



American Association  
for Cancer Research®

FINDING CURES TOGETHER®

PROJECT **GENIE**®  
Genomics Evidence Neoplasia Information Exchange

# GENIE BPC BRCA1.0- PUBLIC COHORT

November 2025

[AACR.org/GENIE](http://AACR.org/GENIE) • #AACRGENIE

© American Association for Cancer Research



# Release Notes

- The GENIE BPC BRCA 1.0-public dataset contains 1,130 breast cancer patients from 3 institutions: DFCI, MSK, and VICC
- **Data Access:**
  - A subset of the data is available through [cBioPortal](#). Both the genomic and clinical (phenomic) data can be evaluated in cBioPortal with opportunities for data exploration and visualization using a user-friendly interface.
  - The complete, post-processed data are available on [Synapse](#).
- **What is included in GENIE BPC data?**
  - **Genomic Data:** Clinical-grade next-generation sequencing data for each patient from the GENIE Registry. Genomic profiling was performed between 2013 and 2018; patients were aged 18-56 at the time of genomic sequencing and include male breast cancers.
  - **Cancer Diagnosis:** Breast cancer diagnosis is considered the index tumor for this patient cohort. There are data about other cancer diagnoses antecedent to the breast cancer and subsequent to the breast cancer.
    - Breast cancer specific fields such as, ER (Estrogen Receptor) status, PR (Progesterone Receptor) status, HER2 (Human Epidermal Growth Factor Receptor 2) status and summary, Oncotype DX recurrence score, multigene signature method and results, band breast subtype classification were also collected.
  - **Pathologic Information:** Each pathology specimen from diagnosis through death or last follow-up is curated with specimen type, site, and histology.

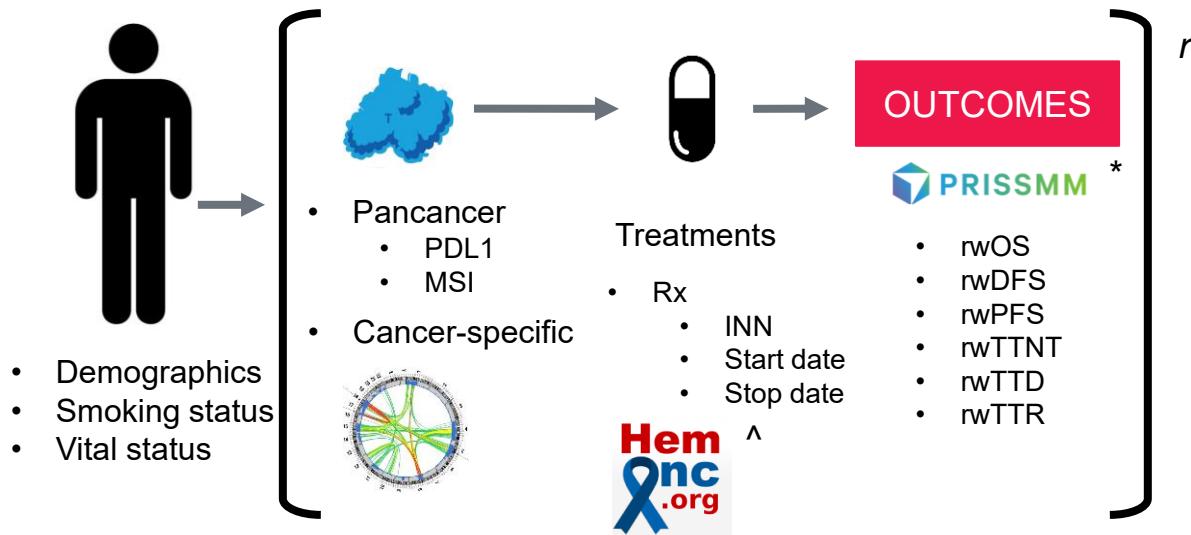
# Release Notes

- **Treatment Histories:** All anti-neoplastic systemic therapies—intravenous and oral chemotherapies—are included in the data set. Dates are provided as intervals from diagnosis to start and stop of each drug. Investigational drugs are masked, no dosing information is included.
- **Imaging Information:** Each CT, MRI, PET-CT scan from diagnosis through death or last follow-up is curated for the presence or absence of cancer and an evaluation of whether the cancer was stable, responding, or progressing. These data are used to compute progression-free survival-imaging (PFS-I). Sites of tumor involvement are also recorded.
- **Medical Oncologist's Evaluations:** Medical oncology notes (1/month) have been curated to ascertain the presence or absence of cancer and whether the cancer was stable, responding, or progressing. These data are used to compute progression-free survival-medonc (PFS-M) from diagnosis through death or date of last follow-up. The ECOG or Karnofsky Performance Status (KPS) were curated when available in the medical oncology note.
- **Overall Survival:** Overall survival is based on death, with censoring at the date last known alive. Ascertainment of death varies by institution.
- **Additional Relevant Biomarkers:** Information about select biomarkers not included on the NGS panels, including PD-L1, MMR, and MSI are also curated.
- **Patient-Reported Outcomes:** No patient-reported outcomes are available in this dataset.
- **Date Masking:** Exact dates are masked to preserve confidentiality; however, date intervals are available, allowing calculation of event times such as diagnosis, treatment start, treatment end, PFS-I, PFS-M, and OS

