors that may have influenced in-person versus telemedicine attendance.

4.1 Evaluation of factors associated with attendance

This retrospective chart review collected and analyzed attendance status, demographic information, personal and family cancer history, logistical aspects of the cancer genetic counseling consultation, and pedigree information for each eligible patient record in this study. The study population was divided into two cohorts based on the date of the patient's initial visit consultation (cohort 1: pre-telemedicine/pandemic; cohort 2: telemedicine/pandemic). The pre-telemedicine cohort consisted of 496 patients seen for an initial new patient consult between April 3, 2018, and March 17, 2020. The telemedicine cohort consisted of 304 patients seen for an initial new patient consult between March 18, 2020, and April 2, 2021. In total, 800 patients met the study's criteria.

In the full sample, the attendance rate at the first follow-up visit was 78% (553 patients attended their first follow up out of the 707 patients scheduled) and a no-show rate of 22% (154 patients missed their first follow up visit out of the 707 patients scheduled). In addition to the first follow-up visit, attendance rate was also analyzed for attendance at any follow-up visit and this analysis identified that 658/707 patients attended at least one of their scheduled follow-up visits, for an overall return rate of 93%. Only 49/707 patients never attended any follow-up visit (7%). Alternatively stated, 7% of patients never returned for their follow-up visit, 78% of patients returned to their first follow-up visit, and 15% of patients eventually returned at a later visit.

The impact of telemedicine on attendance rate was striking. The results of this study identified that patients in the telemedicine cohort were significantly more likely to attend their first follow-up visit than patients in the pre-telemedicine cohort (88% vs 72%, $p<0.001$). Patients in the telemedicine cohort were also more likely to attend at least one follow-up visit than not attend at all, although this increase did not meet statistical significance ($p=0.23$). More patients in the pre-telemedicine cohort never returned for their scheduled follow-up visit, while more patients in the telemedicine cohort returned at their first scheduled follow-up visit ($p<0.001$).

Additional factors were also evaluated to identify any that needed to be further analyzed, as there may have been other variables, aside from telemedicine, that differed between cohorts and played a role in attendance prediction. Through univariate analyses it was identified that patient age (categorized as less than 65 years old vs 65 years or older at the time of initial visit, $p = 0.019$), race/ethnicity ($p=0.041$), place of service ($p = 0.002$), insurance type ($p = 0.023$), personal history of cancer ($p = 0.049$), previous germline testing ($p = 0.005$), previous known germline mutation ($p < 0.001$), sample type ($p < 0.001$), day of sample collection ($p = 0.002$), number of days to sample collection ($p < 0.001$), and number of days from initial visit to the date results reported ($p = 0.050$) were associated with attendance, so these variables were included in a multivariate analysis. These results are discussed in detail in the following sections.

Multivariate analyses (binary logistic regression) identified that insurance type, personal history of cancer, previous germline genetic testing, previously known germline mutation, sample type, sample collection date, clinic location, and patient's age (categorized as less than 65 years old vs 65 years or older at the time of initial visit) did not predict whether a patient was more or less likely to attend their first follow-up visit. However, although these factors did not reach statistical significance, there were interesting trends identified. The analysis showed a

trend of decreasing attendance at first follow-up visits for patients with government insurance (Medicare/Medicaid/TriCare) compared to those with private commercial insurance, which has been reported previously in the literature (Dantas et al., 2018).

Additionally, the logistic regression model suggested that patients older than 65 years of age were less likely to attend their first follow-up (although this finding did not reach statistical significance) which contradicts prior research in other medical specialties which identified younger adults as more likely to miss their appointments (Dantas et al., 2018). A reasonable conjecture may be that older individuals are more likely to be affected with cancer and thus less able to keep their appointments. It is also plausible that younger patients may be more aware of genetic advances and more interested in learning about their genetic make-up.

The logistic regression model also suggested that patients seen at the Chao Comprehensive Cancer Center (CCC) in Orange, CA were less likely to attend their first follow-up visit compared to patients seen at the Chao Digestive Disease Center (CDDC) in Costa Mesa, CA. This trend is likely due to the CDDC's clinic catchment area (Newport Beach, CA), which is an affluent socioeconomic region in Southern California and supports previous associations in the literature regarding attendance rate and socioeconomic status. Furthermore, many of the patients seen at the CDDC are referred due to their history of colon polyps and do not have a personal cancer diagnosis themselves, which may have made them more likely to attend. However, inspection of the data indicates this may not be the explanation for the increased attendance rate in the Costa Mesa clinic, as there was no significant association found between personal history of cancer and clinic location ($p=0.63$)

It was anticipated that patients with a personal history of cancer may be more motivated to attend their appointments and thus have a higher likelihood of attendance. In contrast to this

expectation, those with a personal history of cancer were actually less likely to attend their first follow-up, although this difference not statistically significant. It is reasonable to assume that patients with a cancer diagnosis are under significant stress that may impact their ability or desire to attend their follow-up visit with genetics. These patients may be too ill to attend their follow-up visit or burdened with treatment and other appointments that likely take precedence. Therefore, it is reasonable to infer that patients with a personal history of cancer would be more likely to reschedule than those without.

This study identified several factors that were found to significantly, and independently, predict attendance status at first follow-up visit. First, patients with a family history of cancer were 1.08 times more likely to attend their first follow-up visit with every one additional relative affected with cancer. This was an initial hypothesis of the study; namely, a family history of cancer and those with more affected relatives would be more likely to return to their follow-up visits than those without a family history or with fewer relatives affected, possibly due to a higher perception of hereditary cancer risk that increased their motivation to attend.

The second factor identified as independently predicting return to first follow-up was race/ethnicity. An association between race/ethnicity and attendance has been demonstrated in previous research, with White or Asian ethnicities being more likely to attend their medical appointments than minority ethnicities (Hispanic/Latino patients, American Indian/Alaskan Native patients, and Black/African American patients) (Dantas et al., 2018; Shitmosu et al., 2016; Smith et al., 1994). The results of this analysis identified that patients of Asian descent were 2.59 times more likely to attend their first follow-up visit than White patients. In addition, patients categorized as ‘other’ in the study sample, which consisted of Hispanic/Latino patients, American Indian/Alaskan Native patients, Black/African American patients, and Native

Hawaiian/Pacific Islander, were less likely to attend than White patients, although this was not a statistically significant difference.

