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Evaluating the effectiveness of outreach efforts and testing workflow on genetic testing participation in a high-risk population

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Introduction: Genetic testing enables precision medicine by improving disease risk awareness, prevention, and treatment. Despite national guidelines, fewer than 20% of eligible US patients with a personal or family history of breast or ovarian cancer undergo testing, with notable disparities by race, age, and insurance. Population-scale programs and point-of-care strategies, such as risk assessments during mammography, aim to address these gaps. This study evaluates the effectiveness of three outreach methods and clinic workflow variations on genetic testing participation among high-risk patients.

Methods: The study was conducted at eight Providence Health and Services clinics in California. To evaluate the effectiveness of three outreach methods on genetic testing participation, high-risk patients were randomized to receive one of three methods: mailed brochure, email, and SMS text message. The effectiveness of two workflows was assessed retrospectively, comparing genetic testing among patients who were offered testing in the same building to those who were required to go to a different building. Descriptive and regression analyses were used to examine associations between outreach and workflow and test order rates. A stratified analysis by workflow was used to further examine associations between patient characteristics and genetic testing.

Results: A total of 7,112 patients received outreach methods, and 16,965 were included in the retrospective analysis by workflow. Overall, genetic testing following outreach was low, less than 3%, and did not differ by outreach method. The different building workflow was associated with a lower order rate than the same building workflow (IRR = 0.72, 95% CI = 0.65–0.80). The differences in order rates by patient characteristics were larger in the different building workflow.

Conclusion: The findings suggest that while outreach yields low engagement, low-cost methods such as email are feasible, and point-of-care access is critical for improving participation and equity. Health systems should prioritize same-day testing and provider capacity to expand access and reduce barriers.

KEYWORDS
genetic testing, high-risk population, location, outreach, participation, routine care, workflow

1 Introduction

Genetic testing can transform health care through personalized delivery of care and information, also referred to as precision medicine (1). This approach aims to increase the awareness of disease risk and improve disease prevention and early detection. Genetic testing can also inform treatment once a disease is present; an estimated 10% of breast cancers and 15% of ovarian cancers are attributable to hereditable mutations, and identifying which patients have these mutations can help tailor cancer therapies. Even though there are established national guidelines for hereditary cancer risk assessment and genetic testing, less than one in five patients with a personal or family history of breast and ovarian cancer meeting the National Comprehensive Cancer Network (NCCN) Guidelines have undergone cancer genetic testing in the United States. This translates to 1.2–1.3 million women in the United States who are eligible but have not received genetic testing (2). Among women with a family history of breast or ovarian cancer, but without a previous diagnosis, an estimated 3.6% had genetic testing completed (3).

Previous studies have demonstrated underutilization of and disparities in genetic testing by patient characteristics, such as race, age, education, and insurance coverage (4–6). In fact, a recent article from the Centers of Disease Control calls for equity in the implementation of genomics and precision medicine to be a public health imperative to prevent widening of health disparities in the coming decades (7).

Novel genetics service delivery models, such as population-scale genetic testing programs, may help bridge these gaps and improve the identification of high-risk, but otherwise healthy, patients (1). For example, one potential workflow is to conduct cancer risk assessments during routine mammograms, thereby reaching patients at point of care (4). As the implementation of cancer risk assessment and subsequent genetic testing tools begins to expand outside of specialty genetics clinics, it is critical to understand which processes are most effective in connecting patients to the testing and care they need.

Outreach is often the first method of engagement to provide eligible participants with educational information about genetic testing. Previous studies have employed a variety of methods of outreach for recruitment, though which is the most effective is still largely inconclusive (8, 9). How best to integrate genetic testing into more routine care is a priority area for research as well (10, 11). More research is needed to understand how to best integrate testing in order to successfully lower barriers and increase the likelihood of eligible patients completing genetic testing and receiving the best-informed care. Then, once a patient has engaged, it is important to identify the workflows that are most effective as well as accessible.

Providence Health and Services offers a population-scale cancer genetics risk assessment and screening program that engages patients in preventive care settings such as mammography. The program leverages technology such as the Ambry CARE platform to enable risk assessment electronically at scale, and develops and supports clinical workflows that extend the reach of genetics services. Importantly, the program serves a diverse patient population across eight clinics; this makes it an ideal learning system as many previous genomics programs have been conducted in populations of predominantly European ancestry (1, 10, 12). As there may be differential disease prevalence, risks, and/or treatments for individuals of different ethnic backgrounds, genomics programs must have effective methods of engaging diverse individuals to best understand these differences and optimize care for all. In the population-scale cancer risk assessment program pilot fewer than 20% of eligible patients ended up completing genetic testing. To better understand how to increase participation in genetic testing among high-risk patients, we studied how variations in outreach and the genetic test workflow influence uptake in this real-world setting. The objectives of this study were: (1) to examine the effectiveness of three outreach methods on genetic testing participation among eligible patients, and (2) to explore the effectiveness of genetic testing workflows on participation rates.

