Supplementary Online Content

Kurian AW, Ward KC, Hamilton AS, et al. Uptake, results, and outcomes of germline multiple-gene sequencing after diagnosis of breast cancer. *JAMA Oncol*. Published online May 10, 2018. doi:10.1001/jamaoncol.2018.0644

This supplementary material has been provided by the authors to give readers additional information about their work.

Online-Only Material

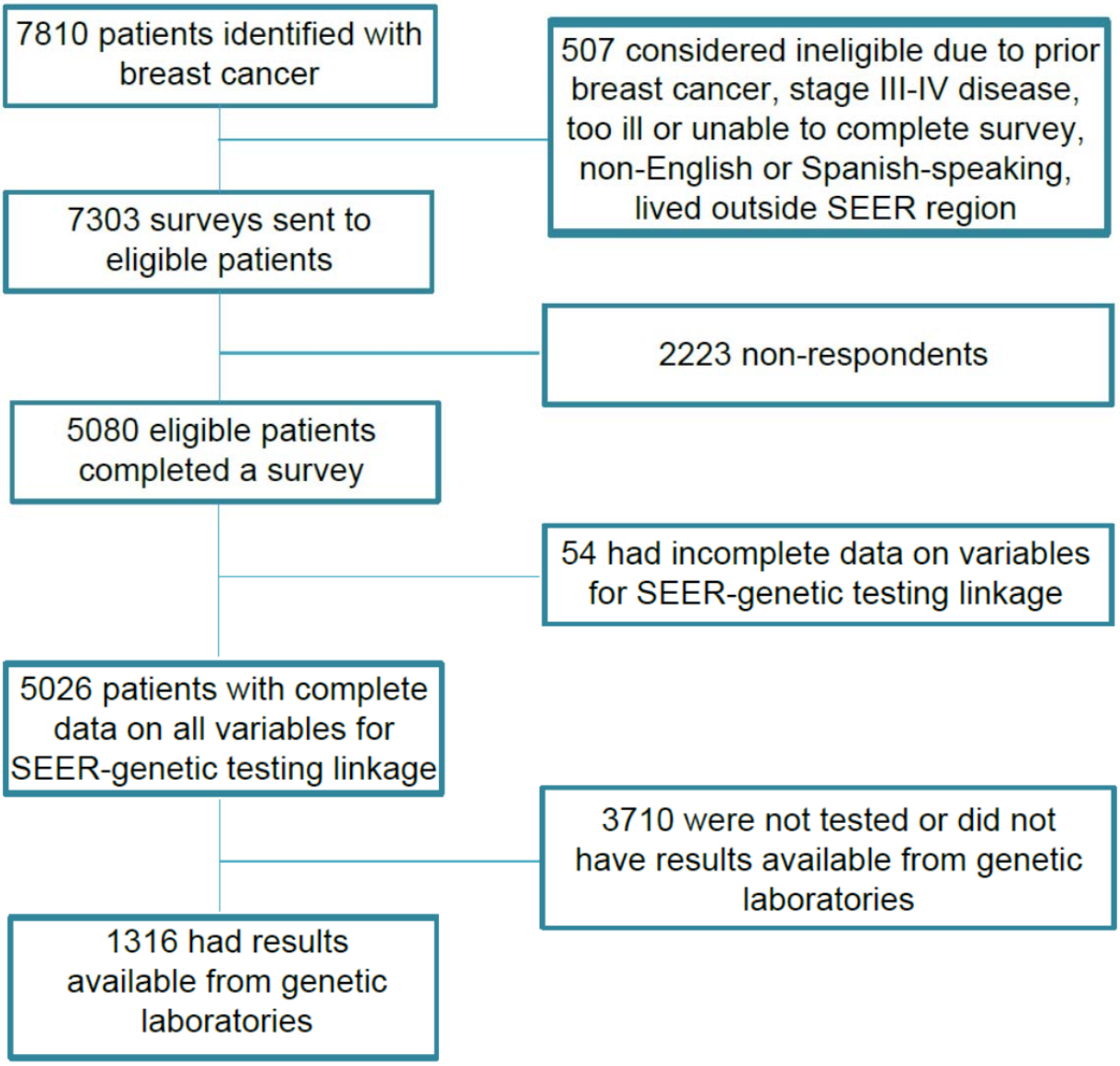
eFigure 1. Patient flow diagram, depicting the flow of patients into the study from those initially identified to the final analytic sample.

eTable 1. Demographic and clinical characteristics of patients by genetic test type

eFigure 2. Multivariable analysis among tested patients of the correlates of receiving multiple-gene sequencing versus a *BRCA1/2*-only test, n=1,316 patients with complete information for all variables in the model. Diamonds represent point estimates and bars represent 95% confidence intervals; the X-axis is on a log scale.