Additionally, the length of time between a patient's initial visit and their genetic test results report date was a significant predictor of attendance status at first follow-up visit; with each additional week, patients were 0.99 times less likely to return. Delays between the patient's initial visit and their report date impacted their likelihood to return to their first follow-up visit and receive their results, however, this finding could be explained by the patient being advised to reschedule their visit by the administrative team (i.e., UCI schedulers and administrative assistants). Delays with sample collection or insurance authorization likely prevented the test results from being ready in time for the scheduled follow-up visit, and thus the patient could have been advised to reschedule their visit for a later date.

As stated previously, the most notable finding from this study, and the initial purpose of the research, was the substantial impact of cohort on attendance rate at first follow-up visit. This was initially identified in the univariate analysis and remained a significant predictor of attendance in the multivariate analysis, which identified that patients in the telemedicine cohort were 3.54 times more likely to attend their first follow-up visit than those in the pre-telemedicine cohort. This remained a significant predictor of attendance status even when all remaining covariates were accounted for, demonstrating that none of the other significant predictors could explain the increased attendance in the telemedicine cohort. Although this research cannot identify what specific aspects of telemedicine are responsible for the increased attendance rate, the results document that there was improved attendance, and therefore access to care, in the telemedicine period.

The focus of this research was to explore associations/predictors of attendance at first follow-up since appointment-keeping at this visit is valuable for providers and patients alike, contributing not only to clinic efficiency but also improving communication, medical recommendations, and follow-through between provider and patient. However, additional analyses were pursued to assess differences between patients who never attended a follow-up and those who attended at least one follow-up. Almost all variables lost significance in this analysis due to an increasingly small sample in the reference group. The number of relatives with cancer was the only variable that reached significance, identifying that with every one additional relative affected with cancer, patients were 1.16 times more likely to attend at least one follow-up visit compared to patients who never attended a follow-up visit. In terms of service delivery model, the logistic regression model suggested that patients in the telemedicine cohort were more likely to attend any follow-up visit, although this difference did not reach statistical significance. A further multinomial approach also identified a difference in effect for the cohort variable, with those in the telemedicine cohort 2.21 times more likely to return at first follow-up visit (see Appendix J, Model 1).

4.2 Study limitations and future research directions

As with any research, limitations exist. An important limitation of this study is that the research focused on one patient sample in Southern California, and thus cannot be generalized to the entire cancer genetic counseling patient population. The demographics of the UCI patient sample are not representative of all populations in the United States, so it would be beneficial to investigate these questions about the impact of telemedicine in additional cancer genetic

counseling clinics across the country to assess whether these findings remain true across a more diverse study sample.

Limitations were also present during initial data collection. For example, insurance information was extracted from the medical records at the time of data collection (November 2021 to January 2022), which may not have been representative of the insurance that patients had at the time of their genetic counseling consultations. Moreover, an initial hypothesis of this study was that patients with late-stage cancers would be less likely to attend their follow-up visits overall but more likely to attend during the telemedicine period, however, this hypothesis could not be investigated because cancer staging could not be consistently collected across patient records. Due to variability in cancer staging reporting and collection, this variable was not analyzed. Future studies should further explore this hypothesis to identify if telemedicine benefits patients with late-stage cancer diagnoses as this may be a useful intervention to deliver valuable genetic information.

Patients' zip codes were collected during the chart review data collection; however, this variable was not analyzed due to constraints of the statistical software used for analysis. Although no data were explored on the association between distance to clinic and telemedicine attendance, place of service (clinic location) can be substituted as a proxy for socioeconomic status.

Additionally, this study focused on patient attendance at follow-up visits as an extension of prior research completed at this institution (Spiewak, 2019). For this reason, the study did not collect nor analyze attendance status for initial new patient consultations or predictors of attendance for this initial consultation. Cancellations for these initial consultations were also not easily trackable or identifiable in the medical record system, especially for patients who missed

their initial consultation and were never rescheduled. It would be worthwhile to apply the same study methodology to attendance at new patient consultations in future research, as this could further identify telemedicine's impact on attendance and access to cancer genetic counselors.

Furthermore, due to the continuous timeframe of this study, 46 patients in the pre-telemedicine cohort were scheduled for a follow-up visit during the telemedicine cohort, which means that the cohorts in this study are not entirely separable. It would be interesting to evaluate the data with more stringent cohort inclusivity, for example, eliminating the 46 patients from the dataset, or adding these patients to the telemedicine cohort, since their attendance at follow-up would be more accurately measured in that period.

Given that this was a retrospective chart review that analyzed predictors of attendance, it was not possible to identify the *reasons* that patients attended or did not attend their follow-up visits. Future research could explore personal motivations and explanations from patients who attended their follow-up visit/s and patients who did not through a qualitative survey. A qualitative study would be a valuable approach to explore the "why" behind attendance status and could also help solidify if telemedicine was truly the cause for the increased attendance, or if this significant predictor of attendance is explainable by another unknown factor. Results from a qualitative study could provide insight for the development of targeted approaches that may increase the likelihood to attend, for example, developing and testing an intervention.

4.3 Conclusions

The purpose of this retrospective chart review was to explore differences in attendance rate between patients in a pre-telemedicine period compared to patients in a telemedicine period, in part due to previous research suggesting that this alternate service delivery model could be a useful approach for increasing access to genetic services.

The results of this study identified improved attendance at first follow-up visit in the telemedicine cohort. This was present in the univariate analyses and in the multivariate analyses, where other significant variables were considered and where an estimate of *how much* attendance improved could be garnered. The results of the multivariate analysis identified that patients in the telemedicine period were 3.54 times more likely to attend their first follow-up visit, and that this result was independent of any other significant factor.

Although demographic and clinical history information were not a primary focus of this research, comparisons were explored between these factors to investigates differences among patients who attended and patients who did not attend. Other predictors of patient attendance at first follow-up included race/ethnicity, with patients of Asian descent more likely to attend their follow-up, and family history of cancer, with patients with more relatives affected by cancer more likely to attend their follow-up. In addition, lead times between initial visit and report date were an important predictor as well, with longer lead times resulting in higher likelihood of non-attendance.

The results of this study are consistent with the service delivery model itself, i.e., telemedicine, being responsible for this increase in attendance. These findings lay the groundwork for further studies to explore and test the effectiveness of offering a telemedicine option for cancer genetic counseling, particularly for groups who are known to be at a higher risk for non-attendance, thereby increasing attendance and access to cancer genetic counseling.