2 Methods and materials

2.1 Study setting

The study was conducted among patients with mammogram appointments at eight Providence Health and Services clinics in California. Clinics were characterized by different patient populations, regions of California, size, and number of years offering the population-scale cancer risk assessment program. The clinics were all participating in the Providence population-scale cancer risk assessment program and at the time of this study all utilized the Ambry CARE platform for the electronic risk assessment (13). Briefly, the program included clinic staff sending patients the CARE electronic risk assessment survey following NCCN guidelines prior to their mammogram appointment (14). Pre-test genetic counseling was not routinely conducted. Patients received pre-test educational materials, including an educational video, and provided informed consent before testing. After completing the electronic assessment, patients who were evaluated as having high risk for hereditary cancer were informed that they were eligible for the genetic testing panel and genetic counseling from Providence genetic counselors. The genetic counselors oversaw all patients who completed testing, reviewed personal and family history, and evaluated results. Post-test genetic counseling was recommended for patients with strong family histories, positive results, or other findings where additional discussion was appropriate. These patients were encouraged to return for follow-up counseling. Patients could follow a link to more information about testing and the consent process. They could also electronically opt out of the test. At the mammogram encounter, mammography technician staff offered eligible patients informational handouts about the genetic testing option and confirmed the patient's decision about testing. Staff gave interested patients information about how and where to complete the test (see workflow in Section 2.3). The genetic test offered was a large multigene pan-cancer hereditary cancer panel. To have a genetic test ordered, first an eligible patient expressed interest in genetic testing, then the patient completed the consent for the test, and finally program staff ordered a test for the patient. To be succinct, this process of staff ordering a genetic test on behalf of the patient is referred to as "ordered" throughout the paper. The eight clinics use either blood or saliva collection methods, and one clinic offers a choice of in-office blood collection or a saliva collection kit. We did not observe a significant impact of collection method on order rate (data not shown).

2.2 Population and design

The study population was drawn from adult patients at participating clinics who had a mammography appointment in 2023 and 2024, and who were identified as high-risk for hereditary cancer per NCCN guidelines through the pre-appointment screening and for whom clinic staff found no definitive record of previous genetic testing in patient's electronic health record (EHR).

For objective 1, which was prospective, the outreach attempts began in July 2024 and test orders were assessed following outreach. Patients were eligible for outreach if they met the above criteria, had a mammogram appointment in 2024, did not formally agree to testing at the time of their visit, and had not electronically opted out of testing. Objective 2 was conducted retrospectively starting in mid-2025. Appointment records and testing outcomes for patients meeting the above criteria with mammography appointments in 2023 and 2024 were reviewed and analyzed after all appointments had occurred and opportunities for testing were complete. The objective 2 population is inclusive of the objective 1 population. Supplementary Figure 1 outlines the populations, activities, and exclusion criteria.

Many patients had more than one appointment in the study window; we included a single encounter per patient in the population. Due to population overlap with the outreach objective, we selected each patient's most recent encounter for analysis in objective 2 unless an earlier encounter within the study period resulted in a genetic test being ordered. For objective 2, the workflow a patient experienced was based on which clinic they attended for their mammogram.

2.3 Outreach and workflow

Each patient in objective 1 was assigned to one of three outreach groups: SMS text, email, or mailed brochure. The outreach materials for the three groups can be found in the Supplementary material. The outreach materials were developed by the study team and reviewed by Providence program staff for content. The materials were designed for readability at fifth-grade level. Patients were randomly distributed among the three groups by appointment month and clinic, although due to cost constraints associated with mailing, the mailed brochure group was assigned fewer overall participants. Data for patient contact was incomplete for a handful of patients; if patient was assigned to an outreach method and missing the necessary contact information, the patient was reassigned to another outreach group. Outreach occurred in three waves in 2024 and early 2025; each patient received one outreach attempt. The amount of time between a patient's mammography appointment and outreach varied between one and seven months. Outreach materials and messaging were offered in English and Spanish, based on language selected for the pre-appointment assessment. Very few patients had a language besides English or Spanish listed in the data, which is why materials were not further translated. The eligible patients with assessment language other than English or Spanish were sent English language outreach materials. The outreach message content included a reminder that the patient was told at their last mammogram appointment that they were at high risk for hereditary cancer, they were again invited to receive genetic testing and given a number to call to pursue the opportunity.

In objective two, each of the eight clinics followed one of two workflows for delivering genetic testing to patients. One workflow provided genetic testing in the same building, and in some cases the same room as where the patient received their mammogram. Patients had the option to schedule a follow-up return for the sample collection if they preferred not to do the collection following their mammogram. This workflow was implemented by five of the eight clinics. The second workflow required patients to go to a different building to receive their genetic testing following their mammogram appointment. Patients did not need to make an additional appointment in this workflow but did have to go to a different location. Three of the eight clinics implemented this workflow. The variation in genetic testing location occurred naturally across clinics, and the implementing partners were interested in understanding whether going to a different building influenced uptake to guide decisions about scaling and expansion.

2.4 Data collection

The mammogram appointment date, genetic test order status, patient contact information, and patient-reported demographics data were sourced from the data portal of the genetic testing provider and CARE risk assessment platform, Ambry. Patient demographics, including language, age, race, and ethnicity, were derived from the patient response to the pre-appointment screening. The patients' insurance payor for the mammogram appointment was derived from Providence EHRs and matched using their individual medical record number and appointment date. Previous genetic testing was used as an exclusion criterion for the study population and was assessed by clinic staff from patient's EHR record.