eTable 2. Tested genes and pathogenic variants

eFigure 1. Patient flow diagram, depicting the flow of patients into the study from those initially identified to the final analytic sample.



eTable 1. Demographic and Clinical Characteristics of Patients by Genetic Test Type			
	No Genetic Test[1] n=3,710	**Multiple-Gene Sequencing[1] n=588**	***BRCA1/2*-Only[1] n=728**
Test Results[2]			
Negative	-	61.6	91.7
Variant of Uncertain Significance only	-	29.8	3.2
BRCA1/2 Pathogenic Variant	-	4.1	5.1
Other Gene Pathogenic Variant	-	4.6	0.0
Age (Years)			
≥50	94.3	64.6	59.6
<50	5.7	35.4	40.4
Geographic Site[3]			
Georgia	52.0	61.3	54.4
Los Angeles County	48.0	38.7	45.6
Race/Ethnicity			
White, non-Hispanic	53.2	61.7	61.7
Black	19.3	15.2	13.2
Hispanic	15.4	10.8	15.0
Asian	9.6	9.9	7.5
Other or unknown	2.5	2.4	2.5
Education			
High school graduate or less	32.5	17.8	16.6
Some college	30.4	25.3	31.7
College graduate or more	34.9	53.8	51.0
Missing	2.1	3.2	0.7
Marital Status			
Not married	41.7	31.8	29.3
Married or partnered	58.3	68.2	70.7
Income			
<$20,000	16.3	8.6	7.6
$20,000 - $60,000	28.9	24.5	25.3
≥$60,000	35.3	54.6	52.6
Missing	19.5	12.3	14.7
Insurance			
Medicaid	10.5	8.6	7.0
Medicare and/or Veteran's Affairs	35.3	16.5	16.9

Private or other	53.2	73.4	75.7
None	1.0	1.6	0.5
Comorbidities			
None	54.6	63.6	61.9
One	30.3	26.1	30.1
Two or more	15.1	10.3	8.0
Tumor Grade			
Grade 1	23.8	20.2	19.3
Grade 2	46.3	39.7	44.5
Grade 3	26.6	34.7	32.5
Unknown	3.3	5.4	3.7
Stage			
0	25.8	29.0	26.5
I	49.1	46.9	45.6
II	24.2	22.5	27.4
Missing	0.9	1.6	0.6
Tumor T Stage and Size			
Tis (*in situ*)	25.8	29.0	26.5
T1 (<2 centimeters (cm))	55.2	52.1	49.7
T2 (2-5 cm)	18.2	17.8	23.2
TX (missing)	0.8	1.1	0.6
Estrogen/Progesterone Receptor (ER/PR)			
ER positive only	12.5	11.4	10.6
PR positive only	0.7	0.4	0.9
ER and PR both positive	73.6	72.4	72.7
Neither ER nor PR positive	13.2	15.8	15.8
HER2 Status			
HER2 negative	63.9	61.6	65.3
HER2 positive	8.8	9.4	10.5
Missing or borderline	27.3	29.0	24.2
Axillary Lymph Node Involvement			
No	47.8	42.8	40.0
Yes	51.8	56.8	60.0
Missing	0.4	0.4	0.0
Surgical Treatment			
Breast conserving surgery	66.4	47.5	49.9

Unilateral mastectomy	20.2	13.2	14.2
Contralateral prophylactic mastectomy	11.9	38.1	35.4
Missing	1.5	1.2	0.5
Patient Pre-Test Risk of Mutation[4]			
Average risk	81.1	45.5	46.5
Higher risk	18.9	54.5	53.5
Tumor Laterality			
Unilateral	95.5	90.5	91.0
Bilateral	4.6	9.5	9.0

