Information Sharing Patterns in a Population Genetic Screening Pilot Study

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Abstract

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Population genetic screening for preventable adult-onset disease is an emerging public health paradigm. There is limited information about the information sharing patterns of population screening participants. This thesis explored intent to share results by participants in a relatively small pilot population genetic screening study at three time points: invitation to participate (T0), consent to participate (T1), and after results disclosure (T2). More participants intend to share their results than not share at all time points. Intent to share is stratified by result at the T2 time point, with a higher proportion of those with positive screening results intending to share with family or friends and with their doctor. Following result disclosure, the proportion of participants in both groups answering “Don’t know” is decreased, suggesting less uncertainty about sharing regardless of result. Qualitative analysis of free text survey responses at the T1 and T2 timepoints showed that the two most common motivations to share information are to provide family members with important health information and to seek emotional support. Materials developed to promote information sharing after population genetic screening should emphasize both these benefits of sharing. Future research is needed to understand barriers to sharing information, particularly sharing with healthcare providers.

I. Introduction

Population genetic screening

Population genetic screening, which involves offering genetic testing for specific disorders to all members of a population regardless of known risk factors, is an emerging public health paradigm. It is estimated that 1 to 2 percent of the population carries a pathogenic variant which puts them at an increased risk of a preventable adult onset disease, which translates into millions of individuals at risk.[1] These individuals could benefit from proven, effective interventions to reduce their risk for disease. The Centers for Disease Control and Prevention (CDC) Office of Public Health Genomics has identified so-called "Tier 1" genetics conditions as priority conditions to consider integrating into public health programs.[2] These are conditions that are underdiagnosed by current practice, which have diseases associated with them causing a significant public health burden and have evidence-based interventions available which could significantly reduce morbidity and mortality if undertaken at an early or presymptomatic stage.

The CDC Tier 1 conditions include specific hereditary cancer syndromes and familial hypercholesterolemia.[2] Between 5 and 10% of colon cancer and female breast cancer, and up to 25% of ovarian cancer, are due to inherited genetic mutations. Those with a genetic mutation may have more than a 70% chance of developing cancer in their lifetime, and risk reduction interventions can reduce this possibility significantly. National guidelines have established criteria for which individuals without cancer, but with a family history suggestive of a hereditary cancer syndrome, should be offered genetic testing.[3,4] Research has shown that current cancer genetic testing guidelines may miss a number of those who carry clinically relevant genetic mutations,[5] and that population genetic screening may be a more cost effective strategy than screening based on family or personal history.[6,7] The prevalence of familial hypercholesterolemia has been estimated at 1 in 200 to 1 in 250 individuals.[8] A significant portion of those with FH in the general population are felt to be undiagnosed.[9] Early identification of those at risk and aggressive, early intervention to reduce elevated cholesterol can lead to lower rates of atherosclerosis, premature coronary artery disease, and sudden cardiac death.

Existing paradigms of genetic testing

The existing model of delivering clinical genetic testing presents a number of barriers for patients seeking care. The criteria for genetic testing vary depending on the national guideline referenced, and require expertise to interpret and apply.[10] Even when individuals meet clinical criteria for testing, insurance companies may not cover the cost of genetic testing unless formal genetic counseling is provided.[11] Limited numbers of trained genetic counselors or other genetic providers in some areas of the country mean long delays for patients. There are also inequities in the access to genetic services for some members of the population. It is well recognized that members of the African American and Hispanic ethnic groups have lower rates of referral for and uptake of genetic testing, even when they meet clinical testing criteria and the results of genetic testing would significantly impact treatment decisions for those with cancer.[12,13]

The rising popularity of direct-to-consumer (DTC) genetic testing for disease susceptibility, in which an individual orders their own testing directly from a non-clinical testing lab, suggests that there is demand for genetic testing outside clinical guidelines.[14,15] A 2018 survey performed in the Kaiser Permanente system of over 10,000 individuals suggested 3 times more people had undergone DTC testing than clinical genetic testing, and that non-Hispanic black and Hispanic individuals were as likely as non-Hispanic white individuals to have had DTC genetic testing, although many of these individuals sought testing for ancestry information rather than disease susceptibility.[16]

Genetic information sharing and cascade screening

HIPAA privacy restrictions only allow release of clinical genetic test results to the individual tested. Research testing is generally undertaken with the expectation of confidentiality as well. Therefore, current practice relies on an individual tested to be the gatekeeper of information and share it appropriately with those members of their family who could be impacted by the test results.[17] In addition, those who undergo testing through research protocols or DTC testing often must share their results with their healthcare provider themselves in order to access appropriate screening and prevention within a clinical setting.

The majority of disorders included in the CDC Tier 1 guidelines are inherited in an autosomal dominant fashion. This means that a first-degree relative of the individual found to carry a mutation (a parent, child, or sibling) has a 50% chance of carrying the same mutation. So-called 'cascade' screening of family members can amplify the benefit of testing a single person by allowing rapid identification of multiple other relatives who will benefit from screening and prevention interventions as well as those who do not need such interventions. It is also suggested that cascade screening of first degree relatives improves the economic value of population genetic screening.[7,18]

Prior research has shown that patients found to carry hereditary cancer gene mutations after clinical cancer genetic testing have rates of sharing their results with family members of 67-98%, with highest rates of sharing with first-degree family members.[19–21] Participants in risk factor based hereditary cancer genetic research have also been found to share their results with family members nearly 2/3 of the time.[22] In contrast, only 51% of those who received an abnormal result from a health-related DTC test shared their results with a first-degree relative, and this rate was even lower in non-Hispanic Black individuals (33%).[16]

There is limited information to date about information sharing patterns after population genetic screening. A study of Israeli Ashkenazi Jews undergoing population BRCA1 and BRCA2 screening for the three common Ashkenazi founder variants showed that 88% of participants found to carry a pathogenic variant reported sharing their screening results with at least one family member, comparable to clinical genetic testing information sharing rates.[23] Ninety-six percent (96%) of participants in a US-based multisite genomic screening study who received actionable pathogenic or likely pathogenic results reported sharing their results with at least one first degree family member, but only one third shared with all first degree family members.[24]

Sharing of genetic test results does not always lead to family members undergoing testing, and information sharing can be motivated by reasons other than promoting cascade testing in family members.

Reviews report that uptake of cascade testing in families with a known hereditary cancer gene mutation is commonly less than 50%.[25,26] Patients identify that their motivation for sharing information is to seek emotional support as often as it is to convey important medical information to family members.[27,28] In prior studies of family communication after clinical genetic testing for hereditary cancer syndromes, emotional closeness of family members has repeatedly been shown to influence likelihood to share test results.[29–31] Additionally, research has shown that less support from a partner after genetic testing for hereditary cancer can be associated with increased distress post disclosure.[32]

In general, individuals who share clinical cancer genetic test results with their family are more likely to be female, have a personal history of cancer, have greater self-efficacy in health management, and perceive less ambiguity in cancer prevention recommendations.[33–35] Barriers to family communication about cascade screening which have been identified include concern for family member reactions, complexity of information, lack of closeness to family, and family conflict.[36,37] Stigma about cancer diagnosis and shame about inherited disease have been identified as particular barriers in cultural minority populations.[38]

II. Study objective(s)/Research aims

Numerous research groups, including the National Institutes of Health *All of Us* Research Program[39], are undertaking large-scale population recruitment to screen for a variety of genetic diseases. Challenges to implementing population studies include the appropriate age for screening, what genes to include in the screening, who will perform the screening, how participants will be recruited and results returned, and how to assist participants in sharing their results with relevant family members.[40] Among those important considerations, this study will attempt to address the last of these concerns to assess genetic result sharing among those opting in to a population genetic screening program.

The objectives of this study are to describe the information sharing patterns of participants in a relatively small pilot population genetic screening study, undertaken to evaluate the potential of large-scale general population genetic screening. First, the overall rates of plans to share genetic screening results will be described and compared at three different time points in the study. Which family members or other acquaintances were identified as receivers of the information will also be described. Second, the rates of information sharing after receipt of positive and uninformative genetic screening results will be compared. Finally, qualitative analysis of participants' survey responses will be used to investigate why participants intend to share or not share their results.