2.5 Analysis

The outcome for both objectives was whether program/clinic staff ordered a genetic test for the patient—referred to as "ordered" or "order rate." Ninety-four percent of the patient population with an ordered test had a completed test result. In the data, we could not determine the reason for incomplete tests (i.e., whether it was a lab error or a patient changing their mind at a later date), and therefore we defined the primary outcome as an ordered test to reflect the patient's consent for and intention to participate in testing. To examine the effectiveness of outreach and test workflow across the breadth of our patient population, we included age at mammogram appointment, language, race/ethnicity, and insurance payor as additional factors in our frequency tables and covariates in our analyses. Patient age was categorized into five categories: 18–39, 40–45, 46–55, 56–65, and 66 years and older. Due to small numbers, languages other than English were combined, and "another" race and "multiple" races were combined into a single category for analysis. The five final race/ethnicity categories in the analysis were White non-Hispanic, Hispanic, Black, Asian, and another/multiple. Commercial, military, and worker's compensation were grouped into commercial/other insurance.

To handle missing demographic data, we first tested for an association between having a missing demographic variable and order rate for both objectives. The association was not significant for either objective, so we excluded patients with incomplete demographics from our analytic populations. This excluded fewer than 5% of patients from the eligible pool for both objectives.

For objective 1, we summarized and compared the characteristics of the population for each outreach method. We investigated the association of outreach method and demographic covariates on order rate using frequency tables and Pearson's chi-square test, and visually represented the outreach timing and the association with order rate using a histogram.

For objective 2, we first summarized the population demographics by testing workflow. Then we described the order rate by workflow and by patient demographics using Pearson's chi-square test for significant associations with order rate. To quantify the association between method and order status independent of demographic covariates we conducted a multivariable regression using a modified Poisson regression to estimate incidence risk ratio. We next investigated the demographic variable associations with order rate within populations stratified by testing location workflow using Pearson's chi-square test. We created a bar chart showing rate per clinic with 95% confidence interval bars. Figures were created using the ggplot2 package and analyses were conducted using R version 4.2.2 (15, 16).

3 Results

3.1 Outreach methods

A total of 7,112 patients were contacted using one of the three outreach methods. Table 1 presents the characteristics of patients in the three outreach groups. As the sample was designed, there are no differences between the groups by age, race/ethnicity, assessment language, and insurance payor. Overall, the majority were White non-Hispanic, English speaking, and had commercial insurance coverage.

Overall, the proportion of patients for whom a genetic test was ordered following outreach was low, less than 3%, and the rate did not differ by outreach method. A greater proportion of patients aged 45 or younger received genetic testing following outreach (4.4%—4.5%) compared to the other age groups (all < 2.5%). Those who pursued genetic testing on average received

TABLE 1 Characteristics of outreach groups.

Characteristic	Overall, $N = 7,112$	Brochure, $N = 932$	Email, $N = 3,153$	SMS, $N = 3,027$	p-value
Age					0.84
18–39	290 (4.1%)	34 (3.6%)	122 (3.9%)	134 (4.4%)	
40–45	885 (12%)	115 (12%)	392 (12%)	378 (12%)	
46–55	1,699 (24%)	238 (26%)	742 (24%)	719 (24%)	
56–65	1,864 (26%)	242 (26%)	820 (26%)	802 (26%)	
66+	2,374 (33%)	303 (33%)	1,077 (34%)	994 (33%)	
Assessment language					0.14
English	7,009 (99%)	923 (99%)	3,112 (99%)	2,974 (98%)	
Not English	103 (1.4%)	9 (1.0%)	41 (1.3%)	53 (1.8%)	
Race/ethnicity					0.26
Another/multiple	344 (4.8%)	39 (4.2%)	146 (4.6%)	159 (5.3%)	
Asian	934 (13%)	118 (13%)	444 (14%)	372 (12%)	
Black	198 (2.8%)	30 (3.2%)	88 (2.8%)	80 (2.6%)	
Hispanic	1,403 (20%)	171 (18%)	609 (19%)	623 (21%)	
White non-hispanic	4,233 (60%)	574 (62%)	1,866 (59%)	1,793 (59%)	
Payor					0.60
Commercial/other	5,392 (76%)	700 (75%)	2,370 (75%)	2,322 (77%)	
Medicaid	269 (3.8%)	34 (3.6%)	120 (3.8%)	115 (3.8%)	
Medicare	1,451 (20%)	198 (21%)	663 (21%)	590 (19%)	
Appointment to outreach (days)	108 (45)	110 (44)	108 (45)	107 (45)	0.10

Values are expressed as n (col %) for categorical variables and mean ± SD, for appointment to outreach. P-values are from chi-squared tests.

outreach closer to their appointment than those who did not ($\mu_{ordered} = 98$ days vs. $\mu_{notordered} = 107$ days, $p < 0.003$) (Table 2; Supplementary Figure 2).

3.2 Workflow

A total of 16,965 patients were included in the objective 2 analysis, which examined the association between genetic testing workflow and the rate of genetic tests ordered among a population screened to be high risk for hereditary cancer. The populations across the two testing location workflows differed significantly by age, race/ethnicity, assessment language, and insurance payor (Table 3).

The overall genetic test order rate in this high-risk population was 11.7%. The "same building" workflow was associated with higher order rates than the "different building" workflow (13% vs. 9%, $p < 0.001$, Table 4). Order was inversely associated with age, with higher order rates corresponding to lower ages. Although they represent a small percentage of the population, non-English speakers were overall less likely to order a test than English speakers (12% English vs. 6.8% non-English, $p < 0.05$). There was little difference in order rate between patients insured through Medicaid and insured through commercial or other insurance (11% vs. 12%), while Medicare was associated with lower rates (9%). Order rate did vary by race/ethnicity, with patients who were Hispanic (13%) and another/multiple races (16%) having the highest order rates and patients who were White (12%), Asian (10%), and Black (11%) having the lowest order rates. There was a significant difference in the proportion of patients who pursued genetic testing between clinics within workflow; one clinic in each of the two workflows had either significantly higher or lower order rates compared to the other clinics in the same workflow (Supplementary Figure 3).

