

ADDITIONAL FILE 1

Implementing genomic screening in diverse populations

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Supplementary Tables:

1. **Table S1.** Questions from a return of genomic results preference survey administered to previously enrolled BioMe Biobank participants.
2. **Table S2.** Demographic characteristics of BioMe participants who were respondents of a return of genomic results preference survey (N = 72), and characteristics of all adult BioMe participants enrolled at the time of the survey (N = 31,213).
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1. **Fig. S1. A model for returning genomic results to biobank research participants without prior knowledge of genomic risk.** After genomics-first identification of variant positive individuals, they receive genetic counseling and are then referred to specialty provider(s) for further evaluation and initiation of risk management.
2. **Fig. S2. Pre-pilot survey to understand BioMe participants' (N = 72) preferences regarding the hypothetical return of results.** **A)** Decision to enroll into biobank research if the program returned genomic results. **B)** Selected reasons for receiving or not receiving genomic results. **C)** Selected categories of genomic results participants would want to receive.

Table S1. Questions from a return of genomic results preference survey administered to previously enrolled BioMe Biobank participants.

Question	Answer options
If, during your enrollment in <i>BioMe</i> , the recruiter told you that you COULD receive genetic research results from your participation, do you think you still would have enrolled?	<ul style="list-style-type: none"> • Definitely yes • Probably yes • Not sure • Probably not • Definitely not
What do you think are good reasons to receive genetic research results? (Check all that apply)	<ul style="list-style-type: none"> • To help myself (for example, by finding out what diseases I am at risk for) • To help my family (for example, by finding out what diseases could run in the family) • To help me make decisions about having children (for example, by finding out what diseases could be passed on to them) • I feel ownership of my genetic research results • Other (please specify)
What do you think are good reasons NOT to receive genetic research results? (Check all that apply)	<ul style="list-style-type: none"> • Concerns about my privacy • Concerns about discrimination (health insurance, life insurance, employment, or other) • Cannot make health changes based on genetic research results • Receiving genetic research results would cause me or my family anxiety • Other (please specify)
If given the choice, what type of genetic research results would you want to receive?	<ul style="list-style-type: none"> • Only genetic research results that the researcher thinks are important • Only genetic research results about specific diseases that I think are important • Only genetic research results about specific diseases that experts in genetics think are important and should be received by everyone • All genetic research results, including those that are uncertain and/or cannot be interpreted at the moment • None (I would not want to receive genetic research results)
If you were to receive genetic research results, how would you want to be informed?	<ul style="list-style-type: none"> • By phone • By a letter in the mail • In person • Not applicable (I would not want to receive genetic research results)
If you were to receive genetic research results, who would you want to inform you?	<ul style="list-style-type: none"> • My primary care doctor that I see regularly for my healthcare • A genetic counselor (a health professional trained in genetic diseases, particularly in returning and discussing implications of genetic testing results) • A medical geneticist (a doctor who is specially trained in diagnosing and treating genetic diseases) • A <i>BioMe</i> Biobank researcher or research coordinator • Not applicable (I would not want to receive genetic research results)

Table S2. Demographic characteristics of BioMe participants who were respondents of a return of genomic results preference survey (N = 72), and characteristics of all adult BioMe participants enrolled at the time of the survey (N = 31,213).

Demographic characteristics (number of survey respondents)	Survey respondents N (%)	BioMe participants N (%)	Chi-squared P value
Female (72)	43 (59.7)	18449 (59.1)	0.9
Age range (72)			
18 to 30 years	27 (37.5)	2149 (6.9)	<0.0001
31 to 50 years	16 (22.2)	8823 (28.3)	
51 to 70 years	26 (36.1)	13538 (43.4)	
71 years and over	3 (4.2)	6703 (21.5)	
Born in the U.S. (71)	62 (87.3)	19692 (63.1)	<0.0001
Self-reported ancestry (72)			
African American/African	9 (12.5)	7670 (24.6)	0.07
East/Southeast Asian	2 (2.8)	866 (2.8)	
Hispanic/Latinx	24 (33.3)	11072 (35.5)	
European	30 (41.7)	9459 (30.3)	
Native American, Other, or Multiple Selected	7 (9.7)	2146 (6.9)	
Jewish (70)	20 (28.6)	-	-
Identify as religious (69)	39 (56.5)	-	-
Have children (70)	26 (37.1)	-	-
Highest level of school completed or highest degree (70)			
Less than high school degree	1 (1.4)	-	-
High school degree or equivalent (e.g. GED)	4 (5.7)	-	-
Some college but no degree	16 (22.9)	-	-
Associate degree	4 (5.7)	-	-
Bachelor degree	26 (37.1)	-	-
Graduate degree	19 (27.1)	-	-
Average household income (66)			
Less than \$20,000	9 (13.6)	-	-
\$20,000-\$39,000	6 (9.1)	-	-
\$40,000-\$59,000	14 (21.2)	-	-
\$60,000-\$79,000	9 (13.6)	-	-
\$80,000-\$149,000	10 (15.1)	-	-
\$150,000 or more	18 (27.2)	-	-

Table S3. Clinically confirmed pathogenic, likely pathogenic, and downgraded variants in a pilot genomic screening program.