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APPENDIX A

Clinical characteristics of the study population:

	Descriptive Statistics				
	Group 1 Pre-telemed N = 496	**Group 2 Telemed N = 304**	**Overall Total**		
Clinical characteristics (cat.) *N = 800 unless otherwise specified*	**N (%)**	**N (%)**	**N (%)**	**χ2 (d.f.)**	**p-value**
Insurance *N = 784*					
Private (HMO, PPO, EPO)	243 (50.0)	181 (60.7)	424 (54.1)	8.67 (2)	0.013
Government (Medicare, Medicaid)	196 (40.3)	96 (32.2)	292 (37.2)		
Other	47 (9.7)	21 (7.0)	68 (8.7)		
Insurance *N = 784*					
Private	243 (50.0)	181 (60.7)	424 (54.1)	8.58 (1)	0.003
Government/Other	243 (50.0)	117 (39.3)	360 (45.9)		
Insurance Authorization					
Auth Required	179 (36.1)	97 (31.9)	276 (34.5)	2.54 (2)	0.281
No Auth Required	278 (56.0)	175 (57.6)	453 (56.6)		
Unknown	39 (7.9)	32 (10.5)	71 (8.9)		
Referral Indication					
Personal history of cancer	17 (3.4)	24 (7.9)	41 (5.1)	9.79 (3)	0.020
Family history of cancer	182 (36.7)	96 (31.6)	278 (34.8)		
Both	295 (59.7)	181 (59.5)	476 (59.5)		
Neither	2 (0.4)	3 (1.0)	5 (0.6)		
Referral Indication *N = 795*					
Personal history of cancer	17 (3.4)	24 (8.0)	41 (5.2)	8.76 (2)	0.012
Family history of cancer	182 (36.7)	96 (31.9)	278 (35.0)		
Both	295 (59.7)	181 (60.1)	476 (59.9)		
Personal History of Cancer					
Yes	312 (62.9)	205 (67.4)	517 (64.6)	1.69 (1)	0.193
No **Note: among those with no personal history of cancer, only 5 did not have a family history as well.*	184 (37.1)	99 (32.6)	283 (35.4)		

Cancer Type *N = 519* Ovarian Colorectal Breast Prostate Uterine Melanoma Non-melanoma Skin Renal Pancreatic Brain Neuroendocrine Gastric Multiple Lung Appendiceal Hematologic Thyroid Testicular Bladder Ocular Cervical Other	 52 (16.6) 43 (13.7) 42 (13.4) 20 (6.4) 24 (7.7) 12 (3.8) 10 (3.2) 15 (4.8) 8 (2.6) 5 (1.6) 3 (1.0) 3 (1.0) 52 (16.6) 3 (1.0) 3 (1.0) 0 (0.0) 4 (1.3) 1 (0.3) 3 (1.0) 1 (0.3) 0 (0.0) 9 (2.9)	 25 (12.1) 30 (14.6) 19 (9.2) 18 (8.7) 10 (4.9) 8 (3.9) 9 (4.4) 6 (2.9) 9 (4.4) 5 (2.4) 8 (3.9) 7 (3.4) 36 (17.5) 2 (1.0) 2 (1.0) 2 (1.0) 1 (0.5) 0 (0.0) 3 (1.5) 0 (0.0) 1 (0.5) 5 (2.4)	 77 (14.8) 73 (14.1) 61 (11.8) 38 (7.3) 34 (6.6) 20 (3.9) 19 (3.7) 21 (4.0) 17 (3.3) 10 (1.9) 11 (2.1) 10 (1.9) 88 (1.7) 5 (1.0) 5 (1.0) 2 (0.4) 5 (1.0) 1 (0.2) 6 (1.2) 1 (0.2) 1 (0.2) 14 (2.7)	25.23 (21)	0.237
Referral Source Provider Self	 432 (87.1) 64 (12.9)	 260 (85.5) 44 (14.5)	 692 (86.5) 108 (13.5)	0.39 (1)	0.528
Previous Germline Genetic Testing Yes No	 69 (13.9) 427 (86.1)	 44 (14.5) 260 (85.5)	 113 (14.1) 687 (85.9)	0.05 (1)	0.825
Previous Somatic Genetic Testing Yes No	 14 (2.8) 482 (97.2)	 13 (4.3) 291 (95.7)	 27 (3.4) 773 (96.6)	1.22 (1)	0.269
Prior Germline Mutation (Patient) Yes No	 26 (5.2) 470 (94.8)	 17 (5.6) 287 (94.4)	 43 (5.4) 757 (94.6)	0.05 (1)	0.831

Prior Germline Mutation (Relative) Yes No	76 (15.3) 420 (84.7)	36 (11.8) 268 (88.2)	112 (14.0) 688 (86.0)	1.89 (1)	0.168
Sample Type *N = 713* Blood Saliva Buccal No sample submitted	389 (88.2) 48 (10.9) 3 (0.7) 1 (0.2)	2 (0.7) 252 (92.6) 0 (0.0) 18 (6.6)	391 (54.8) 300 (42.1) 3 (0.4) 19 (2.7)	529.67 (3)	< 0.001
Sample Type *N = 691* Blood Saliva	389 (89.0) 48 (11.0)	2 (0.8) 252 (99.2)	391 (56.6) 300 (43.4)	508.99 (1)	< 0.001
Genetic Testing Laboratory *N = 799* Lab A Lab B Lab C Other	406 (82.0) 33 (6.7) 38 (7.7) 18 (3.6)	175 (57.6) 83 (27.3) 42 (13.8) 4 (1.3)	581 (72.7) 116 (14.5) 80 (10.0) 22 (2.8)	81.50 (3)	< 0.001
Genetic Test Type Panel Specific Site Analysis Both	467 (94.2) 26 (5.2) 3 (0.6)	287 (94.4) 16 (5.3) 1 (0.3)	754 (94.3) 42 (5.3) 4 (0.5)	0.29 (2)	0.866
Genetic Testing Results Positive Negative VUS *No results (no sample submitted) *Note: not included in chi-square analysis*	102 (20.6) 272 (54.8) 122 (24.6) 0 (0.0)	66 (21.7) 149 (49.0) 71 (23.4) 18 (5.9)	168 (21.0) 421 (52.6) 193 (24.1) 18 (2.3)	0.79 (2)	0.674
Attendance at 1st follow-up *N = 707* Attended Did not attend	325 (72.4) 124 (27.6)	228 (88.4) 30 (11.6)	553 (78.2) 154 (21.8)	24.59 (1)	< 0.001