In the multivariable regression, patients in the "same building" workflow group had a 28% higher rate of genetic testing orders compared to those in the "different building" workflow (IRR = 0.72; 95% CI: 0.65, 0.80), after adjusting for patient demographics (Table 5). Age remained inversely correlated with order rate after adjusting for workflow and demographic covariates. Individuals of Asian race/ethnicity had a 20% lower order rate compared to individuals who were White non-Hispanic, and individuals using a language other than English in the assessment had a 44% lower order rate than those using English.

We further examined associations between population characteristics and order rate within each testing workflow (Table 6). In both workflows, a greater proportion of adults under 45 years of age had tests ordered than older adults. However, patients between the ages of 18 and 39 were less likely to have a test ordered in the "different building" method than those in the 40–45 year old group (11% vs. 15%). There were greater differences among language and race/ethnicity levels in the "different building" group, with particularly low order rates associated with patients using a language other than English (0%) and individuals identifying as Black or Asian (2.3% and 6.5%, respectively).

4 Discussion

This study examined the effectiveness of outreach methods and workflows on genetic testing participation among high-risk mammography patients. The results showed that outreach to patients who had neither explicitly declined nor pursued genetic testing within a month or more after their appointment resulted in a modest 3% test order rate. There was no difference between outreach methods. The study found that offering genetic testing in the same building was associated with a significantly higher order rate compared to the testing workflow in a different building.

Overall, the percent of patients who pursued genetic testing following all three outreach methods was relatively low. Another study examined the effectiveness of the three similar outreach methods to recruit patients into a population-scale whole genome sequencing research program, Geno4ME (8). The Geno4ME program found that outreach resulted in 7.5% enrollment in the

TABLE 2 Rate of ordering by population characteristic (row percentages).

Characteristic	Ordered, $N = 196$	Not ordered, $N = 6,916$	p-value
Outreach method			0.65
Brochure	30 (3.2%)	902 (97%)	
Email	84 (2.7%)	3,069 (97%)	
SMS	82 (2.7%)	2,945 (97%)	
Appointment to outreach (days)	98 (43)	107 (43)	0.003
Age			0.0045
18–39	13 (4.5%)	277 (96%)	
40–45	39 (4.4%)	846 (96%)	
46–55	45 (2.6%)	1,654 (97%)	
56–65	44 (2.4%)	1,820 (98%)	
66+	55 (2.3%)	2,319 (98%)	
Assessment language			0.12
English	196 (2.8%)	6,813 (97%)	
Not English	0 (0%)	103 (100%)	
Race/ethnicity			0.38
Another/multiple	13 (3.8%)	331 (96%)	
Asian	32 (3.4%)	902 (97%)	
Black	6 (3.0%)	192 (97%)	
Hispanic	40 (2.9%)	1,363 (97%)	
White non-Hispanic	105 (2.5%)	4,128 (98%)	
Payor			0.11
Commercial/other	161 (3.0%)	5,231 (97%)	
Medicaid	5 (1.9%)	264 (98%)	
Medicare	30 (2.1%)	1,421 (98%)	

Values are expressed as n (row %) for categorical variables and mean ± SD for appointment to outreach. P-values are from independent t-tests (continuous variables) or chi-squared test (categorical variables).

TABLE 3 Characteristics of population offered genetic testing, by testing workflow.

Characteristic	Overall, $N = 16,965$	Same building, $N = 12,142$	Different building $N = 4,823$	*p*-value
Age group				<0.001
18–39	804 (4.7%)	637 (5.2%)	167 (3.5%)	
40–45	2,192 (13%)	1,676 (14%)	516 (11%)	
46–55	4,209 (25%)	3,127 (26%)	1,082 (22%)	
56–65	4,490 (26%)	3,157 (26%)	1,333 (28%)	
66+	5,270 (31%)	3,545 (29%)	1,725 (36%)	
Assessment language				0.004
English	16,788 (99%)	12,000 (99%)	4,788 (99%)	
Not English	177 (1.0%)	142 (1.2%)	35 (0.7%)	
Race/ethnicity				<0.001
Another/multiple	425 (2.5%)	334 (2.8%)	91 (1.9%)	
Asian	2,383 (14%)	1,953 (16%)	430 (8.9%)	
Black	648 (3.8%)	605 (5.0%)	43 (0.9%)	
Hispanic	2,837 (17%)	2,327 (19%)	510 (11%)	
White non-Hispanic	10,672 (63%)	6,923 (57%)	3,749 (78%)	
Payor				<0.001
Commercial/other	12,841 (76%)	9,364 (77%)	3,477 (72%)	
Medicaid	550 (3.2%)	356 (2.9%)	194 (4.0%)	
Medicare	3,574 (21%)	2,422 (20%)	1,152 (24%)	

Values are expressed as *n* (col %). *P*-values are from chi-squared tests.

program, and of those who enrolled, approximately 70% completed an at-home DNA kit (8). This enrollment was slightly higher than our order rate following outreach, which was approximately 3%. We expected higher engagement in the present study because it focused on a high-risk population and the outreach was performed as follow-up after they were notified of their eligibility during their appointment. In contrast, Geno4ME outreach occurred in the general population, and while they were engaged in care at the health system, the outreach was a cold contact for participation in a research study. There were other key differences that could explain the discrepancy. For example, Geno4ME was offered free of charge, whereas our population was offered genetic testing as part of clinical care, which includes insurance billing and may have costs associated. The associated cost is a possible contributing factor the lower participation in our population compared to the free test population. Additionally, the Geno4ME approach included multiple outreach attempts, whereas in our study there was only one outreach attempt, which may contribute to the slightly higher response in the Geno4ME population. Other qualitative studies found that repetition was helpful in encouraging patients to receive testing (17, 18).