Gene	CHR:POS:REF:ALT	cDNA Position	Protein Position	# Heterozygous Carriers	Interpretation ^a
BRCA1	17:43057062:T:TG	c.5266dupC	p.Gln1756fs	2	Pathogenic
	17:43124027:ACT:A	c.68_69delAG	p.Glu23fs	4	Pathogenic
	17:43094472:C:T	c.1059G>A	p.Trp353Ter	1	Pathogenic
	17:43063917:A:C	c.5109T>G	p.Tyr1703Ter	1	Pathogenic
	17:43049191:TG:T	c.5335delC	p.Gln1779fs	1	Pathogenic
	17:43092615:TC:T	c.2915delG	p.Gly972fs	1	Pathogenic
	17:43091455:T:TGC	c.4074_4075dupGC	p.Gln1359fs	1	Likely pathogenic
BRCA2	13:32340128:C:T	c.5773C>T	p.Gln1925Ter	1	Pathogenic
	13:32338277:G:T	c.3922G>T	p.Glu1308Ter	2	Pathogenic
	13:32319298:G:T	c.289G>T	p.Glu97Ter	1	Pathogenic
	13:32380085:C:T	c.9196C>T	p.Gln3066Ter	1	Pathogenic
	13:32340300:GT:G	c.5946delT	p.Ser1982fs	3	Pathogenic
	13:32336781:T:G	c.2426T>G	p.Leu809Ter	1	Pathogenic
	13:32338783:CA:C	c.4429delA	p.Ile1477fs	1	Pathogenic
	13:32370955:G:A	c.8488-1G>A		1	Pathogenic
	13:32339489:G:T	c.5134G>T	p.Gly1712Ter	1	Pathogenic
	13:32340836:GACAA:G	c.6486_6489delACAA	p.Lys2162fs	1	Pathogenic
	13:32336684:G:GA	c.2330dupA	p.Asp777fs	1	Pathogenic
	13:32333282:G:T	c.1804G>T	p.Gly602Ter	1	Pathogenic
MLH1	3:37012098:C:T	c.676C>T	p.Arg226Ter	1	Pathogenic
MSH6	2:47799823:TC:T	c.1842delC	p.Cys615fs	1	Pathogenic
PMS2	7:6005918:C:A	c.137G>T	p.Ser46Ile	1	Pathogenic
	7:5986838:G:A	c.1927C>T	p.Gln643Ter	1	Pathogenic
	7:5986933:A:AT	c.1831dupA	p.Ile611fs	1	Pathogenic
	7:6003793:C:A	c.251-1G>T		1	Likely pathogenic
APOB	2:21006288:C:T	c.10580G>A	p.Arg3527Gln	1	Pathogenic
	2:21002392:CAT:C	c.13028_13029delAT	p.Tyr4343fs	2	Uncertain
	2:21006128:G:C	c.10740C>G	p.Asn3580Lys	2	Uncertain
	2:21005155:TG:T	c.11712delC	p.Asn3904Lysfs	1	Pathogenic ^b
LDLR	19:11116198:A:G	c.1691A>G	p.Asn564Ser	1	Likely pathogenic
	19:11105441:G:A	c.535G>A	p.Glu179Lys	1	Likely pathogenic
	19:11120143:C:T	c.1897C>T	p.Arg633Cys	1	Pathogenic
	19:11123263:C:T	c.2230C>T	p.Arg744Ter	1	Pathogenic
	19:11105567:G:A	c.661G>A	p.Asp221Asn	1	Pathogenic
	19:11116153:G:A	c.1646G>A	p.Gly549Asp	1	Pathogenic
	19:11113608:G:A	c.1432G>A	p.Gly478Arg	1	Likely pathogenic
	19:11113343:G:A	c.1252G>A	p.Glu418Lys	1	Uncertain
	19:11120106:G:T	c.1860G>T	p.Trp620Cys	1	Uncertain
	19:11120188:T:G	c.1942T>G	p.Ser648Ala	2	Uncertain
	19:11131285:A:G	c.2552A>G	p.Gln851Arg	1	Uncertain
19:11105507:G:A	c.601G>A	p.Glu201Lys	1	Uncertain	
19:11105572:C:T	c.666C>T	p.D222=	1	Uncertain	
TTR	18:31598655:G:A	c.424G>A	p.Val142Ile	33	Pathogenic
	18:31592974:G:A	c.148G>A	p.Val50Met	1	Pathogenic

^a Only pathogenic and likely pathogenic variants associated with conditions included in the pilot genomic screening program were disclosed to consenting participants.