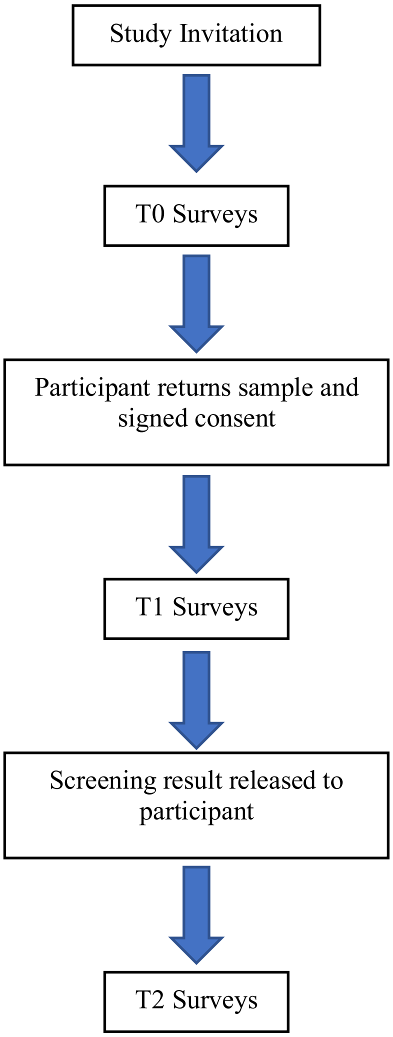
IV. Methods

Setting

This is a sub study of the "Genetic Screening for Inherited Disease Risk" project, a pilot study at the University of Washington with a goal of establishing the feasibility and utility of large-scale, general population genetic screening. The study was approved by the University of Washington Institutional Review Board (00009032). Participants were identified by a UW Medical Center medical record search and were invited to participate via email. Inclusion criteria were adults ages 25-60 who had had at least 2 UW Medical Center clinic visits within the past 5 years. Patients identified as racial and ethnically minorities through their electronic health records (EHR) were preferentially selected for recruitment with the goal of sequencing at least 2,500 participants. We sought a diverse group of participants so that the feasibility of population genetic screening could be assessed among a diverse population. Exact enrichment targets for self-identified racial and ethnic minorities were defined by our partners to meet the needs of a separate project and were 10% were African American, 46% Asian American, 10% Hispanic, 6% Native American or Pacific Islander, 20% White and 8% identifying as Other or Multiracial. In order to ensure input from sexual and gender minorities 1000 invitations were targeted at individuals self-identifying as LGTBQ+. Exclusion criteria were lack of English language proficiency indicated in the EHR, inability to consent, inability to use email or electronic forms, and prior bone marrow transplant. Individuals who had coded EHR information indicating previous orders for genetic testing for a hereditary cancer panel at the University of Washington Department of Laboratory Medicine or send-out genetic testing ordered through the University of Washington were excluded, but there was no detailed medical record review to exclude individuals who may have received genetic testing prior to entry into the UW health system or testing not recorded formally in the EHR.

Surveys were administered via REDCap[41] at three time points: study invitation (T0), consent to participate (T1), and after results disclosure (T2). (Figure 1)

Figure 1: Study flow chart



Participants answered the first surveys (T0) prior to written consent after they had responded to the invitation to participate and read about the study. After T0 surveys participants could request a saliva test kit sent to their home. The second (T1) survey email request was sent after receipt of a study sample and written consent. Participants who consented and returned a saliva sample underwent a 25 gene screening panel (including 23 genes for hereditary cancer and 2 for familial hypercholesterolemia). Prior to sending the T2 surveys, results were entered into REDCap, including a "positive results" field with Yes/No answers. Those participants with uninformative testing results, i.e. individuals where no pathogenic or likely pathogenic variants were identified, obtained their results through a web-based portal, while participants with positive testing results were first contacted by a study genetic counselor with recommendations for follow up including clinical testing. Study genetic counselors recorded information about their conversation with the participants with positive screening results in REDCap, including if they were aware of their result due to prior clinical testing. T2 survey emails were sent to participants about 1 to 2 weeks after result delivery. Research test results were not entered into the participant's electronic medical record or shared with family members by the study team. The study team only communicated with participant's healthcare providers about results if specifically requested to guide follow-on care.

Only those who have received their screening results at least 2 weeks prior to the data extraction (to allow time to access the final surveys), and completed the question in the T2 survey asking "*Have you or do you plan to share the results of your genetic test with relatives or friends?*" (with answer options "Yes", "No", or "Don't know") are included in this analysis.

Survey questions

Detailed demographic data including age, gender, sexual orientation, race, ethnicity, education level, and household income were collected in the T1 survey. (Although sex assigned at birth was collected in the survey for genetic testing quality control, this analysis will use only self-identified gender.) Participants were also asked about personal history of heart attack or coronary artery disease, cancer diagnosis, family cardiac and cancer history, prior genetic testing, and known genetic risk in the family.

At each time point, participants were asked if they planned to or had shared their genetic screening results with anyone. Those who answered "Yes" or "Don't know" were then asked to choose all that apply from a list of 10 types of people they could potentially share their results with. (See Table S1 in appendix) Following the T1 information sharing questions all respondents were asked "*Will you please tell us more about why you would or would not share your genetic test results with the people you indicated above?*" in a free text field. After return of results (T2), participants answering "Yes" or "Don't know" to the information sharing question were then asked "*Will you please tell us more about why you plan to share your genetic test results with the people you indicated above*?"

Quantitative analysis

Data were exported from REDCap into the R statistical program[42] for analysis. Descriptive statistics were generated for age, gender, sexual orientation, race, ethnicity, education level, and household income for the entire cohort and for the groups with positive screening results or uninformative screening results. Proportions of participants responding "Yes", "No", or "Don't Know" to the information sharing question at each time point were calculated, as well as proportions of participants selecting each category of recipient at each time point.

Invited participants in the parent genetic screening study were not required to answer information sharing survey questions to participate in the screening study. The groups who answered only at the T0 time point or at the T0 and T1 time point only and then dropped out were compared by age and how they answered the information sharing questions with the cohort in the final analysis to evaluate for any systematic differences. Because many who dropped out after the T0 survey did not answer the detailed demographic questions in the T1 survey, further comparison on demographic characteristics was not possible.

Data from the T2 time point was divided by positive results or uninformative results. Result disclosure notes from the study genetic counselor were reviewed in REDCap for those with positive results who reported a history of genetic testing to confirm which participants were aware of their results prior to receiving screening results. The answers to the information sharing with others, information sharing with doctor, and with whom were compared between the groups with positive and uninformative results. Comparison of the proportion of each answer at each time point was performed separately for those with positive results and those with uninformative results. Statistical analysis for categorical variables was performed by Pearson's Chi squared test using the chisq.test function in R.

To identify factors potentially influencing intent to share information, an exploratory analysis of different demographic factors was performed by generating descriptive statistics of answers at each time point stratified by gender, race, age (<45 vs. 45 and over), education, personal cancer history, and family history of cancer in a first degree relative. At the T2 time point, multivariate analysis was performed to assess for association between those characteristics found to show a significant influence on answer of the information sharing question. For this analysis, a new binary outcome variable was created for answering "Yes" (1) versus answering "No" or "Don't know" (0). To correct for multiple comparisons, tests were considered significant at a Bonferroni-adjusted p-value of 0.01.

Qualitative analysis

Free text responses are short blocks of text in the participants' own words, without follow up questions. Qualitative analysis of free text responses may be different from qualitative analysis of semi-structured interviews or longer texts. An approach that has been used in previous surveys of individuals receiving hereditary cancer risk assessment is to examine who answers the free text questions compared to who does not and what common topics emerge in these answers.[43,44]

To identify topics in the answers, I performed a conventional content analysis of the free text responses.[45] A codebook was created using a combination deductive and inductive approach.[46] An initial deductive codebook was created based on prior qualitative studies about information sharing after clinical genetic testing.[27,28,30,31] Emergent codes were added as I performed the first round of coding on data available as of February 15, 2022 (see below). Excerpts were coded with all codes that applied. I then refined the codebook to condense those codes that were redundant or expressed the same concept. A second coder (N.R.) then used the refined codebook to code all the free text excerpts independently. We met to review the few discrepancies which were identified, and consensus was reached as to a final applicable code or codes. I finally grouped the codes into domains which summarized common topics.