While we show only modest engagement following the three different outreach methods, we found that all methods resulted in comparable uptake of genetic testing. The Geno4ME study mentioned above that examined the same outreach methods for recruitment to genetic testing also saw minimal differences in their effectiveness (8). In the general Geno4ME population, 7.8% of those who received a brochure plus email and SMS text enrolled, which was similar to the 7.3% who enrolled after only receiving digital outreach (email and SMS). This is similar to our study, but in our more select population (individuals with personal and/or family history of cancer), we saw no discernible difference between the three outreach methods. We did, however, find that fewer days between the appointment and outreach resulted in slightly greater participation in testing. If facilities or health systems with similar populations to our study population wish to conduct outreach with their high-risk populations, our findings suggest they should use whichever of the three methods is the most feasible, based on time and cost, to implement, as there was no difference in participation between the outreach methods. While uptake was low following outreach, the low-cost options such as email may present an easily accessible option for health systems to support at least some increased engagement, and our findings suggest improved engagement when reaching out to patients shortly after their appointment. Due to the low engagement following outreach, we were unable to stratify our results by outreach approach to understand if there was variability in effectiveness for different demographics but, overall, following receipt of outreach, there were no differences in testing uptake by race and ethnicity or language selected for the assessment.

Participation in genetic testing was higher in the workflow where the testing was offered at the same building as the mammogram compared to when testing was located in another building. Another study in a NCCN-defined high-risk population

TABLE 4 Genetic testing order rate by workflow and demographics ($N = 16{,}965$).

Characteristic	Ordered, $N = 1{,}983$	Not ordered, $N = 14{,}982$	p-value
Workflow			<0.001
Same building	1,550 (13%)	10,592 (87%)	
Different building	433 (9%)	4,390 (91%)	
Age group			<0.001
18–39	163 (20%)	641 (80%)	
40–45	380 (17%)	1,812 (83%)	
46–55	519 (12%)	3,690 (88%)	
56–65	475 (11%)	4,015 (89%)	
66+	446 (8%)	4,824 (92%)	
Assessment language			0.041
English	1,971 (12%)	14,817 (88%)	
Not English	12 (7%)	165 (93%)	
Race/Ethnicity			0.002
Another/multiple	68 (16%)	357 (84%)	
Asian	241 (10%)	2,142 (90%)	
Black	73 (11%)	575 (89%)	
Hispanic	361 (13%)	2,476 (87%)	
White non-Hispanic	1,240 (12%)	9,432 (88%)	
Payor			<0.001
Commercial/other	1,594 (12%)	11,247 (88%)	
Medicaid	60 (11%)	490 (89%)	
Medicare	329 (9%)	3,245 (91%)	

Values are expressed as *n* (row %). *P*-values are from chi-squared tests.

observed the same trend; patients attending clinics with "point-of-care" testing, which offer patients tests at the clinic on the same day (or a later date, if preferred) had genetic testing rates double of those who were referred out and had to make an appointment with another provider (19). This magnitude of difference is greater than what we saw in our study, which may be partially explained by the fact that in our study, the patients that had to go to another building for testing did not have to call and schedule an appointment, which may lower the barrier to entry and attenuate the difference between the two groups. In Wang et al. and Brabender et al., 35% and 50.1% of point-of-care testing patients completed genetic testing, respectively, which is much greater than our order rate of 13% in the same building group (19, 20). The three study populations are high-risk, as defined by NCCN, but other differences in patient demographics or provider and clinic factors may have contributed to this difference. The order rates in our study are closer to the 15% order rate in a qualitative study in a similar Southern California Providence-based population (17) and a 15.3% order rate pooling 3 years of the National Health Interview Survey (2).

There was variation by clinic in the percentage ordered both within and between workflow (Supplementary Figure 3). One clinic offering testing in the same building had a substantially lower order rate than the other four, and one "different building" clinic had a much higher order rate than the other two. It is likely that clinic and provider characteristics play an important role in the order rates at the study clinics. Other qualitative studies have shown that a provider's ability to communicate clearly and provide the information on genetic testing plays a significant role in a patient's decision and motivation to complete genetic testing (6, 10, 17). Furthermore, having a trusted provider, for example a primary care provider, that the patient sees regularly vs. a new mammogram technician recommend testing has also been shown to been a factor in completing genetic testing (6, 17, 21).

Our analysis of order rate showed a strong and consistent correlation with age, which is similar to other studies of decision to participate in genetic testing among patients who have been identified as high risk and/or with a history of breast and ovarian cancer (19, 22, 23). Patients in our youngest age group [18–39] had the highest genetic test order rates. They are below the typical recommended age for mammograms in the general population (24), so their indication for mammography (such as family history of breast cancer under age 40 or physical symptoms like a mass or breast changes) may heighten their awareness of risk and influence their willingness to participate in genetic testing compared to the rest of the population. In healthy populations, previous studies have not found a relationship between age and genetic testing (6, 25).