^b This *APOB* variant is associated with hypobetalipoproteinemia.

cDNA and protein position provided for NM_007294.3 (*BRCA1*), NM_000059.3 (*BRCA2*), NM_000249.3 (*MLH1*), NM_000179.2 (*MSH6*), NM_000535.5 (*PMS2*), NM_000384.2 (*APOB*), NM_000527.4 (*LDLR*), and NM_000371.3 (*TTR*); Human reference genome build 38 (GRCh38).

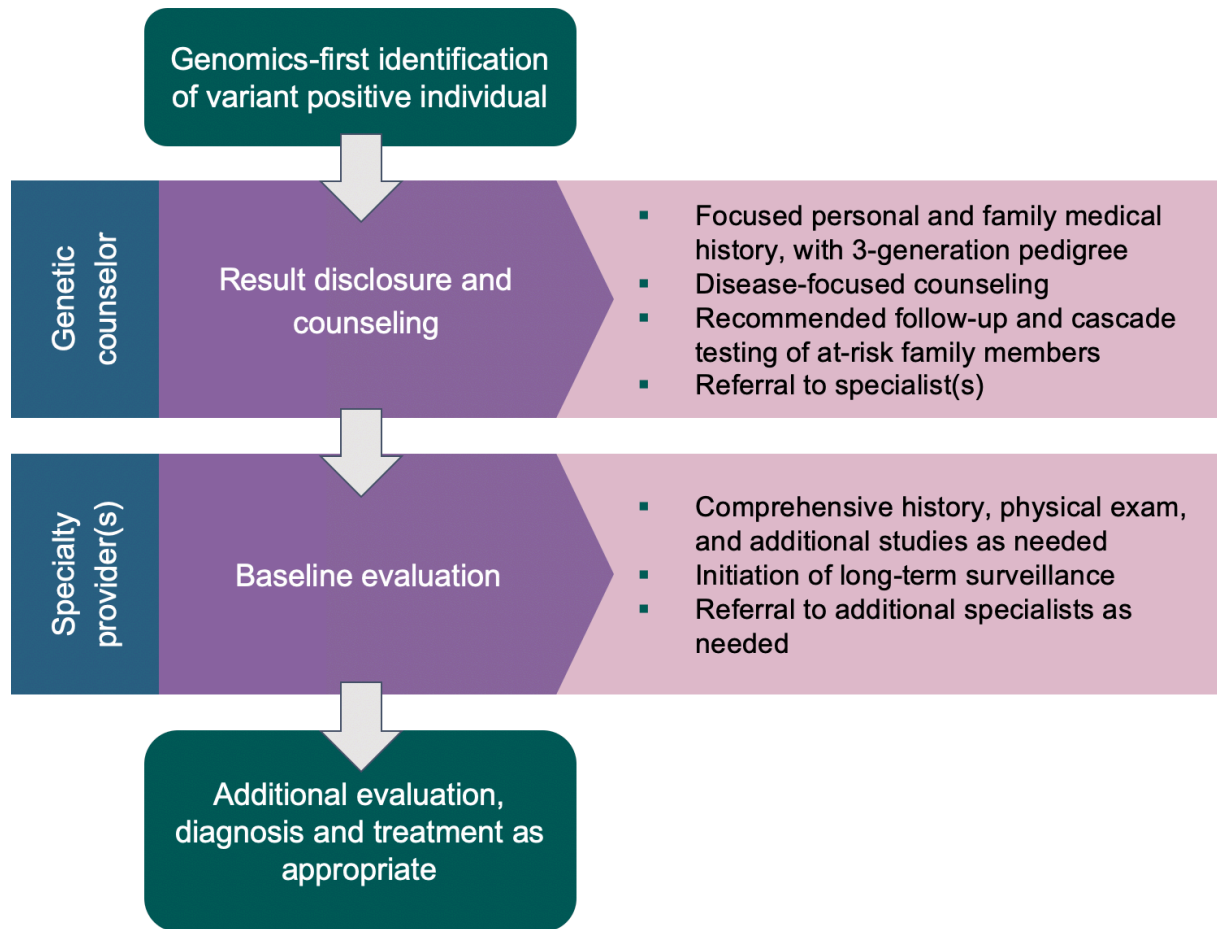
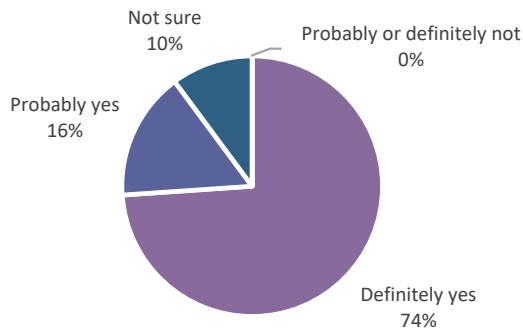
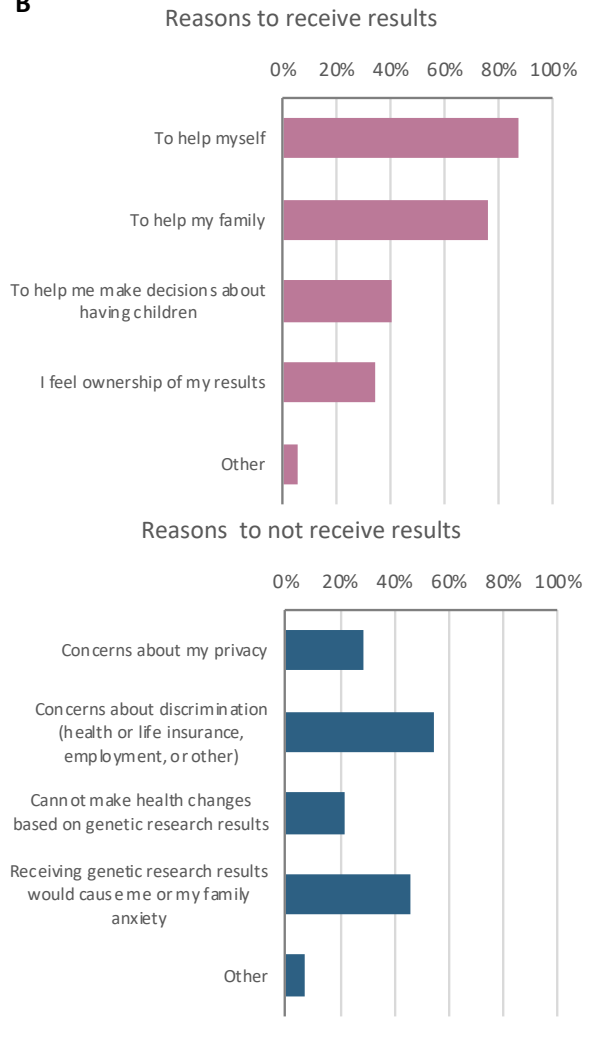