As of February 15, 2022, a total of 653 individuals had received results. At this time, free text fields for relevant questions from these participants were exported from REDCap into Excel for analysis. The free text responses from the remaining participants have not yet been coded. I compared demographic characteristics (age, gender, race, ethnicity, education, income, personal cancer history, family cancer history, and result category) of those who answered the free text questions at each time point with those who did not answer. The data set was divided based on answer ("Yes", "No", or "Don't know") at T1, and by result (positive or uninformative) and answer ("Yes" or "Don't know") at T2 to examine differences in identified topics. The same codebook was used to code all the subsets. Because the free text questions were asked of different groups (all respondents at T1, and only those who answered "Yes" or "Don't Know" at T2), some distinct codes were used based on time point.

IV. Results

Response to questionnaires

Overall, 2017 participants had received their screening results at least 2 weeks prior to the time data was extracted from REDCap for this analysis and were eligible for inclusion. A total of 1150 participants (57%) completed the T2 survey question about information sharing and were included in the final analysis. The group who dropped out after the T0 survey (n=346) were younger (mean age 38.2 ± 9.6 years) and were more likely to answer "No" to the T0 information sharing question (11.8%) than the cohort used in this analysis. Those who dropped out after the T1 survey (n=532) were of similar age and had similar answers to the T0 information sharing question compared to the cohort used in this analysis but were more likely to answer "Yes" to the T1 information sharing question (80.6%). (See Table S2 in appendix.)

Demographics

Table 1 shows the demographic characteristics of the participants in the analysis. The average age of participants was 41.1 years ±10.3 (range 25-60). Of the participants 339 (29.4%) identified as male, 608 (52.9%) identified as female, 17 (1.5%) identified as Other, and 186 (16.2%) preferred not to answer. Participants were asked to self-report all races that applied to them. A total of 1013 (88.1%) participants chose more than one race.

Overall, the cohort was highly educated. Nearly 75% of participants were college graduates or held an advanced degree. No participants reported less than a high school education. Household income was reported as over $100,000 for nearly half of participants. This distribution reflects the demographic characteristics of the population invited to participate in the study.

Quantitative results

At study invitation (T0), 803 (69.8%) of participants answered “Yes”, they did intend to share their results with someone else, 65 (5.7%) answered “No” and 281 (24.4%) answered “Don’t know”. At sample collection (T1), 806 (70.1%) of participants answered “Yes”, 30 (13.5%) answered “No”, and 155 (13.5%) answered “Don’t know” to the information sharing question. At the T1 timepoint, 159 participants (13.8%) did not answer the information sharing question. As both the T0 and T1 surveys were administered prior to return of results, it is possible that some participants elected not to answer what appeared to be a duplicate question from the prior set of surveys. Following return of results (T2), 753 (65.4%) of participants said “Yes,” they had or planned to share their results, 262 (22.8%) answered “No”, and 135 (11.7%) answered “Don’t know”. Between T0 and T2 there was a slight decrease in those intending to share information (answering “Yes”), but a notable shift from those answering “Don’t know” to those answering “No”. (Figure 2)

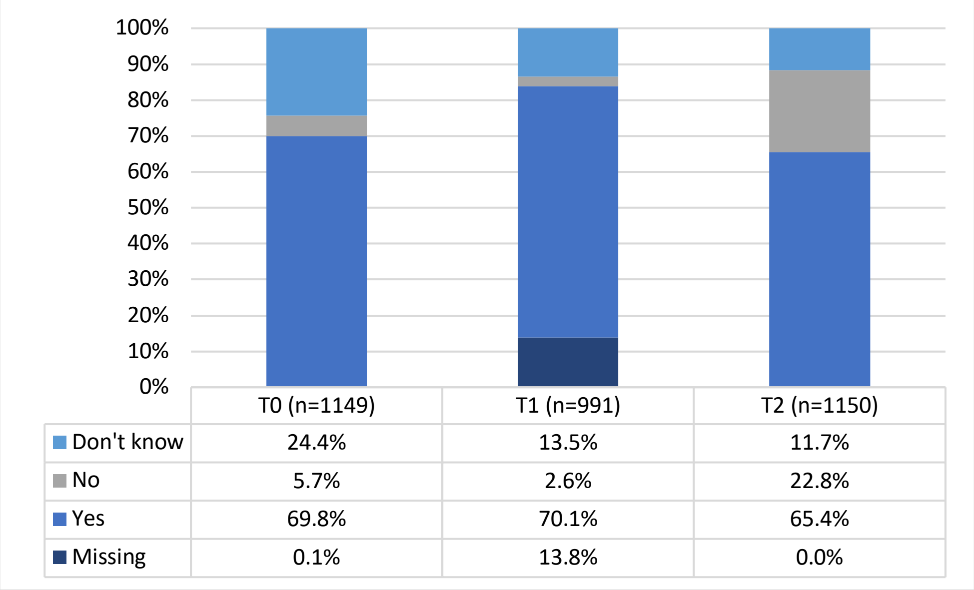
No difference in answers to information sharing questions were observed when stratified by gender, race, age (under 45 vs. 45 and over), education level, or personal history of cancer. Those with a family history of cancer in a first degree relative did show a statistical difference between the three answers with a higher percentage answering “Yes” and a lower percentage answering “Don't know”. (See Table S3 in Appendix.)

Table 1: Demographic characteristics of study participants

	TOTAL **N=1150**	**POSITIVE** **N=48 (4.2%)**	**UNINFORMATIVE** **N=1102 (95.8%)**
AGE RANGE	25-60 years	25-59 years	25-60 years
MEAN AGE (SD)	41.1 years (±10.3)	41.2 years (±10)	41.1 years (±10.3)
GENDER			
MALE	339 (29.4%)	9 (18.8%)	330 (29.9%)
FEMALE	608 (52.9%)	32 (66.7%)	576 (52.3%)
OTHER	17 (1.5%)	1 (2.1%)	16 (1.5%)
PREFER NOT TO ANSWER	186 (16.2%)	6 (12.5%)	180 (16.3%)
SEXUAL ORIENTATION			
ASEXUAL	36 (3.1%)	1 (2.1%)	35 (3.2%)
BISEXUAL	65 (5.7%)	5 (10.4%)	60 (5.4%)
LESBIAN OR GAY	82 (7.1%)	6 (12.5%)	76 (6.9%)
QUEER	33 (2.9%)	3 (6.3%)	30 (2.7%)
STRAIGHT	746 (64.9%)	29 (60.4%)	717 (65.1%)
SOMETHING ELSE	11 (1%)	0	11 (1%)
DON'T KNOW	5 (0.4%)	0	5 (0.5%)
PREFER NOT TO ANSWER	172 (15%)	4 (8.3%)	168 (15.2%)
RACE[1]			
ALASKA NATIVE	12 (1%)	0	12 (1.1%)
AMERICAN INDIAN	59 (5.1%)	3 (6.3%)	56 (5.1%)
ASIAN	530 (46.1%)	18 (37.5%)	512 (46.5%)
BLACK/AFRICAN AMERICAN	96 (8.3%)	5 (10.4%)	91 (8.3%)
NATIVE HAWAIIAN	4 (0.3%)	1 (2.1%)	3 (0.3%)
OTHER PACIFIC ISLANDER	25 (2.2%)	0	25 (2.3%)
WHITE	466 (40.5%)	24 (50%)	442 (40.1%)
OTHER	48 (4.2%)	1 (2.1%)	47 (4.3%)
DON'T KNOW	3 (0.3%)	0	3 (0.3%)
PREFER NOT TO ANSWER	143 (12.4%)	5 (10.4%)	138 (12.5%)
ETHNICITY			
HISPANIC	133 (11.6%)	8 (16.7%)	125 (11.3%)
NON-HISPANIC	854 (74.2%)	35 (72.9%)	819 (74.3%)
PREFER NOT TO ANSWER	163 (14.2%)	5 (10.4%)	158 (14.3%)
EDUCATION LEVEL			
LESS THAN HIGH SCHOOL	0	0	0
HIGH SCHOOL/GED	18 (1.6%)	0	18 (1.6%)
SOME COLLEGE	123 (10.7%)	7 (14.6%)	116 (10.5%)
COLLEGE GRADUATE	434 (37.7%)	19 (39.6%)	415 (37.7%)
ADVANCED DEGREE	433 (37.7%)	18 (37.5%)	415 (37.7%)
PREFER NOT TO ANSWER	142 (12.3%)	4 (8.3%)	138 (12.5%)
HOUSEHOLD INCOME			
LESS THAN $50,000	128 (11.1%)	5 (10.4%)	123 (11.2%)
$50-100,000	253 (22%)	12 (25%)	241 (21.9%)
MORE THAN $100,000	547 (47.6%)	25 (52.1%)	522 (47.4%)
PREFER NOT TO ANSWER	222 (19.3%)	6 (12.5%)	216 (19.6%)