In the stratified analysis by workflow there were variations in the percent of genetic tests ordered by patient characteristics. In the clinics that required patients to go to another building, there were significant differences in ordering by language selected for their assessment and by race and ethnicity. Although the numbers are small, the stratified analysis showed that none of the patients who selected a language other than English had a genetic test ordered if they had to go to another building to receive it, whereas there was no difference in ordering by assessment language for those who could receive testing at the same building. Black or Asian patients had much lower order rates than patients of other race and ethnicities at the clinics where they had to go elsewhere for testing, compared to "same building" clinics where they are within a percentage point or two of both Hispanic and White non-Hispanic patients. Another study in a high-risk population also found that Black patients were less likely to complete genetic testing if they were referred elsewhere, but this was not the case if offered testing at the point of care (26). These populations have been found to face additional barriers to care generally and genetic testing specifically, including receiving care in their preferred language, mistrust in providers, and other system-level access inequities (6, 27). Additionally, a lower percentage of younger patients ordered a genetic test when they had to go elsewhere for a test, compared to the overall sample and those who received testing in the same building. The findings suggest that providing testing at the same building lowers barriers to testing and provides testing more equitably.

The study had several limitations. First, while the testing workflow was intended as a proxy for convenience and accessibility of the test, there are potentially unmeasured and important variations by clinic due to differential implementation, such as the capacity of staff to discuss genetic testing in the appointment (see Supplementary Figure 3). Due to the small number of clinics, we were unable to account for these facility-level differences and for

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TABLE 5 Univariate and multivariable regression on order status ($N = 16{,}965$).

Characteristic	Univariate			Multivariable		
	IRR	95% CI	*p*-value	IRR	95% CI	*p*-value
Workflow						
Same building	—	—		—	—	
Different building	0.70	0.63, 0.78	<0.001	0.72	0.65, 0.80	<0.001
Age group						
18–39	2.40	2.00, 2.86	<0.001	2.45	2.03, 2.96	<0.001
40–45	2.05	1.79, 2.35	<0.001	2.15	1.83, 2.51	<0.001
46–55	1.46	1.28, 1.65	<0.001	1.55	1.33, 1.80	<0.001
56–65	1.25	1.10, 1.42	<0.001	1.31	1.14, 1.52	<0.001
66+	—	—		—	—	
Assessment language						
English	—	—		—	—	
Not English	0.58	0.31, 0.97	0.058	0.56	0.32, 0.99	0.045
Race/ethnicity						
White non-Hispanic	—	—		—	—	
Another/multiple	1.38	1.07, 1.74	0.010	1.23	0.99, 1.54	0.06
Asian	0.87	0.76, 0.99	0.048	0.80	0.70, 0.91	0.001
Black	0.97	0.76, 1.22	0.80	0.93	0.74, 1.17	0.55
Hispanic	1.10	0.97, 1.23	0.13	0.97	0.87, 1.09	0.65
Payor						
Commercial/other	—	—		—	—	
Medicaid	0.88	0.67, 1.12	0.33	0.88	0.69, 1.14	0.33
Medicare	0.74	0.66, 0.83	<0.001	1.09	0.94, 1.26	0.27

IRR denotes the Incidence Rate Ratio for the outcome of order status, estimated using a modified Poisson regression with robust error variance. Multivariable models adjust for Workflow and all patient demographic covariates shown.

potential within-clinic patient similarities. For both objectives, the population was limited to those that had not received previous genetic testing, based on what program staff could identify in Providence system EHRs. A limitation of this approach was our inability to identify and exclude patients who may have received genetic testing elsewhere (i.e., other hospital systems). Consequently, our population may include individuals who have already been tested, potentially leading to an underestimation of our success rate due to an inflated denominator that includes those unlikely to pursue testing again. We were unable to see a patient's personal history of cancer in the data and were unable to account for this in the analysis. This is a limitation, as a personal history of cancer could influence a patient's decision to pursue genetic testing. Our study was conducted among patients who were identified as high risk for hereditary cancer using the NCCN guidelines. While the high-risk population is a critically important target for genetic testing, this may limit the generalizability of our findings to a more general, unselected population. A final limitation is that the CARE program cites the genetic test as being low cost and likely covered by insurance; however, the burden of both the cost and finding out details of coverage differ by patient, and our payor variable is an insufficient proxy for this barrier.

This study adds to the growing body of research on how to best implement and expand the reach of cancer genetic testing services outside of specialty clinical settings. Offering genetic testing in person and at the point of care resulted in the highest uptake, underscoring the importance of immediate access in promoting participation. While engagement was modest following outreach, all outreach methods performed comparably. Therefore, low-cost options, such as email, may provide an easy way for health systems to increase engagement. Future research could examine how different phrasing or language used to talk about genetic testing in outreach may influence uptake. Investing in provider and facility capacity to deliver same-day genetic testing services in the same location is essential. This includes equipping providers with the tools and training needed to effectively counsel patients on the benefits and purposes of genetic testing. Future research and evaluation should focus on identifying best practices for building provider and clinic capacity to provide point-of-care genetic testing in non-specialty settings. These efforts will not only expand access to genetic testing across the population but also promote equity by ensuring that eligible, at-risk groups can benefit, ultimately driving transformative improvements in public health outcomes.