Fig. S1. A model for returning genomic results to biobank research participants without prior knowledge of genomic risk. After genomics-first identification of variant positive individuals, they receive genetic counseling and are then referred to specialty provider(s) for further evaluation and initiation of risk management.

A If you had been told you could receive genomic results from BioMe, do you think you still would have enrolled?



B



C Types of results you would want to receive

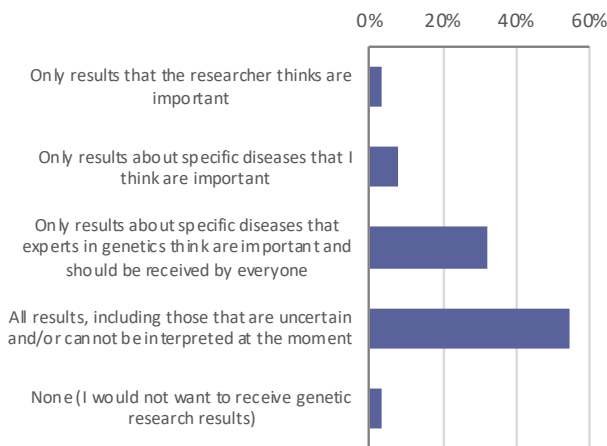


Fig. S2. Pre-pilot survey to understand BioMe participants' (N = 72) preferences regarding the hypothetical return of results. A) Decision to enroll into biobank research if the program returned genomic results. B) Selected reasons for receiving or not receiving genomic results. C) Selected categories of genomic results participants would want to receive.