[1] *Totals to >100% as participants were invited to select all that apply*

Figure 2: Intent to share at each time point



	T0 (n=1149)	T1 (n=991)	T2 (n=1150)
■ Don't know	24.4%	13.5%	11.7%
■ No	5.7%	2.6%	22.8%
■ Yes	69.8%	70.1%	65.4%
■ Missing	0.1%	13.8%	0.0%

Overall, at all time points, the most common individual identified for receipt of this information was spouse (78.7% at T0, 73.6% at T1 and 72.1% at T2) followed by first degree relatives (parent- 59.5%, 67.1%, 52.5%; child- 33.5%, 46.5%, 30.6%; sibling- 54.6%, 67.1%, 52%).(Table 2) There was little noted change in proportion selecting each group between T0 and T2 other than a decrease in the selection of friend at the T2 time point.

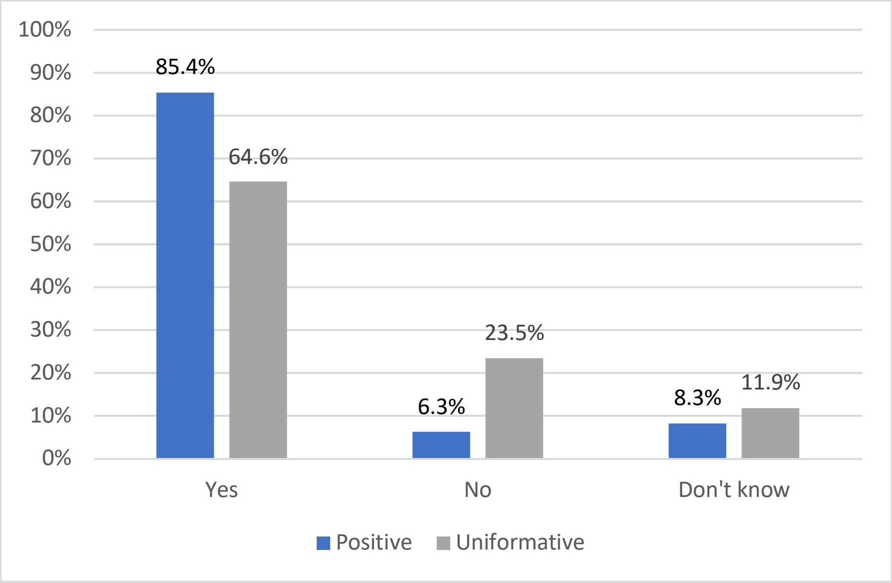
Table 2: Intent to share with whom by time point

	T0 **N=1084**	**T1** **N=961**	**T2** **N=888**	**% CHANGE BETWEEN T0 AND T2**
SPOUSE	853 (74.2%)	707 (73.6%)	640 (72.1%)	-2.1%
FIRST DEGREE RELATIVES:				
PARENT	645 (56.1%)	645 (67.1%)	466 (52.5%)	-3.6%
CHILD	363 (31.6%)	447 (46.5%)	272 (30.6%)	-1%
SIBLING	592 (51.5%)	645 (67.1%)	462 (52%)	+0.5%
2^{ND}/3^{RD} DEGREE RELATIVES:				
GRANDPARENT	61 (5.3%)	129 (13.4%)	24 (2.7%)	-2.6%
AUNT/UNCLE/COUSIN	155 (13.5%)	256 (26.6%)	80 (9%)	-4.5%
NON-RELATIVES:				
FRIEND	385 (33.5%)	404 (42%)	203 (22.9%)	-10.6%
SPIRITUAL LEADER	26 (2.3%)	38 (4%)	9 (1%)	-1.3%
COWORKER	50 (4.4%)	86 (9%)	45 (5.1%)	+0.7%
EMPLOYER	18 (1.6%)	24 (2.5%)	7 (0.8%)	-0.8%
NONE SELECTED	23 (2%)	40 (4.2%)	15 (1.7%)	-0.3%

A total of 48 (4.2%) participants were identified to carry a pathogenic or likely pathogenic variant in at least one of the tested genes, 45 in hereditary cancer genes and 3 in familial hypercholesterolemia genes. Of these, 13 (27.1%) were aware of their genetic result prior to participation in this study, although one of these individuals was identified to have a previously unknown pathogenic variant in a second gene. This percentage of positive results, even when leaving out those who were previously aware of their genetic variant (3.1%), is higher than the estimated 1-2% population carrier rate.[1] When examined, rates of positive screening results were similar in the groups of participants who did not complete the last survey, indicating the T2 results are not skewed due to dropout.

When grouped by result, significantly more participants with positive results (85.4%) than uninformative results (64.6%) reported at T2 that they did plan to or had shared their results with another person (OR=3.2, p=0.0048). (Figure 3)

Figure 3: Intent to share with others at T2 by result



From T0 to T2, the uninformative results group showed a slight decrease in likelihood to share with all categories of persons. Conversely, those with positive results showed a stable to increased intent to share with all of their genetic relatives. Small sample size makes it difficult to interpret the change in information sharing plans with non-spouse unrelated individuals. (Table 3)

Table 3: Intent to share by result, pre- vs. post-result

	POSITIVE			**UNINFORMATIVE**		
	T0 n=45	**T2 n=45**	**% Change**	**T0 n=1039**	**T2 n=843**	**% Change**
SPOUSE	35 (77.8%)	32 (71.1%)	-6.7%	818 (78.7%)	608 (72.1%)	-6.6%
FIRST DEGREE RELATIVES:						
PARENT	28 (62.2%)	28 (62.2%)	0.0%	617 (59.4%)	438 (52%)	-7.4%
CHILD	15 (33.3%)	19 (42.2%)	+8.9%	348 (33.5%)	253 (30%)	-3.5%
SIBLING	24 (53.3%)	31 (68.9%)	+15.6%	568 (54.7%)	431 (51.1%)	-3.6%
2ND/3RD DEGREE RELATIVES:						
GRANDPARENT	1 (2.2%)	2 (4.4%)	+2.2%	60 (5.8%)	22 (2.6%)	-2.6%
AUNT/UNCLE/COUSIN	3 (6.7%)	10 (22.2%)	+15.5%	152 (14.6%)	70 (8.3%)	-6.3%
NON-RELATIVES:						
FRIEND	16 (35.6%)	13 (28.9%)	-6.7%	369 (35.5%)	190 (22.5%)	-13%
SPIRITUAL LEADER	1 (2.2%)	1 (2.2%)	0.0%	25 (2.4%)	8 (0.9%)	-1.5%
COWORKER	1 (2.2%)	6 (13.3%)	+11.1%	49 (4.7%)	39 (4.6%)	-0.1%
EMPLOYER	0	2 (4.4%)	+4.4%	18 (1.7%)	5 (0.6%)	-1.1%
NONE SELECTED	2 (4.4%)	1 (2.2%)	-2.2%	21 (2%)	14 (1.7%)	-0.3%

Participants with positive screening results were more likely than those with uninformative results to have a family history of cancer in a first degree relative (60.4% vs. 45.6%). Because a family history of cancer was associated with a higher likelihood to share results in the overall cohort, the potential of this confounding the association between positive results and intent to share was examined. The higher intent to share by those with positive results remained statistically significant (p=0.00634) when controlled for family history of cancer. (see Table S4 in Appendix.)