Attendance at any follow-up *N = 707* Attended at least one Did not attend any	414 (92.2) 35 (7.8)	244 (94.6) 14 (5.4)	658 (93.1) 49 (6.9)	1.43 (1)	0.233
Clinical characteristics (cont.)				**t (d.f.)**	**p-value**
Number of living children Mean S.D. Median Range	1.77 1.39 2.00 0 – 9	1.57 1.34 2.00 0 – 6	1.69 1.38 2.00 0 – 9	1.98 (796)	0.048
Number of relatives with cancer Mean S.D. Median Range	4.68 3.40 4.00 0 – 19	4.06 3.07 4.00 0 – 24	4.44 3.29 4.00 0 – 24	2.58 (792)	0.010
Referral to initial visit (days) *N = 705* Mean S.D. Median Range	64.17 66.49 48.00 0 – 683	77.61 69.79 61.50 1 – 517	69.32 68.04 54.00 0 – 683	-2.56 (703)	0.011
Initial visit to sample collection (days) *N = 686* Mean S.D. Median Range	5.28 29.80 0.00 0 – 287	26.02 31.93 16.00 0 – 226	12.65 32.13 0.00 0 – 287	-8.51 (684)	< 0.001
Sample collection to report date (days) *N = 680* Mean S.D. Median Range	21.46 35.86 15.00 5 – 432	26.37 75.84 13.50 5 – 761	23.22 53.74 15.00 5 – 761	-1.14 (678)	0.253

Initial visit to report date (days) *N = 701* Mean S.D. Median Range	 26.89 46.59 16.00 5 – 432	 51.66 80.46 33.00 8 – 771	 35.99 62.35 20.00 5 – 771	 -5.14 (692)	 < 0.001
Time from initial visit to first follow-up visit (days) *N = 707* Mean S.D. Median Range	 59.63 70.59 42.00 7 – 735	 65.17 44.65 56.00 3 – 367	 61.65 62.41 43.00 3 – 735	 -1.14 (705)	 0.256

APPENDIX B

Comparisons of demographic characteristics between patients who attended their first follow-up visit and those who did not:

	Attendance at 1st Follow-Up Visit		Statistical Analysis	
	Attended N = 553	**No-Show N = 154**		
Demographic Comparisons *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**$\chi 2$ (d.f.)**	**p-value**
Cohort				
Group 1 (pre-telemedicine)	325 (72.4)	124 (27.6)	24.59 (1)	< 0.001
Group 2 (telemedicine)	228 (88.4)	30 (11.6)		
Gender				
Female	383 (77.7)	110 (22.3)	0.27 (1)	0.604
Male	170 (79.4)	44 (20.6)		
Age (years)				
Q1: 18 – 41	152 (83.5)	30 (16.5)	7.61 (3)	0.055
Q2: 42 – 55	146 (77.2)	43 (22.8)		
Q3: 56 – 65	133 (80.1)	33 (19.9)		Test of linear association: $\chi 2$ (1) = 5.39, p = 0.02
Q4: 66 – 93	122 (71.8)	48 (28.2)		
65 Cutoff				
≤ 65 years old	431 (80.3)	106 (19.7)	5.47 (1)	0.019
> 65 years old	122 (71.8)	48 (28.2)		
70 Cutoff				
≤ 70 years old	484 (79.0)	129 (21.0)	1.47 (1)	0.225
> 70 years old	69 (73.4)	25 (26.6)		
Race/Ethnicity *N = 698*				
White	299 (78.1)	84 (21.9)	6.77 (3)	0.080
Hispanic or Latino	87 (75.7)	28 (24.3)		
Asian	105 (86.1)	17 (13.9)		
Other	56 (71.8)	22 (28.2)		
Race/Ethnicity *N = 698*				
White	299 (78.1)	84 (21.9)	6.37 (2)	0.041
Asian	105 (86.1)	17 (13.9)		
Other	143 (74.1)	50 (25.9)		

Race/Ethnicity N = 698 White Other	 299 (78.1) 248 (78.7)	 84 (21.9) 67 (21.3)	 0.05 (1)	 0.833
Language English Spanish Other	 496 (78.7) 27 (65.9) 30 (83.3)	 134 (21.3) 14 (34.1) 6 (16.7)	 4.33 (2)	 0.115
Language English Not English	 496 (78.7) 57 (74.0)	 134 (21.3) 20 (26.0)	 0.89 (1)	 0.345

APPENDIX C

Comparisons of clinical characteristics between patients who attended their first follow-up visit and those who did not:

	Attendance at 1st Follow-Up Visit		Statistical Analysis	
	Attended N = 553	**No-Show N = 154**		
Clinical Comparisons *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**$\chi 2$ (d.f.)**	**p-value**
Place of Service				
CCC (Orange, CA)	258 (73.3)	94 (26.7)	9.97 (1)	0.002
CDDC (Costa Mesa, CA)	295 (83.1)	60 (16.9)		
Insurance				
Private	310 (82.0)	68 (18.0)	7.56 (2)	0.023
Government	189 (73.8)	69 (26.2)		
Other/Unknown	43 (71.7)	17 (28.3)		
Insurance				
Private				
Government	310 (82.0)	68 (18.0)	6.09 (1)	0.014
**other/unknown excluded*	189 (73.8)	67 (26.2)		
Insurance				
Private	310 (82.0)	68 (18.0)	7.43 (1)	0.006
Government + *Other/Unknown*	232 (73.4)	84 (26.6)		
Insurance Authorization				
Authorization required	180 (74.7)	61 (25.3)	2.78 (2)	0.249
No authorization required	322 (80.3)	79 (19.7)		
Unknown	51 (78.5)	14 (21.5)		
Referral Indication *N = 703*				
Personal history of cancer	21 (72.4)	8 (27.6)	4.20 (2)	0.122
Family history of cancer	210 (82.4)	45 (17.6)		
Both	319 (76.1)	100 (23.9)		
Personal History of Cancer				
Yes	340 (75.9)	108 (24.1)	3.88 (1)	0.049
No	213 (82.2)	46 (17.8)		

Cancer Type (top 5) *N = 450* Breast CRC Ovarian Uterine Multiple Other	 29 (67.4) 55 (78.6) 55 (78.6) 27 (81.8) 60 (75.9) 117 (75.5)	 14 (32.6) 15 (21.4) 15 (21.4) 6 (18.2) 19 (24.1) 38 (24.5)	2.87 (5)	0.719
Cancer Category *N = 450* Female Cancer Male Cancer GI Cancer Multiple Other	 127 (76.5) 21 (77.8) 76 (74.5) 35 (72.9) 84 (78.5)	 39 (23.5) 6 (22.2) 26 (25.5) 13 (27.1) 23 (21.5)	0.81 (4)	0.938
Referral Source Provider Self	 475 (77.9) 78 (80.4)	 135 (22.1) 19 (19.6)	0.32 (1)	0.573
Prior Germline Genetic Testing Yes No	 32 (62.7) 521 (79.4)	 19 (37.3) 135 (20.6)	7.72 (1)	0.005
Prior Somatic Genetic Testing Yes No	 16 (69.6) 537 (78.5)	 7 (30.4) 147 (21.5)	1.05 (1)	0.307
Prior Germline Mutation (Patient) Yes No	 11 (44.0) 542 (79.5)	 14 (56.0) 140 (20.5)	17.81 (1)	< 0.001
Prior Germline Mutation (Relative) Yes No	 79 (82.3) 474 (77.6)	 17 (17.7) 137 (22.4)	1.08 (1)	0.298
Sample Type Blood Buccal No Sample Saliva	 280 (74.3) 1 (33.3) 2 (40.0) 258 (87.2)	 97 (25.7) 2 (66.7) 3 (60.0) 38 (12.8)	25.64 (3)	< 0.001