TABLE 6 Genetic testing order rate by demographic characteristics, stratified by testing workflow ($N = 16,965$).

Characteristic	Same building			Different building		
	Ordered, $N = 1,550$	Not ordered, $N = 10,592$	p-value	Ordered, $N = 433$	Not ordered, $N = 4,390$	p-value
Age group			<0.001			<0.001
18–39	144 (23%)	493 (77%)		19 (11%)	148 (89%)	
40–45	304 (18%)	1,372 (82%)		76 (15%)	440 (85%)	
46–55	426 (14%)	2,701 (86%)		93 (8.6%)	989 (91%)	
56–65	356 (11%)	2,801 (89%)		119 (8.9%)	1,214 (91%)	
66+	320 (9.0%)	3,225 (91%)		126 (7.3%)	1,599 (93%)	
Assessment language			0.12			0.07
English	1,538 (13%)	10,462 (87%)		433 (9.0%)	4,355 (91%)	
Not English	12 (8.5%)	130 (92%)		0 (0%)	35 (100%)	
Race/ethnicity			0.04			0.011
Another/Multiple	52 (16%)	282 (84%)		16 (18%)	75 (82%)	
Asian	213 (11%)	1,740 (89%)		28 (6.5%)	402 (93%)	
Black	72 (12%)	533 (88%)		1 (2.3%)	42 (98%)	
Hispanic	313 (13%)	2,014 (87%)		48 (9.4%)	462 (91%)	
White non-Hispanic	900 (13%)	6,023 (87%)		340 (9.1%)	3,409 (91%)	
Payor			<0.001			0.23
Commercial/other	1,269 (14%)	8,095 (86%)		325 (9.3%)	3,152 (91%)	
Medicaid	41 (12%)	315 (88%)		19 (9.8%)	175 (90%)	
Medicare	240 (9.9%)	2,182 (90%)		89 (7.7%)	1,063 (92%)	

Values are expressed as n (row %). P-values are from chi-squared tests (among characteristic levels within workflow).

Data availability statement

The raw data supporting the conclusions of this article will be made available by the authors, without undue reservation.

Ethics statement

The studies involving humans were approved by the studies involving humans were approved by the Providence St. Joseph Health IRB (IRB approval #2024000036). The studies were conducted in accordance with the local legislation and institutional requirements. The studies were conducted in accordance with the local legislation and institutional requirements. Written informed consent for participation was not required from the participants or the participants' legal guardians/next of kin in accordance with the national legislation and institutional requirements.

Author contributions

LD: Formal analysis, Writing – original draft, Visualization, Methodology, Data curation, Investigation. EB: Methodology, Writing – original draft, Investigation. JR: Project administration, Writing – original draft, Investigation. KE: Funding acquisition, Conceptualization, Writing – review & editing. KC: Writing – review & editing. SB: Writing – review & editing. OG: Writing – review & editing. KV: Supervision, Conceptualization, Methodology, Writing – review & editing, Investigation, Funding acquisition.

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The author(s) declared that generative AI was not used in the creation of this manuscript.

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Supplementary material

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fcacs.2026.1765262/full#supplementary-material

DATASHEET 1
Outreach materials.

SUPPLEMENTARY FIGURE 1
Study population flowchart.

SUPPLEMENTARY FIGURE 2
Count of patients and percent of order by number of days between mammogram and outreach.

SUPPLEMENTARY FIGURE 3
Percent of order by clinic.

References

1. Lemke AA, Amendola LM, Thompson J, Dunnenberger HM, Kuchta K, Wang C, et al. Patient-reported outcomes and experiences with population genetic testing offered through a primary care network. *Genet Test Mol Biomarkers.* (2021) 25:152–60. doi: 10.1089/gtmb.2020.0275

2. Childers CP, Childers KK, Maggard-Gibbons M, Macinko J. National estimates of genetic testing in women with a history of breast or ovarian cancer. *J Clin Oncol.* (2017) 35:3800–6. doi: 10.1200/JCO.2017.73.6314

3. Han X, Jemal A. Recent Patterns in Genetic Testing for Breast and Ovarian Cancer Risk in the US. *Am J Prev Med.* (2017) 53:504–7. doi: 10.1016/j.amepre.2017.04.014

4. Anderson B, McLosky J, Wasilevich E, Lyon-Callo S, Duquette D, Copeland G. Barriers and facilitators for utilization of genetic counseling and risk assessment services in young female breast cancer survivors. *J Cancer Epidemiol.* (2012) 2012:298745. doi: 10.1155/2012/298745

5. Choi JJ, Fikre T, Fischman A, Buck AK, Ko NY. The role of race and insurance status in access to genetic counseling and testing among high-risk breast cancer patients. *Oncologist.* (2022) 27:832–8. doi: 10.1093/oncolo/oyac132

6. Shen EC, Sriniva S, Passero LE, Allen CG, Dixon M, Foss K, et al. Barriers and facilitators for population genetic screening in healthy populations: a systematic review. *Front Genet.* (2022) 13:865384. doi: 10.3389/fgene.2022.865384

7. Khoury MJ, Bowen S, Dotson WD, Drzymalla E, Green RF, Goldstein R, et al. Health equity in the implementation of genomics and precision medicine: a public health imperative. *Genet Med.* (2022) 24:1630–9. doi: 10.1016/j.gim.2022.04.009

8. Dickey L, Gronowski B, Jones K, Rinaldi JB, Emery K, Clemens J, et al. Participation in genetic screening: testing different outreach methods across a diverse hospital system based patient population. *Front Genet.* (2023) 14:1272931. doi: 10.3389/fgene.2023.1272931