Participants with positive screening results showed no significant change in answer over the three time points regarding sharing of information with family or acquaintances (p-value=0.71). The group with uninformative results did show significant change in answer over the three time points, with more participants answering “No” at T2 (p-value<$2.2x10^{-16}$). (Figure 4)

The majority of participants with positive results answered “Yes” (89.6%) they did plan to or had shared their results with their doctor, while 6.3% answered “No” and 4.2% answered “Don’t know.” In contrast, those with uninformative results were nearly evenly divided between “Yes” (29.8%), “No” (36.6%) and “Don’t know” (33.5%). (Figure 5)

Figure 4: Intent to share at each time point by result, positive vs. uninformative results

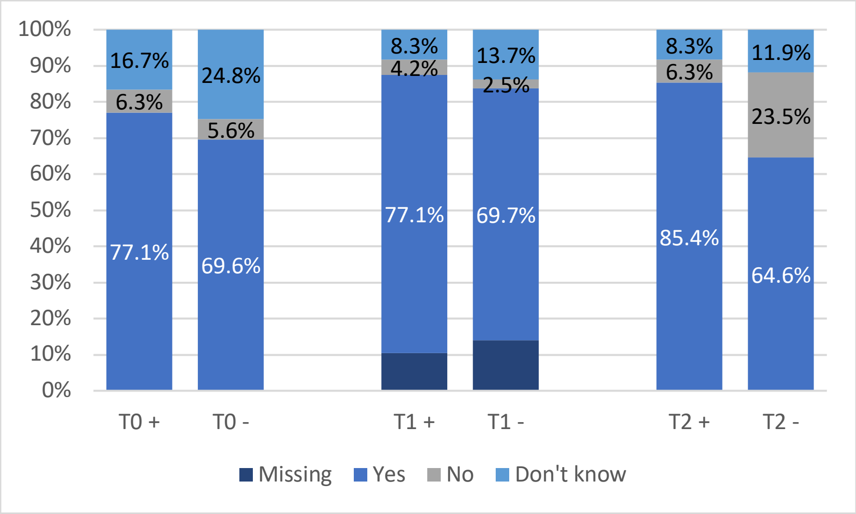
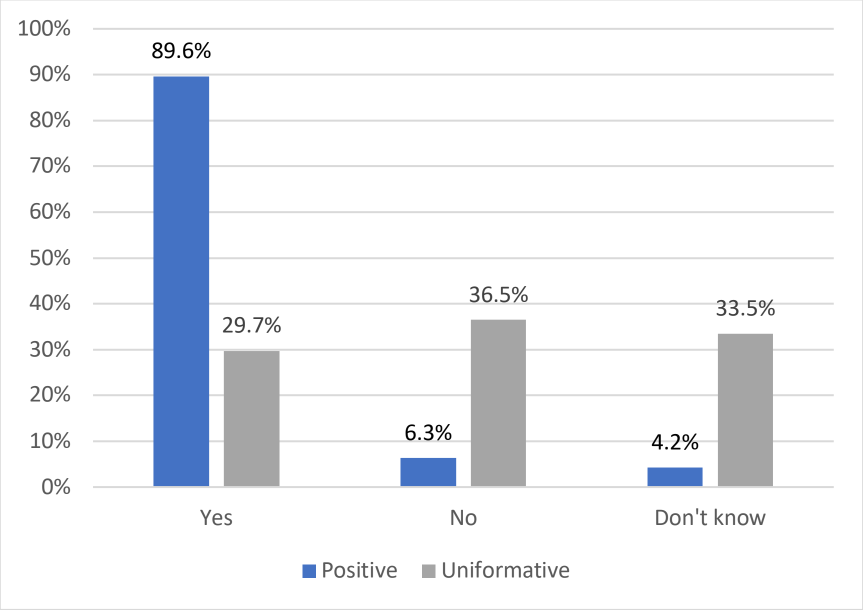


Figure 5: Intent to share with doctor at T2 by result



Qualitative results

A total of 474 participants provided text responses to the T1 question “*Will you please tell us more about why you would or would not share your genetic test results with the people you indicated* *above?*" and 179 participants did not. (See Table S5 in Appendix.) In general, the group who did not provide a free text answer at T1 had a higher proportion of not answering the other demographic questions, making it difficult to draw conclusions about the group characteristics. This group was less likely to have reported a personal or family history of cancer. Of those who responded, 394 answered "Yes", 13 answered "No", and 67 answered "Don't know." At the T2 free text field, 383 participants provided an answer and 270 did not. Of those who answered, 333 had responded "Yes" and 50 had responded "Don't know" to the information sharing question. Analysis of the group characteristics at T2 suggest that more of those who answered the free text question were female and had a positive screening result than those who did not answer.

We identified a total of thirteen codes: eleven throughout the free text responses, and two emerged only in the T2 excerpts. The codes fell into three domains: Motivation to share, Neutral about sharing, and Hesitation about sharing.

Codebook: Codes, Code definitions, and Domains identified

Domain	Code	Definition
Motivation to share	Health knowledge for family	Information shared for family members so they will get genetic testing, understand risk, or change their lifestyle; also sharing uninformative results to inform family for the family member's sake
	Informational/interesting	Share information to increase general health literacy or increase general awareness of genetic testing; share information with others only because it is interesting
	Support and trust	Share information for emotional support; share result with others only because they knew participant was undertaking screening
	Reassurance/Good news (T2 only)	Shared results because they were uninformative, this was "good news" to share; shared in order to reassure others that result was not concerning for the participant themselves
Neutral about sharing	No real reason	State they have no reason for sharing or not sharing; sharing just for fun
	Open book	Describe themselves as an open book; always share information with spouse/friends/family and genetic information is no different; why not?
	If they want to know	Will share only if someone asks for the information or will ask if they want to know before sharing
	Depends on result (T1 only)	Will decide to share or not share after results are disclosed
Hesitation about sharing	Privacy (T1 only)	Concern about privacy, genetic information is personal, no one needs to know; also concern about unsolicited advice if they share
	Don't want to worry	Concern about genetic screening results causing worry/anxiety in others
	Family not close	Adopted, no contact with family, no close family, no one who would be receptive to information
	Needs confirmation	Screening test is not a diagnosis, so decision about sharing will be deferred
	Nothing to share (T2 only)	Results were uninformative so there is no information to share

Motivation to share

Most of those who answered “Yes” to the information sharing question at both time points gave responses indicating they would share their genetic screening results without hesitation. Respondents most commonly (256/474 (54%) at T1 and 218/383 (56.9%) at T2) indicated they would share their results because family members could change something about their health care, such as seek genetic testing themselves or make lifestyle changes:

> *“For folks genetically close to me, I would want them to know if there are diseases I may be genetically predisposed to so that they could get tested if they want, as well.” (ID#129, T1)*
>
> *“So they will be aware and proactive about their own health.” (ID#2679, Positive result, T2)*

Other responses indicated sharing of information because of trust with a given individual, or to seek emotional support, consistent with the finding that the spouse was the most common person that results would be shared with:

> *“I would share first with my immediate family because I am close with them and they are a strong support network.” (ID#2019, T1)*
>
> *“I believe that if proven to have some sort of genetic problem, and if I would need to make a lifestyle change, I feel that I would need to ask for support from the people closest to me.” (ID#22980, T1)*

Following result disclosure (T2), individuals with uninformative results were less likely share information to seek support, but instead because it was interesting or to promote others’ interest in genetics:

> *"It's interesting and I do not view it as needing to stay private. It may inspire others to do genetic tests and learn more." (ID#17271, Uninformative result, T2)*

Some with uninformative results (34/308 (11%)) also were motivated to share information because they believed it would be reassuring for their family to know:

> *"Since my results show that I am not at greater risk, I want to share the good news" (ID#22798, Uninformative result, T2)*

<u>Hesitation about sharing</u>

There were a number of reasons that participants stated they may hesitate to share their results. Privacy concerns were stated as a distinct reason not to share genetic screening results by 39/474 participants (8.2%) prior to result disclosure, including by those who had answered "Yes" or "Don't know" to the information sharing question:

> *"I'd rather keep my health information private" (ID#17354, T1)*
>
> *"I would want to share it with my friends and spouse … The reason why I won't share with other people is just because I feel it is a private matter." (ID#15424, T1)*

Others felt that they did not want to worry others:

> *"I don't … want to share if there is a bad thing, such as possible disease that is difficult to cure, It will make my family worry about me, and will make my child worry about himself." (ID#940, T1)*

Some participants reported not being close enough to family to share their information or being adopted and having no known biologic family:

> *"Not always in communication with family so it depends whether it's that urgent to talk. Also, I don't know or am not close to parents' families." (ID#20272, T1)*

At the T2 time point, three of 44 participants (6.8%) with uninformative screening results who reported being unsure about sharing information felt that they had nothing to share:

> *"My results show no higher risks for anything, so it seems like there's nothing to tell." (ID#5331, Uninformative result, T2)*

Both participants with positive results at the T2 time point who reported being unsure about sharing were awaiting confirmation of the test result:

> *"First [I] must have it confirmed. Then I guess it's my responsibility to share possible information that may effect[sic] them…" (ID#3696, Positive result, T2)*

Neutral about sharing

Less often, participants responses indicated they did not feel a strong motivation or hesitation about sharing. Some participants had no particular reason for their answer or described themselves as an "open book" who always shares information. A number of respondents at the T1 time point (29/474 (6.1%)) remained neutral about sharing information until after they received their result:

> *"I guess I would make that decision once I receive the results and how I feel about it." (ID#3696, T1)*

V. Discussion

This study was undertaken to characterize the genetic information sharing intentions of participants in a population genetic screening setting before and after receipt of results. Overall, more participants do plan to share their results than not share their results, both before and after receipt of results. The most commonly identified individuals with whom they would share their results are their spouse and first-degree relatives. Parallel with this, qualitative data show participants' motivation to share is both to convey genetic health information but also to seek psychosocial support from individuals they trust, consistent with prior research on genetic information sharing after clinical testing.[27,28]

Quantitative analysis did not show differences in intent to share based on gender, race, age, or personal history of cancer as has been reported in clinical settings[33,35] but did show that those with a family history of cancer in a first degree relative were more likely to share. This is consistent with findings reported by Lieberman et al, that family history of breast or ovarian cancer was a significant predictor of intent to share BRCA screening results in an Ashkenazi population screening study.[23] Intent to share is stratified after results disclosure, with those receiving positive screening results reporting intent to share at rates comparable to that reported after clinical genetic testing[19,21] and prior studies of population genetic screening.[23,24] The proportion of those who received positive results answering "No" remained stable across the time points, suggesting the increase came from those who changed from "Don't know" to "Yes". In contrast, the group with uninformative results showed a shift from answering "Don't know" towards answering "No". In both groups, this implies that receiving results, positive or not, leads to less uncertainty about sharing.

Those who received uninformative results are a group of particular interest for population genetic screening as it is expected that the large majority of those undergoing population genetic screening will receive uninformative results. In this analysis, this group reported less intent to share, most notably with their doctor. While qualitative data was not available from those who answered that they did not intend to share results after receiving uninformative results, those who were unsure about sharing felt that due to the uninformative result there was nothing to share, an understandable hesitation. Those who received uninformative results and did intend to share often felt it was good news that should be shared. There is the risk that this peace of mind could incorrectly translate into a belief that there is no residual risk of cancer or coronary artery disease. However, an exploratory study by Hoell et al. investigating the comprehension and personal value of negative genomic screening found that participants expressed feeling peace of mind after receiving their results, but did seem to understand there was a residual risk of disease. [47]

Strengths and limitations

While previous studies have investigated patterns of family information sharing after clinical genetic testing and after Ashkenazi population BRCA screening, this is among the first to examine genetic information sharing after unselected population genetic screening. This is also the first study to my knowledge to examine genetic information sharing after uninformative results from population screening. Our study population was intentionally selected to be diverse, representing racial and ethnic minorities as well as sexual and gender minorities. This allows us to elicit the perspective of minoritized populations who have had less uptake of genetic services in the past. However, this study population was highly educated and had high household income. We therefore did not capture the full range of socioeconomic status and likely also suggests a high level of health literacy among our participants, which could limit generalizability of these results. Because completion of the survey questions was not required to receive results, the information sharing patterns of the cohort opting in to answer the questions may not represent the overall study population. Similarly, because the qualitative analysis was performed on only a subset of participants, it may not reflect the motivations and hesitations about genetic information sharing in the entire cohort. Finally, we are unable to know from this data if intent to share genetic information translates into actual sharing, and if sharing leads to any behavior changes in family members such as cascade testing or lifestyle changes.

Implications and future directions

As population genetic screening programs move towards implementation, emphasis has fallen on maximizing the secondary benefits of these screening programs by encouraging sharing of genetic screening results for cascade screening. However, our study population identified support from others as another important motivator for sharing information. When developing materials to promote information sharing after population screening, both conveying important health information to family members as well as getting support from others should be emphasized as benefits of sharing.

While most participants in this population screening study plan to share their genetic information with at least one other person, there is still a large proportion who do not intend to share, particularly those with uninformative results. Further investigation should be undertaken to explore what population screening participants see as risks or barriers to sharing their information. This information can help frame how participants can be aided in sharing their information with others.

Finally, participants with uninformative screening results had low rates of intent to share their results with their healthcare provider. Knowledge of what genetic screening has already been performed for a patient could be useful information for their future healthcare, even if it did not identify a pathogenic variant. From a health economics perspective, the value of sharing an uninformative result with a healthcare provider should be explored.

VI. Conclusion

This study demonstrates that participants in population genetic screening often plan to share their screening results with others, especially if those results identify a pathogenic variant. These analyses suggest that motivation to share genetic information after population screening includes both providing health information for family members and seeking support from trusted individuals. Sharing screening results with relatives and healthcare providers is important to increase the public health impact of population genetic screening. While in theory population genetic screening would preclude the need to share genetic screening results with others, it is highly unlikely that there will be universal uptake of screening should it become available. Further investigation to understand the motivations and barriers to information sharing in this setting will allow development of strategies to promote information sharing with family members and others, including health care providers.