Sample Type *N = 673* Blood Saliva	 280 (74.3) 258 (87.2)	 97 (25.7) 38 (12.8)	 17.19 (1)	 < 0.001
Sample Collection Same day Not same day	 298 (73.9) 255 (83.9)	 105 (26.1) 49 (16.1)	 10.04 (1)	 0.002
Genetic Testing Laboratory Lab A Lab B Lab C Other	 418 (78.1) 88 (83.8) 38 (74.5) 8 (53.3)	 117 (21.9) 17 (16.2) 13 (25.5) 7 (46.7)	 7.78 (3)	 0.051
Genetic Test Type *N = 703* Panel Single Site	 516 (77.7) 33 (84.6)	 148 (22.3) 6 (15.4)	 1.03 (1)	 0.311
Genetic Testing Results Positive Negative VUS	 108 (78.3) 314 (78.5) 131 (78.9)	 30 (21.7) 86 (21.5) 35 (21.1)	 0.02 (2)	 0.990
Number of Living Children *N = 706* 0 1 2 3 or more	 142 (78.0) 86 (77.5) 191 (80.6) 134 (76.1)	 40 (22.0) 25 (22.5) 46 (19.4) 42 (23.9)	 1.27 (3)	 0.736 Test of linear association: $\chi 2$ (1) = 0.02, p = 0.884
Parent Status No children Has children	 142 (78.0) 411 (78.3)	 40 (22.0) 114 (21.7)	 0.01 (1)	 0.941
Number of Relatives with Cancer *N = 702* Q1: 0 – 2 Q2: 3 – 4 Q3: 5 – 6 Q4: ≥ 7	 160 (76.6) 152 (76.4) 108 (81.8) 131 (80.9)	 49 (23.4) 47 (23.6) 24 (18.2) 31 (19.1)	 2.39 (3)	 0.495 Test of linear association: $\chi 2$ (1) = 1.71, p = 0.192

Referral to initial visit (days) *N = 618* Q1: 0 – 30 Q2: 31 – 53 Q3: 54 – 91 Q4: ≥ 92	 124 (79.5) 120 (76.9) 121 (78.1) 115 (76.2)	 32 (20.5) 36 (23.1) 34 (21.9) 36 (23.8)	0.56 (3)	0.906 Test of linear association: $\chi2$ (1) = 0.35, p = 0.557
Initial visit to sample collection (days) *N = 668* 0 1 – 14 15+	 298 (73.9) 99 (92.5) 135 (85.4)	 105 (26.1) 8 (7.5) 23 (14.6)	22.29 (2)	< 0.001 Test of linear association: $\chi2$ (1) = 13.5, p = < 0.001
Sample collection to report (days) *N = 663* Q1: 5 – 11 Q2: 12 – 15 Q3: 16 – 21 Q4: ≥ 22	 153 (81.0) 147 (80.8) 118 (77.1) 110 (79.1)	 36 (19.0) 35 (19.2) 35 (22.9) 29 (20.9)	0.96 (3)	0.810 Test of linear association: $\chi2$ (1) = 0.45, p = 0.501
Initial visit to report date (days) *N = 675* Q1: 5 – 14 Q2: 15 – 21 Q3: 22 – 35 Q4: ≥ 36	 144 (75.0) 131 (78.0) 131 (86.8) 133 (81.1)	 48 (25.0) 37 (22.0) 20 (13.2) 31 (18.9)	7.81 (3)	0.050 Test of linear association: $\chi2$ (1) = 4.02, p = 0.045
Initial visit to 1st follow-up (days) *N = 707* Q1: 3 – 35 Q2: 36 – 43 Q3: 44 – 63 Q4: ≥ 64	 173 (77.6) 102 (77.9) 147 (81.2) 131 (76.2)	 50 (22.4) 29 (22.1) 34 (18.8) 41 (23.8)	1.44 (3)	0.695 Test of linear association: $\chi2$ (1) = 0.00, p = 0.986

APPENDIX D

Comparisons of demographic characteristics between patients who attended *any* follow-up visit and those who did not:

	Attendance at Any Follow-Up Visit		**Statistical Analysis**	
	Attended N = 658	**No-Show N = 49**		
Demographic Comparisons *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**$\chi 2$ (d.f.)**	**p-value**
Cohort				
Group 1 (pre-telemedicine)	414 (92.2)	35 (7.8)	1.43 (1)	0.233
Group 2 (telemedicine)	244 (94.6)	14 (5.4)		
Gender				
Male	201 (93.9)	13 (6.1)	0.35 (1)	0.555
Female	457 (92.7)	36 (7.3)		
Age (years)				
Q1: 18 – 41	174 (95.6)	8 (4.4)	3.82 (3)	0.281
Q2: 42 – 55	175 (92.6)	14 (7.4)		
Q3: 56 – 65	150 (90.4)	16 (9.6)		Test of linear association: $\chi 2$ (1) = 1.00, p = 0.317
Q4: 66 – 93	159 (93.5)	11 (6.5)		
65 Cutoff				
≤ 65 years old	499 (92.9)	38 (7.1)	0.07 (1)	0.786
> 65 years old	159 (93.5)	11 (6.5)		
Race/Ethnicity *N = 698*				
White	357 (93.2)	26 (6.8)	2.63 (3)	0.452
Hispanic or Latino	109 (94.8)	6 (5.2)		
Asian	116 (95.1)	6 (4.9)		
Other	70 (89.7)	8 (10.3)		
Race/Ethnicity *N = 698*				
White	357 (93.2)	26 (6.8)	0.72 (2)	0.699
Asian	116 (95.1)	6 (4.9)		
Other	179 (92.7)	14 (7.3)		