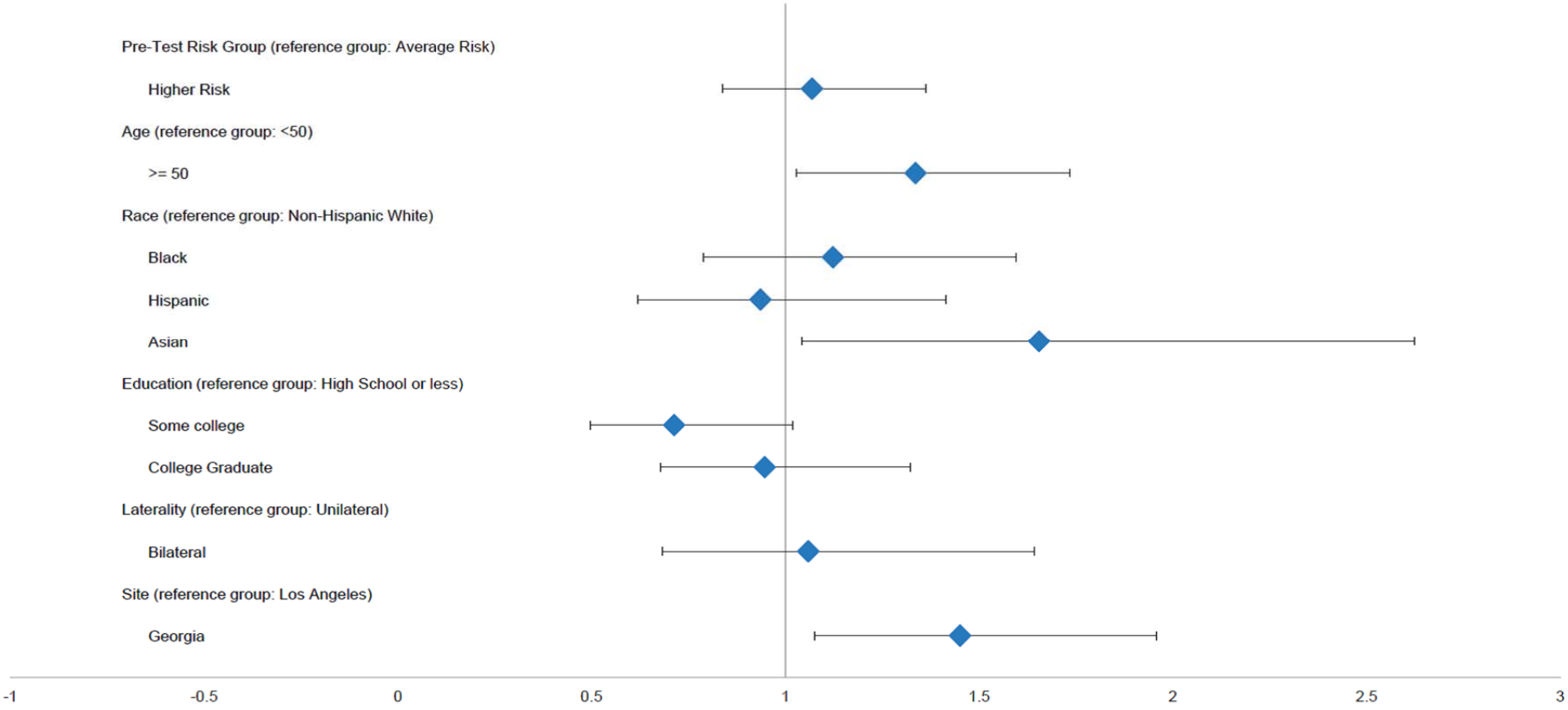
[1]We used survey design and non-response weights to compensate for the differential probability of patient selection and survey non-response among subgroups with various characteristics. Weighted percentages are shown.

[2]Significantly different at 0.01 confidence level based on chi square test

[3]Significantly different at 0.05 confidence level based on chi square test

[4]Patients were considered at higher pre-test risk if they had any of the following: age at breast cancer diagnosis ≤45 years, triple-negative breast cancer diagnosed at age <60; any relative with ovarian cancer, sarcoma or male breast cancer; two or more first-degree relatives with breast cancer (for patients diagnosed at ≤50, one or more first-degree relative with breast cancer); Ashkenazi Jewish ancestry; or family history of a pathogenic variant conferring high risk (e.g., *BRCA1/2*), consistent with criteria for genetic testing according to guidelines of the National Comprehensive Cancer Network.

eFigure 2. Multivariable analysis among tested patients of the correlates of receiving multiple-gene sequencing versus a *BRCA1/2*-only test, n=1,316 patients with complete information for all variables in the model. Diamonds represent point estimates and bars represent 95% confidence intervals; the X-axis is on a log scale.



eTable 2: Tested Genes* and Pathogenic Variants	
Gene Name	Pathogenic Variants (n)
APC	2
ATM[†]	3
AXIN2	0
BAP1	0
BARD1	1
BMPR1A	0
BRCA1[†]	32
BRCA2[†]	32
BRIP1	2
CDH1[†]	0
CDK4	0
CDKN2A	0
CHEK2[†]	4
EPCAM	0
FANCC	0
FH	0
FLCN	0
GREM1	0
MEN1	0
MET	0
MITF	0
MLH1	1
MRE11A	0
MSH2	0
MSH6	1
MUTYH	0
NBN[†]	1
NF1[†]	1
PALB2[†]	3
PMS2	2
POLD1	0
POLE	0
PTEN[†]	0
RAD50	1
RAD51C	2
RAD51D	1
RET	0

SDHA	0
SDHAF2	0
SDHB	0
SDHC	0
SDHD	0
SMAD4	0
SMARCA4	0
STK11[†]	0
TMEM127	0
TP53[†]	0
TSC1	0
TSC2	0
VHL	0
XRCC2	0

*Genes tested in any patient and reported by any of the four participating laboratories were included

[†]Specified as breast cancer susceptibility genes by 2017 National Comprehensive Cancer Network Guidelines