References

1. Evans, J. P., Berg, J. S., Olshan, A. F., Magnuson, T. & Rimer, B. K. We screen newborns, don't we?: Realizing the promise of public health genomics. *Genetics in Medicine* vol. 15 332–334 (2013).
2. Tier 1 Genomics Applications and their Importance to Public Health. https://www.cdc.gov/genomics/implementation/toolkit/tier1.htm (2021).
3. Daly, M. B., Pal, T., Berry, M., Buys, S. & Dickson, P. Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic, Version 2.2021. *J. Natl. Compr. Canc. Netw.* **19**, 77–102 (2021).
4. Gupta, S., Weiss, J., Axell, L., Burke, C. & Chen, L.-M. Genetic/Familial High-Risk Assessment: Colorectal Version 1.2021. *J. Natl. Compr. Canc. Netw.* **19**, (2021).
5. Neben, C. L. *et al.* Multi-Gene Panel Testing of 23,179 Individuals for Hereditary Cancer Risk Identifies Pathogenic Variant Carriers Missed by Current Genetic Testing Guidelines. *J. Mol. Diagn.* **21**, 646–657 (2019).
6. Manchanda, R. *et al.* Cost-effectiveness of Population-Based BRCA1, BRCA2, RAD51C, RAD51D, BRIP1, PALB2 Mutation Testing in Unselected General Population Women. *J. Natl. Cancer Inst.* **110**, 714–725 (2018).
7. Guzauskas, G. F. *et al.* Cost-effectiveness of Population-Wide Genomic Screening for Hereditary Breast and Ovarian Cancer in the United States. *JAMA Netw Open* **3**, e2022874 (2020).
8. Youngblom, E., Pariani, M. & Knowles, J. W. Familial Hypercholesterolemia. in *GeneReviews®* (eds. Adam, M. P. et al.) (University of Washington, Seattle, 2014).
9. Nordestgaard, B. G. *et al.* Familial hypercholesterolaemia is underdiagnosed and undertreated in the general population: guidance for clinicians to prevent coronary heart disease: consensus statement of the European Atherosclerosis Society. *Eur. Heart J.* **34**, 3478–90a (2013).
10. Foulkes, W. D., Knoppers, B. M. & Turnbull, C. Population genetic testing for cancer susceptibility: Founder mutations to genomes. *Nat. Rev. Clin. Oncol.* **13**, 41–54 (2016).
11. Stoll, K., Kubendran, S. & Cohen, S. A. The past, present and future of service delivery in genetic counseling: Keeping up in the era of precision medicine. *Am. J. Med. Genet. C Semin. Med. Genet.* **178**, 24–37 (2018).
12. Pal, T. *et al.* Early onset breast cancer in a registry-based sample of African-American women: BRCA mutation prevalence, and other personal and system-level clinical characteristics. *Breast J.* **19**, 189–192 (2013).
13. Hann, K. E. J. *et al.* Awareness, knowledge, perceptions, and attitudes towards genetic testing for cancer risk among ethnic minority groups: A systematic review. *BMC Public Health* **17**, (2017).
14. Kilbride, M. K. & Bradbury, A. R. Evaluating Web-Based Direct-to-Consumer Genetic Tests for Cancer Susceptibility. *JCO Precis Oncol* **4**, (2020).
15. Francke, U. *et al.* Dealing with the unexpected: Consumer responses to direct-access BRCA mutation testing. *PeerJ* **2013**, (2013).
16. Carroll, N. M. *et al.* Demographic differences in the utilization of clinical and direct-to-consumer genetic testing. *J. Genet. Couns.* **29**, 634–643 (2020).
17. Daly, M. B. A Family-Centered Model for Sharing Genetic Risk. *J. Law Med. Ethics* **43**, 545–551 (2015).
18. Nherera, L., Marks, D., Minhas, R., Thorogood, M. & Humphries, S. E. Probabilistic cost-effectiveness analysis of cascade screening for familial hypercholesterolaemia using alternative diagnostic and identification strategies. *Heart* **97**, 1175–1181 (2011).
19. Stoffel, E. M. *et al.* Sharing Genetic Test Results in Lynch Syndrome: Communication With Close and Distant Relatives. *Clin. Gastroenterol. Hepatol.* **6**, 333–338 (2008).
20. Ricker, C. N. *et al.* Patient communication of cancer genetic test results in a diverse population. *Transl. Behav. Med.* **8**, 85–94 (2018).

21. Cragun, D., Weidner, A., Tezak, A., Clouse, K. & Pal, T. Family communication of genetic test results among women with inherited breast cancer genes. *J. Genet. Couns.* (2020) doi:10.1002/jgc4.1356.
22. Graves, K. D. *et al.* Communication of genetic test results to family and health-care providers following disclosure of research results. *Genet. Med.* **16**, 294–301 (2014).
23. Lieberman, S. *et al.* Familial communication and cascade testing among relatives of BRCA population screening participants. *Genet. Med.* **20**, 1446–1454 (2018).
24. Wynn, J. *et al.* Do research participants share genomic screening results with family members? *J. Genet. Couns.* **31**, 447–458 (2022).
25. Gaff, C. L. *et al.* Process and outcome in communication of genetic information within families: a systematic review. *Eur. J. Hum. Genet.* **15**, 999–1011 (2007).
26. Menko, F. H. *et al.* The uptake of presymptomatic genetic testing in hereditary breast-ovarian cancer and Lynch syndrome: a systematic review of the literature and implications for clinical practice. *Fam. Cancer* **18**, 127–135 (2019).
27. Hughes, C. *et al.* All in the family: evaluation of the process and content of sisters' communication about BRCA1 and BRCA2 genetic test results. *Am. J. Med. Genet.* **107**, 143–150 (2002).
28. Greenberg, M. & Smith, R. A. Support Seeking or Familial Obligation: An Investigation of Motives for Disclosing Genetic Test Results. *Health Commun.* **31**, 668–678 (2016).
29. van Oostrom, I. *et al.* A prospective study of the impact of genetic susceptibility testing for BRCA1/2 or HNPCC on family relationships. *Psychooncology* **16**, 320–328 (2007).
30. Chivers Seymour, K., Addington-Hall, J., Lucassen, A. M. & Foster, C. L. What facilitates or impedes family communication following genetic testing for cancer risk? A systematic review and meta-synthesis of primary qualitative research. *J. Genet. Couns.* **19**, 330–342 (2010).
31. Chopra, I. & Kelly, K. M. Cancer Risk Information Sharing: The Experience of Individuals Receiving Genetic Counseling for BRCA1/2 Mutations. *J. Health Commun.* **22**, 143–152 (2017).
32. Manne, S. *et al.* Associations between relationship support and psychological reactions of participants and partners to BRCA1 and BRCA2 testing in a clinic-based sample. *Ann. Behav. Med.* **28**, 211–225 (2004).
33. Taber, J. M. *et al.* Prevalence and correlates of receiving and sharing high-penetrance cancer genetic test results: Findings from the health information national trends survey. *Public Health Genomics* **18**, 67–77 (2015).
34. Makhnoon, S. *et al.* Relationship between genetic knowledge and familial communication of CRC risk and intent to communicate CRCP genetic information: insights from FamilyTalk eMERGE III. *Transl. Behav. Med.* **11**, 563–572 (2021).
35. Koehly, L. M. *et al.* Characteristics of health information gatherers, disseminators, and blockers within families at risk of hereditary cancer: Implications for family health communication interventions. *Am. J. Public Health* **99**, 2203–2209 (2009).
36. Dean, M. *et al.* Sharing genetic test results with family members of BRCA, PALB2, CHEK2, and ATM carriers. *Patient Educ. Couns.* **104**, 720–725 (2021).
37. Hardcastle, S. J. *et al.* Patients' perceptions and experiences of familial hypercholesterolemia, cascade genetic screening and treatment. *Int. J. Behav. Med.* **22**, 92–100 (2015).
38. Etchegary, H., Potter, B., Perrier, C. & Wilson, B. Cultural differences in family communication about inherited cancer: implications for cancer genetics research. *J. Cult. Divers.* **20**, 195–201 (2013).
39. All of Us Research Program. https://allofus.nih.gov/.
40. Murray, M. F. *et al.* A Proposed Approach for Implementing Genomics-Based Screening Programs for Healthy Adults. *NAM Perspectives* (2018) doi:10.31478/201812a.
41. Harris, P. A. *et al.* Research electronic data capture (REDCap)-A metadata-driven methodology and workflow process for providing translational research informatics support. *J. Biomed. Inform.* **42**, 377–381 (2009).
42. R Core Team. *R: A language and environment for statistical computing*. (2021).

43. Phelps, C., Wood, F., Bennett, P., Brain, K. & Gray, J. Knowledge and expectations of women undergoing cancer genetic risk assessment: a qualitative analysis of free-text questionnaire comments. *J. Genet. Couns.* **16**, 505–514 (2007).
44. Hilgart, J. *et al.* "I have always believed I was at high risk..." The role of expectation in emotional responses to the receipt of an average, moderate or high cancer genetic risk assessment result: a thematic analysis of free-text questionnaire comments. *Fam. Cancer* **9**, 469–477 (2010).
45. Hsieh, H.-F. & Shannon, S. E. Three approaches to qualitative content analysis. *Qual. Health Res.* **15**, 1277–1288 (2005).
46. Fereday, J. & Muir-Cochrane, E. Demonstrating Rigor Using Thematic Analysis: A Hybrid Approach of Inductive and Deductive Coding and Theme Development. *International Journal of Qualitative Methods* **5**, 80–92 (2006).
47. Hoell, C., Aufox, S., Nashawaty, N., Myers, M. F. & Smith, M. E. Comprehension and personal value of negative non-diagnostic genetic panel testing. *J. Genet. Couns.* **30**, 418–427 (2021).