Race/Ethnicity *N = 698* White Other	 357 (93.2) 295 (93.7)	 26 (6.8) 20 (6.3)	 0.05 (1)	 0.816
Language English Spanish Other	 588 (93.3) 37 (90.2) 33 (91.7)	 42 (6.7) 4 (9.8) 3 (8.3)	 0.69 (2)	 0.710
Language English Not English	 588 (93.3) 70 (90.9)	 42 (6.7) 7 (9.1)	 0.63 (1)	 0.429

APPENDIX E

Comparisons of clinical characteristics between patients who attended any follow-up visit and those who did not:

	Attendance at Any Follow-Up Visit		Statistical Analysis	
	Attended N = 658	**No-Show N = 49**		
Clinical Comparisons *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**χ2 (d.f.)**	**p-value**
Place of Service				
CCC (Orange, CA)	323 (91.8)	29 (8.2)	1.86 (1)	0.173
CDDC (Costa Mesa, CA)	335 (94.4)	20 (5.6)		
Insurance *N = 694*				
Private	356 (94.2)	22 (5.8)	4.31 (2)	0.116
Government	232 (90.6)	24 (9.4)		
Other/Unknown	58 (96.7)	2 (3.3)		
Insurance *N = 694*				
Private	356 (94.2)	22 (5.8)	1.55 (1)	0.213
Government + Other/Unknown	290 (91.8)	26 (8.2)		
Insurance Authorization				
Authorization required	223 (92.5)	18 (7.5)	0.94 (2)	0.624
No authorization required	376 (93.8)	25 (6.2)		
Unknown	59 (90.8)	6 (9.2)		
Referral Indication				
Personal history of cancer	23 (79.3)	6 (20.7)	9.28 (2)	0.010
Family history of cancer	241 (94.5)	14 (5.5)		
Both	390 (93.1)	29 (6.9)		
Personal History of Cancer				
Yes	413 (92.2)	35 (7.8)	1.47 (1)	0.225
No	245 (94.6)	14 (5.4)		

Cancer Type (top 5) *N = 450* Breast CRC Ovarian Uterine Multiple Other	 37 (86.0) 66 (94.3) 67 (95.7) 32 (97.0) 72 (91.1) 142 (91.6)	 6 (14.0) 4 (5.7) 3 (4.3) 1 (3.0) 7 (8.9) 13 (8.4)	5.25 (5)	0.387
Cancer Category *N = 450* Female Cancer Male Cancer GI Cancer Multiple Other	 154 (92.8) 24 (88.9) 92 (90.2) 43 (89.6) 103 (96.3)	 12 (7.2) 3 (11.1) 10 (9.8) 5 (10.4) 4 (3.7)	4.05 (4)	0.400
Referral Source Provider Self	 565 (92.6) 93 (95.9)	 45 (7.4) 4 (4.1)	1.37 (1)	0.241
Prior Germline Genetic Testing Yes No	 37 (72.5) 621 (94.7)	 14 (27.5) 35 (5.3)	35.88 (1)	< 0.001
Prior Somatic Genetic Testing Yes No	 20 (87.0) 638 (93.3)	 3 (13.0) 46 (6.7)	1.38 (1)	0.241
Prior Germline Mutation (Patient) Yes No	 14 (56.0) 644 (94.4)	 11 (44.0) 38 (5.6)	55.21 (1)	< 0.001
Prior Germline Mutation (Relative) Yes No	 90 (93.8) 568 (93.0)	 6 (6.3) 43 (7.0)	0.08 (1)	0.778
Sample Type *N = 681* Blood Buccal No Sample Saliva	 355 (94.0) 3 (100.0) 2 (40.0) 283 (95.6)	 22 (5.8) 0 (0.0) 3 (60.0) 13 (4.4)	29.12 (3)	< 0.001

Sample Type *N = 673* Blood Saliva	 355 (94.2) 283 (95.6)	 22 (5.8) 13 (4.4)	 0.701 (1)	 0.402
Genetic Testing Laboratory *N = 706* Lab A Lab B Lab C Other	 504 (94.2) 98 (93.3) 47 (92.2) 8 (53.3)	 31 (5.8) 7 (6.7) 4 (7.8) 7 (46.7)	 	 < 0.001*
Genetic Test Type Panel Single Site	 616 (92.8) 38 (97.4)	 48 (7.2) 1 (2.6)	 1.24 (1)	 0.266
Genetic Testing Results Positive Negative VUS	 120 (87.0) 381 (95.3) 157 (94.6)	 18 (13.0) 19 (4.8) 9 (5.4)	 11.99 (2)	 0.002
Number of Living Children *N = 706* 0 1 2 3 or more	 172 (94.5) 103 (92.8) 221 (93.2) 162 (92.0)	 10 (5.5) 8 (7.2) 16 (6.8) 14 (8.0)	 0.89 (3)	 0.828 Test of linear association: $\chi 2$ (1) = 0.71, p = 0.399
Parent Status No children Has children	 172 (94.5) 486 (92.6)	 10 (5.5) 39 (7.4)	 0.78 (1)	 0.376
Number of Relatives w/ Cancer *N = 702* Q1: 0 – 2 Q2: 3 – 4 Q3: 5 – 6 Q4: ≥ 7	 194 (92.8) 184 (92.5) 125 (94.7) 152 (93.8)	 15 (7.2) 15 (7.5) 9 (5.3) 10 (6.2)	 0.78 (3)	 0.853 Test of linear association: $\chi 2$ (1) = 0.37, p = 0.546

Referral to initial visit (days) *N = 618* Q1: 0 – 30 Q2: 31 – 53 Q3: 54 – 91 Q4: ≥ 92	 147 (94.2) 145 (92.9) 143 (92.3) 140 (92.7)	 9 (5.8) 11 (7.1) 12 (7.7) 11 (7.3)	0.52 (3)	0.916 Test of linear association: $\chi 2$ (1) = 0.33, p = 0.565
Initial visit to sample collection (days) *N = 668* 0 1 –14 15+	 378 (93.8) 103 (96.3) 153 (96.8)	 25 (6.2) 4 (3.7) 5 (3.2)	2.65 (2)	0.266 Test of linear association: $\chi 2$ (1) = 2.49, p = 0.115
Sample Collection Same day Not same day	 378 (93.8) 280 (92.1)	 25 (6.2) 24 (7.9)	0.77 (1)	0.381
Sample collection to report date (days) *N = 663* Q1: 5 – 11 Q2: 12 – 15 Q3: 16 – 21 Q4: ≥ 22	 183 (96.8) 169 (92.9) 143 (93.5) 135 (97.1)	 6 (3.2) 13 (7.1) 10 (6.5) 4 (2.9)	5.19 (3)	0.159 Test of linear association: $\chi 2$ (1) = 0.00, p = 0.994
Initial visit to report date (days) *N = 675* Q1: 5 – 14 Q2: 15 – 21 Q3: 22 – 35 Q4: ≥ 36	 182 (94.8) 155 (92.3) 147 (97.4) 157 (95.7)	 10 (5.2) 13 (7.7) 4 (2.6) 7 (4.3)	4.58 (3)	0.206 Test of linear association: $\chi 2$ (1) = 0.99, p = 0.319