9. Horowitz CR, Sabin T, Ramos M, Richardson LD, Hauser D, Robinson M, et al. Successful recruitment and retention of diverse participants in a genomics clinical trial: a good invitation to a great party. *Genet Med.* (2019) 21:2364–70. doi: 10.1038/s41436-019-0498-x

10. Dusic EJ, Theoryn T, Wang C, Swisher EM, Bowen DJ. Barriers, interventions, and recommendations: improving the genetic testing landscape. *Front Digit Health.* (2022) 4:961128. doi: 10.3389/fdgth.2022.961128

11. Guan Y, McBride CM, Rogers H, Zhao J, Allen CG, Escoffery C. Initiatives to scale up and expand reach of cancer genomic services outside of specialty clinical settings: a systematic review. *Am J Prev Med.* (2021) 60:e85–94. doi: 10.1016/j.amepre.2020.08.029

12. Carey DJ, Fetterolf SN, Davis FD, Faucett WA, Kirchner HL, Mirshahi U, et al. The Geisinger MyCode community health initiative: An electronic health record-linked biobank for precision medicine research. *Genet Med.* (2016) 18:906–13. doi: 10.1038/gim.2015.187

13. Fecteau H, Pfleger H, Nathan D, Siddiqui S, Horton C, Milliard C, et al. Validation of a digital tool that uses national testing guidelines to identify individuals at risk for hereditary cancer. *JNCCN.* (2025) 23:e257025. doi: 10.6004/jnccn.2025.7025

14. Daly MB, Pilarski R, Yurgelun MB, Berry MP, Buys SS, Dickson P, et al. Genetic/familial high-risk assessment: Breast, ovarian, and pancreatic, version 1.2020 featured updates to the NCCN guidelines. *JNCCN.* (2020) 18:380–91. doi: 10.6004/jnccn.2020.0017

15. R Core Team. *R: A Language and Environment for Statistical Computing.* Vienna: R Foundation for Statistical Computing (2022).

16. Wickham Hadley. *Ggplot2 : Elegant Graphics for Data Analysis.* Cham: Springer (2016). doi: 10.1007/978-3-319-24277-4_9

17. Devine C, Emery KR, Childers KK, Brown S, Gordon O, Roth SE. Experiences across a genetic screening and testing programme pathway: a qualitative study of mammogram patient perspectives. *BMJ Open.* (2024) 14:e089884. doi: 10.1136/bmjopen-2024-089884

18. Halverson CME, Wessinger BC, Clayton EW, Wiesner GL. Patients' willingness to reconsider cancer genetic testing after initially declining: mention it again. *J Genet Couns.* (2020) 29:18–24. doi: 10.1002/jgc4.1174

19. Wang C, Lu H, Bowen DJ, Xuan Z. Implementing digital systems to facilitate genetic testing for hereditary cancer syndromes: an observational study of 4 clinical workflows. *Genet Med.* (2023) 25:100802. doi: 10.1016/j.gim.2023.100802

20. Brabender D, Siegel E, Culver JO, Comeaux JG, Date A, Woodworth A. Identification of patients at elevated cancer risk through a community-based genetic testing program. *Ann Surg Oncol.* (2025) 32:9041–9. doi: 10.1245/s10434-025-17820-w

21. Ioffe YJ, Hong L, Joachim-Célestin M, Soret C, Montgomery S, Unternaehrer JJ. Genetic testing in the latinx community: impact of acculturation and provider relationships. *Gynecol Oncol.* (2023) 169:125–30. doi: 10.1016/j.ygyno.2022.12.001

22. Lau-Min KS, McCarthy AM, Nathanson KL, Domchek SM. Nationwide trends and determinants of germline BRCA1/2 testing in patients with breast and ovarian cancer. *JNCCN.* (2023) 21:351–8. doi: 10.6004/jnccn.2022.7257

23. Kurian AW, Ward KC, Howlader N, Deapen D, Hamilton AS, Mariotto A, et al. Genetic testing and results in a population-based cohort of breast cancer patients and ovarian cancer patients. *J Clin Oncol.* (2019) 37:1305–1315. doi: 10.1200/JCO.18.01854

24. American Cancer Society. *American Cancer Society Recommendations for the Early Detection of Breast Cancer*. (2023). Available online at: https://www.cancer.org/cancer/types/breast-cancer/screening-tests-and-early-detection/american-cancer-society-

recommendations-for-the-early-detection-of-breast-cancer.html (Accessed October 26, 2025).

25. Hong YR, Yadav S, Wang R, Vadaparampil S, Bian J, George TJ, et al. Genetic testing for cancer risk and perceived importance of genetic information among us population by race and ethnicity: a cross-sectional study. *J Racial Ethn Health Disparities*. (2024) 11:382–94. doi: 10.1007/s40615-023-01526-4

26. Wagner IM, Xuan Z, Lu H, Wang C. Racial disparities in accessing care along the continuum of cancer genetic service delivery. *Cancer Epidemiol Biomar Prevent*. (2024) 33:55–62. doi: 10.1158/1055-9965.EPI-23-0596

27. Hong YR, Tauscher J, Cardel M. Distrust in health care and cultural factors are associated with uptake of colorectal cancer screening in Hispanic and Asian Americans. *Cancer*. (2018) 124:335–45. doi: 10.1002/cncr.31052