APPENDIX

Table S1: Survey Questions

Timepoint	**Question 1**	**Question 2**	**Question 3**
T0	If you had genetic testing would you share the results of your test with others? YES/NO/DON'T KNOW	Whom would you share them with? (Choose all that apply) • Spouse • Parents • Children • Grandparents/ Grandchildren • Brothers/ Sisters • Aunts/ Uncles/ Cousins • Friends • Spiritual Leader • Coworkers • Employer	N/A
T1	Do you think you would be willing to share the results of your genetic test with relatives or friends? YES/NO/DON'T KNOW	Whom would you share them with? (Choose all that apply) • Same as T0	Will you please tell us more about why you would or would not share your genetic test results with the people you indicated above? FREE TEXT
T2	A. Have you or do you plan to share your genetic results with your doctor? YES/NO/DON'T KNOW B. Have you or do you plan to share the results of your genetic test with relatives or friends? YES/NO/DON'T KNOW	Whom would you share them with? • Same as T0	Will you please tell us more about why you plan to share your genetic test results with the people you indicated above? (if answer to T2B is YES or DON'T KNOW) FREE TEXT

Table S2: Characteristics of groups who dropped out at T0 and T1

	DROPPED OUT AFTER T0 **N=346**	**DROPPED OUT AFTER T1** **N=532**	**ANSWERED T2 SURVEY** **N=1150**
MEAN AGE (SD)	38.2 years (±9.6)	40.1 years (±10.2)	41.1 years (±10.3)
T0 PLAN TO SHARE RESULT			
YES	218 (63%)	356 (66.9%)	803 (69.8%)
NO	41 (11.8%)	40 (7.5%)	65 (5.7%)
DON'T KNOW	87 (25.1%)	135 (25.4%)	281 (24.4%)
NO ANSWER		1 (0.2%)	1 (0.1%)
T1 PLAN TO SHARE RESULT			
YES		594 (80.6%)	806 (70.1%)
NO		32 (4.7%)	30 (2.6%)
DON'T KNOW		117 (14.7%)	155 (13.5%)
NO ANSWER			159 (13.8%)
T2 PLAN TO SHARE RESULT			
YES			753 (65.4%)
NO			262 (22.8%)
DON'T KNOW			135 (11.7%)

Table S3: Association between demographic factors and answer

	T0					**T2**				
VARIABLE	Yes n (%)	No	Don't know	χ^2 statistic (df)	p-value	Yes	No	Don't know	χ^2 statistic (df)	p-value
GENDER										
FEMALE	446 (73.4)	22 (3.6)	140 (23)	8.04 (4)	0.09 NS	416 (68.4)	124 (20.4)	68 (11.2)	6.48 (4)	0.17 NS
MALE	224 (66.3)	21 (6.2)	93 (27.5)			212 (62.5)	85 (25.4)	41 (12.1)		
OTHER	14 (82.4)	1 (5.9)	2 (11.8)			14 (82.4)	3 (17.6)			
AGE										
<45 YEARS	495 (68.4)	43 (5.9)	186 (25.7)	2.25 (2)	0.32 NS	467 (64.4)	175 (24.1)	83 (11.4)	2.22 (2)	0.33 NS
≥45 YEARS	307 (72.6)	22 (5.2)	94 (22.2)			285 (67.4)	86 (20.3)	52 (12.3)		
EDUCATION										
LESS THAN COLLEGE GRAD	105 (74.5)	5 (3.5)	31 (22)	0.88 (2)	0.65 NS	94 (66.7)	34 (24.1)	13 (9.2)	0.69 (2)	0.71 NS
COLLEGE GRAD OR HIGHER	614 (70.9)	41 (4.7)	211 (24.4)			577 (66.6)	192 (22.1)	98 (11.3)		
PERSONAL CANCER HISTORY										
YES	111 (73.5)	8 (5.3)	32 (21.2)	1.01 (2)	0.60 NS	106 (70.2)	30 (19.9)	15 (9.9)	1.01 (2)	0.61 NS
NO	612 (70.5)	40 (4.6)	216 (24.9)			574 (66.1)	199 (22.9)	96 (11)		
FAMILY CANCER HISTORY										
YES	308 (75.1)	16 (3.9)	86 (21)	9.13 (2)	**0.01**	292 (71.2)	77 (18.8)	41 (10)	9.33 (2)	**0.009**
NO	495 (67)	49 (6.6)	195 (26.4)			461 (62.3)	185 (25)	94 (12.7)		

Table S4: Multivariate analysis of association of positive result with sharing, controlled for family history

FACTOR	*β*	*ADJUSTED OR (95% CI)*	*P-VALUE*
POSITIVE RESULT	1.17	3.21 (1.43-7.25)	0.00484
POSITIVE RESULT CONTROLLED FOR FAMILY HISTORY	1.13	3.10 (1.38-7)	0.00634

Table S5: Characteristics of groups who did and did not answer the free text questions

	T1 BLANK N=179	**T1 ANSWERED N=474**	**T2 BLANK N=270**	**T2 ANSWERED N=383**
GENDER				
MALE	43 (24%)	119 (25.1%)	77 (28.5%)	85 (22.2%)
FEMALE	74 (41.3%)	300 (63.3%)	139 (51.5%)	235 (61.4%)
OTHER	0	4 (0.8%)	1 (0.4%)	3 (0.8%)
NO ANSWER	63 (35.2%)	51 (10.8%)	53 (19.6%)	60 (15.7%)
RESULT				
POSITIVE	9 (5%)	24 (5.1%)	6 (2.2%)	27 (7%)
UNINFORMATIVE	170 (95%)	450 (94.9%)	264 (97.8%)	356 (93%)
RACE				
ALASKA NATIVE	2 (1.1%)	6 (1.3%)	2 (0.7%)	6 (1.6%)
AMERICAN INDIAN	8 (4.5%)	32 (6.8%)	14 (5.2%)	26 (6.8%)
ASIAN	67 (37.4%)	221 (46.6%)	136 (50.4%)	152 (39.7%)
BLACK/AFRICAN AMERICAN	6 (3.4%)	30 (6.3%)	14 (5.2%)	22 (5.7%)
NATIVE HAWAIIAN	0	2 (0.4%)	0	2 (0.5%)
OTHER PACIFIC ISLANDER	5 (2.8%)	5 (1.1%)	3 (1.1%)	7 (1.8%)
WHITE	45 (25.1%)	255 (53.8%)	99 (36.7%)	201 (52.5%)
OTHER	9 (5%)	20 (4.2%)	12 (4.4%)	17 (4.4%)
DON'T KNOW	0	2 (0.4%)	1 (0.4%)	1 (0.3%)
NO ANSWER	58 (32.4%)	8 (1.7%)	32 (11.9%)	34 (8.9%)
ETHNICITY				
HISPANIC	19 (10.6%)	68 (14.3%)	37 (13.7%)	50 (13.1%)
NON-HISPANIC	101 (56.4%)	388 (81.9%)	198 (73.3%)	291 (76%)
NO ANSWER	59 (33%)	18 (3.8%)	35 (13%)	42 (11%)
EDUCATION LEVEL				
LESS THAN HIGH SCHOOL	0	0	0	0
HIGH SCHOOL/GED	2 (1.1%)	9 (1.9%)	5 (1.9%)	7 (1.8%)
SOME COLLEGE	14 (7.8%)	67 (14.1%)	32 (11.9%)	49 (12.8%)
COLLEGE GRADUATE	53 (29.6%)	196 (41.4%)	105 (38.9%)	144 (37.6%)
ADVANCED DEGREE	54 (30.2%)	197 (41.6%)	98 (36.3%)	153 (39.9%)
NO ANSWER	56 (31.3%)	5 (1.1%)	30 (11.1%)	30 (7.8%)
HOUSEHOLD INCOME				
LESS THAN $50,000	11 (6.1%)	62 (13.1%)	37 (13.7%)	36 (9.4%)
$50-100,000	35 (19.6%)	116 (24.5%)	63 (23.3%)	88 (23%)
MORE THAN $100,000	63 (35.2%)	258 (54.4%)	116 (43%)	205 (53.5%)
NO ANSWER	70 (39.1%)	38 (8%)	54 (20%)	54 (14.1%)
PERSONAL HISTORY OF CANCER	24 (13.4%)	104 (21.9%)	48 (17.8%)	80 (20.9%)
FAMILY HISTORY OF CANCER	53 (29.6%)	204 (43%)	100 (37%)	157 (41%)