Initial visit to 1st follow up (days) *N = 707* Q1: 3 – 35 Q2: 36 – 43 Q3: 44 – 63 Q4: ≥ 64	 209 (93.7) 123 (93.9) 174 (96.1) 152 (88.4)	 14 (6.3) 8 (6.1) 7 (3.9) 20 (11.6)	8.80 (3)	0.032 Test of linear association: $\chi 2$ (1) = 2.34, p = 0.126

* p-value from Fisher's exact test

APPENDIX F

Binary logistic regression model of attendance status at <u>ANY</u> follow up visit:

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort							
Pre-telemedicine *(reference)*							
Telemedicine	0.515	0.349	1	0.140	1.674	0.844	3.319
Age							
≤ 65 *(reference)*							
> 65	0.013	0.362	1	0.972	1.013	0.498	2.060
Race/Ethnicity							
White *(reference)*			2	0.435			
Asian	0.620	0.509	1	0.224	1.859	0.685	5.044
Other	-0.042	0.346	1	0.904	0.959	0.487	1.890
Number of Relatives with Cancer	0.060	0.052	1	0.250	1.062	0.959	1.177

Outcome variable: 0 = had at least one follow-up visit and never attended
1 = attended at least one follow-up visit

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort							
Pre-telemedicine *(reference)*							
Telemedicine	0.363	0.330	1	0.272	1.437	0.753	2.744
Number of Relatives with Cancer	0.057	0.051	1	0.262	1.058	0.958	1.169

Outcome variable: 0 = had at least one follow-up visit and never attended
1 = attended at least one follow-up visit

APPENDIX G

Demographic comparisons between patients who never returned for follow-up, patients who returned at their first follow-up, and patients who returned at a later follow-up:

	Attendance Ever		
	Never returned N = 49	**Returned at 1st follow-up N = 553**	**Returned at later follow-up N = 105**
Variable *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**N (%)**
Sex			
Female	36 (73.5)	383 (69.3)	74 (70.5)
Male	13 (26.5)	170 (30.7)	31 (29.5)
Age			
18 - 41	8 (16.3)	152 (27.5)	22 (21.0)
42 - 55	14 (28.6)	146 (26.4)	29 (27.6)
56 - 65	16 (32.7)	133 (24.1)	17 (16.2)
66 – 93	11 (22.4)	122 (22.1)	37 (35.2)
Age			
≤ 65	38 (77.6)	431 (77.9)	68 (64.8)
> 65	11 (22.4)	122 (22.1)	37 (35.2)
Race/Ethnicity *N = 698*			
White	26 (56.5)	299 (54.7)	58 (55.2)
Asian	6 (13.0)	105 (19.2)	11 (10.5)
Other	14 (30.4)	143 (26.1)	36 (34.3)
Insurance *N = 694*			
Private	22 (45.8)	310 (57.2)	46 (44.2)
Government	26 (54.2)	232 (42.8)	58 (55.8)

APPENDIX H

Univariate analysis between patients who never returned for follow-up, patients who returned at their first follow-up, and patients who returned at a later follow-up:

	Attendance Ever			Statistical Analysis	
	Never returned N = 49	**Returned at 1st follow-up N = 553**	**Returned at later follow-up N = 105**		
Variable *N = 707 unless otherwise specified*	**N (%)**	**N (%)**	**N (%)**	**χ2 (d.f.)**	**p-value**
Cohort					
Pre-telemedicine	35 (71.4)	325 (58.8)	89 (84.8)	27.15 (2)	< 0.001
Telemedicine	14 (28.6)	228 (41.2)	16 (15.2)		
Age					
≤ 65	38 (77.6)	431 (77.9)	68 (64.8)	8.46 (2)	0.015
> 65	11 (22.4)	122 (22.1)	37 (35.2)		
Race/Ethnicity					
White	26 (56.5)	299 (54.7)	58 (55.2)	6.67 (4)	0.155
Asian	6 (13.0)	105 (19.2)	11 (10.5)		
Other	14 (30.4)	143 (26.1)	36 (34.3)		
Personal cancer history					
Yes	35 (71.4)	340 (61.5)	73 (69.5)	3.93 (2)	0.140
No	14 (28.6)	213 (38.5)	32 (30.5)		
Place of service					
CCC (Orange)	29 (59.2)	258 (46.7)	65 (61.9)	10.07 (2)	0.007
CDDC (Costa Mesa)	20 (40.8)	295 (53.3)	40 (38.1)		

No. of relatives w/ cancer 0 - 2 3 - 4 5 - 6 7 - 24	 15 (31.9) 15 (31.9) 7 (14.9) 10 (21.3)	 160 (29) 152 (27.6) 108 (19.6) 131 (23.8)	 34 (32.7) 32 (30.8) 17 (16.3) 21 (20.2)	 2.47 (6)	 0.872 Test of linear association: $\chi 2$ (1) = 0.26, p = 0.607
No. of days to report 5- 14 15 - 21 22 - 35 36+	 10 (29.4) 13 (38.2) 4 (11.8) 7 (20.6)	 144 (26.7) 131 (24.3) 131 (24.3) 133 (24.7)	 38 (37.3) 24 (23.5) 16 (15.7) 24 (23.5)	 10.84 (6)	 0.093 Test of linear association: $\chi 2$ (1) = 0.71, p = 0.400

APPENDIX I

MODEL 1: BINARY LOGISTIC REGRESSION. Variables that were significant in the logistic regression for first follow-up attendance were then incorporated into regression analysis comparing **those who never returned** for follow-up to **those who returned at a later visit**.

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort							
Pre-telemedicine *(reference)*							
Telemedicine	-0.518	0.552	1	0.348	0.596	0.202	1.757
Age							
≤ 65 *(reference)*							
> 65	0.915	0.523	1	0.080	2.496	0.895	6.957
Race/Ethnicity							
White *(reference)*			2	0.522			
Asian	0.014	0.755	1	0.985	1.015	0.231	4.457
Other	0.541	0.480	1	0.260	1.717	0.670	4.399
Personal cancer history							
Yes *(reference)*							
No	0.114	0.492	1	0.816	1.121	0.428	2.938
Number of relatives with cancer	0.074	0.078	1	0.347	1.076	0.923	1.254
Place of service							
CCC (Orange, CA) *(reference)*							
CDDC (Costa Mesa, CA)	-0.340	0.454	1	0.454	0.712	0.292	1.733
Days from initial visit to report	0.008	0.006	1	0.219	1.008	0.995	1.020

Outcome: 0 = never returned for follow-up
1 = returned at a later visit

MODEL 2: BINARY LOGISTIC REGRESSION.

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort Pre-telemedicine *(reference)* Telemedicine	-0.681	0.529	1	0.198	0.506	0.180	1.428
Age ≤ 65 *(reference)* > 65	0.837	0.507	1	0.099	2.309	0.855	6.241
No. of relatives w/ cancer	0.087	0.076	1	0.252	1.091	0.940	1.266
Days from initial visit to report	0.007	0.006	1	0.245	1.007	0.995	1.020

Outcome: 0 = never returned for follow-up
1 = returned at a later visit

MODEL 3: BINARY LOGISTIC REGRESSION.

Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
						Lower	Upper
Cohort Pre-telemedicine *(reference)* Telemedicine	-0.756	0.420	1	0.072	0.469	0.206	1.070
Age ≤ 65 *(reference)* > 65	0.585	0.403	1	0.147	1.795	0.815	3.953

Outcome: 0 = never returned for follow-up
1 = returned at a later visit

APPENDIX J

Distribution of sample size across 3 outcomes: never returned for follow-up, returned at first follow-up, returned at a later follow-up:

	Outcome	**N**	**Valid Percentage**
Variable: Attend Overall	Never returned for follow-up	49	6.9%
	Returned to 1st follow-up	553	78.2%
	Returned at later follow-up	105	14.9%
Total		707	100%
	EXCLUDED: No follow-up scheduled	*93*	
Total		800	

APPENDIX K

MODEL 1: MULTIVARIATE LOGISTIC REGRESSION - MULTINOMIAL. Including all variables that were included in the final binary logistic regression model for first follow-up visit

	Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
							Lower	Upper
Returned to 1st follow-up	**Intercept**	1.651	0.424	1	< 0.001			
	Cohort	0.795	0.444	1	0.073	2.215	0.928	5.285
	Age	0.320	0.471	1	0.497	1.377	0.547	3.464
	Race/Ethnicity	0.114	0.223	1	0.608	1.121	0.725	1.735
	Personal cancer history	0.340	0.426	1	0.424	1.406	0.610	3.236
	Number of relatives with cancer	0.129	0.073	1	0.079	1.137	0.985	1.313
	Place of service	0.228	0.381	1	0.549	1.257	0.595	2.652
	Days from initial visit to report	0.001	0.004	1	0.870	1.001	0.992	1.009
	Variable	**B**	**S.E.**	**d.f.**	**Sig.**	**Exp(B)**	**95% C.I. for Exp(B)**	
							Lower	**Upper**
Returned at a later follow-up	**Intercept**	0.359	0.471	1	0.447			
	Cohort	-0.628	0.522	1	0.229	0.533	0.192	1.484
	Age	0.893	0.505	1	0.077	2.442	0.908	6.568
	Race/Ethnicity	0.246	0.245	1	0.317	1.279	0.790	2.068
	Personal cancer history	0.047	0.472	1	0.921	1.048	0.415	2.645
	Number of relatives with cancer	0.103	0.079	1	0.191	1.108	0.950	1.293
	Place of service	-0.134	0.426	1	0.753	0.874	0.379	2.016
	Days from initial visit to report	0.004	0.004	1	0.302	1.004	0.996	1.013

MODEL 2: MULTIVARIATE LOGISTIC REGRESSION - MULTINOMIAL

	Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
							Lower	Upper
Returned to 1st follow-up	**Intercept**	1.812	0.397	1	< 0.001			
	Cohort	0.836	0.431	1	0.052	2.308	0.992	5.369
	Age	0.283	0.469	1	0.546	1.327	0.529	3.328
	Race/Ethnicity	0.104	0.222	1	0.640	1.110	0.717	1.716
	Number of relatives with cancer	0.145	0.071	1	0.043	1.156	1.005	1.330
	Days from initial visit to report	0.001	0.004	1	0.853	1.001	0.992	1.009
	Variable	**B**	**S.E.**	**d.f.**	**Sig.**	**Exp(B)**	**95% C.I. for Exp(B)**	
							Lower	**Upper**
Returned at a later follow-up	**Intercept**	0.299	0.44	1	-0.501			
	Cohort	-0.651	0.508	1	0.200	0.521	0.192	1.412
	Age	0.892	0.503	1	0.076	2.439	0.910	6.535
	Race/Ethnicity	0.235	0.245	1	0.338	1.265	0.782	2.045
	Number of relatives with cancer	0.110	0.077	1	0.152	1.117	0.960	1.298
	Days from initial visit to report	0.005	0.004	1	0.299	1.005	0.996	1.013

MODEL 3: MULTIVARIATE LOGISTIC REGRESSION - MULTINOMIAL

	Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
							Lower	Upper
Returned to 1st follow-up	**Intercept**	2.006	0.298	1	<0.001			
	Cohort	0.542	0.332	1	0.103	1.719	0.897	3.295
	Age	-0.045	0.361	1	0.900	0.956	0.471	1.940
	Number of relatives with cancer	0.0641	0.051	1	0.211	1.066	0.964	1.179
	Variable	**B**	**S.E.**	**d.f.**	**Sig.**	**Exp(B)**	**95% C.I. for Exp(B)**	
							Lower	**Upper**
Returned at later follow-up	**Intercept**	0.705	0.342	1	0.039			
	Cohort	-0.819	0.421	1	0.052	0.441	0.193	1.005
	Age	0.580	0.402	1	0.149	1.787	0.812	3.931
	Number of relatives with cancer	0.024	0.058	1	0.680	1.024	0.914	1.149

MODEL 4: MULTIVARIATE LOGISTIC REGRESSION - MULTINOMIAL

	Variable	B	S.E.	d.f.	Sig.	Exp(B)	95% C.I. for Exp(B)	
							Lower	Upper
Returned to 1st follow-up	**Intercept**	2.228	0.178	1	<0.001			
	Cohort	0.562	0.328	1	0.087	1.754	0.922	3.334
	Variable	**B**	**S.E.**	**d.f.**	**Sig.**	**Exp(B)**	**95% C.I. for Exp(B)**	
							Lower	**Upper**
Returned at later follow-up	**Intercept**	0.933	0.200	1	<0.001			
	Cohort	-0.800	0.417	1	0.055	0.449	0.199	1.017