# Release Notes

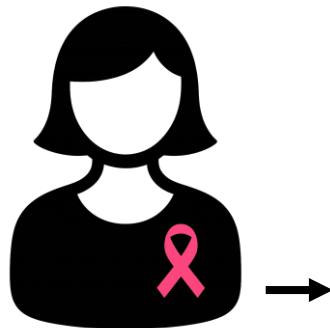
- **Analytical Data Guide:** A more comprehensive overview of the data can be found in the data guide, and a description and location of the variables collected can be found in the variable synopsis spreadsheet.
- **Other Resources:** There is a dedicated [project wiki](#) that describes each of the files.
- **Training Videos:**
  - Demo of GENIE Data on the Synapse and cBioPortal Platforms: [here](#)
  - BPC- specific cBioPortal video training playlist: [here](#)
- **PRISSMM™:** the BPC BrCa dataset uses the PRISSMM™ system licensed and enhanced by Memorial Sloan-Kettering Cancer Center, Memorial Hospital for Cancer and Allied Diseases, and Sloan-Kettering Institute for Cancer Research (collectively “MSK”) is for informational and research purposes only. The content is not intended as a substitute for professional medical advice, diagnosis, or treatment. Original system and improvements © 2019-2022 Dana-Farber Cancer Institute, Inc. Additional functionality and enhancements © 2023 MSK. All rights reserved. Additional information can be found in the analytic data guide and information about licensing PRISSMM™ can be obtained by emailing [PRISSMM@mskcc.org](mailto:PRISSMM@mskcc.org)

# GENIE Data Model



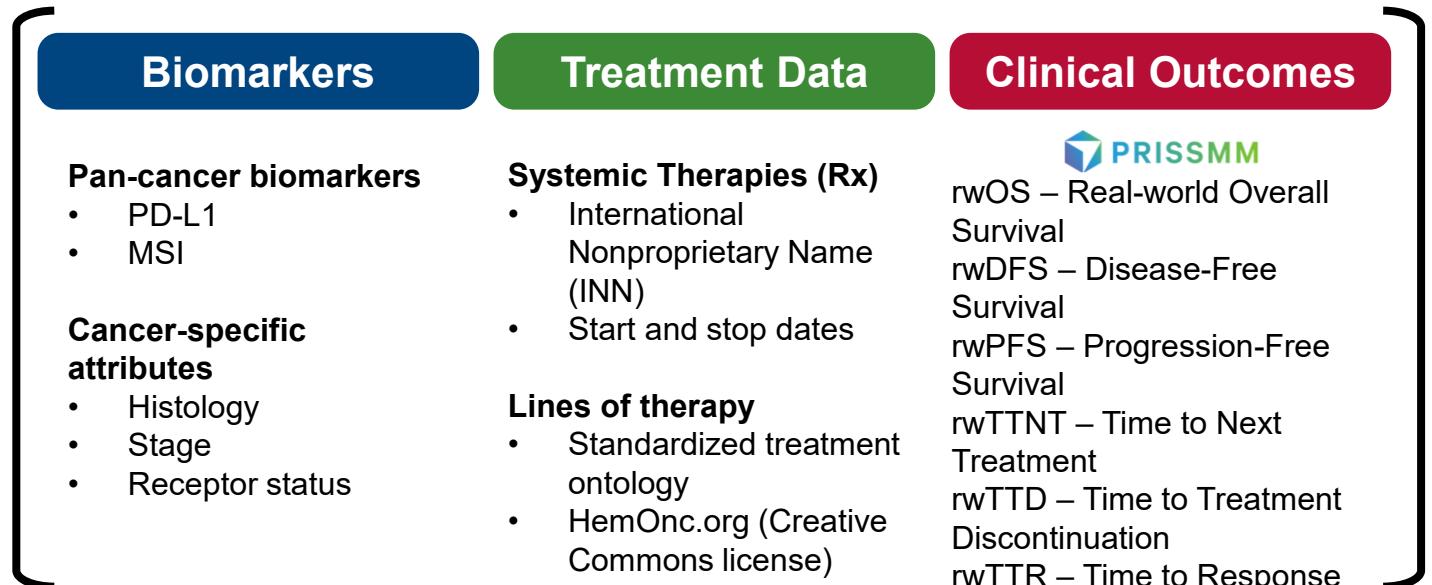
\*PRISSMM is licensed from the DFCI  
^HemOnc is available through a creative commons license

# GENIE BPC Data Model



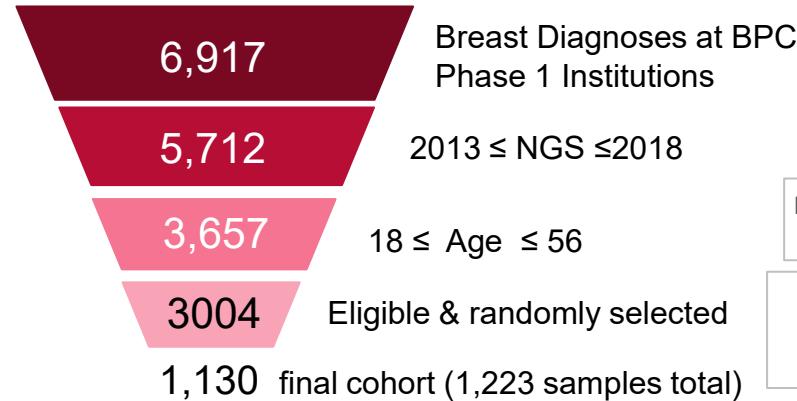
## Core Patient-Level Data

- Demographics
- Smoking history
- Vital status

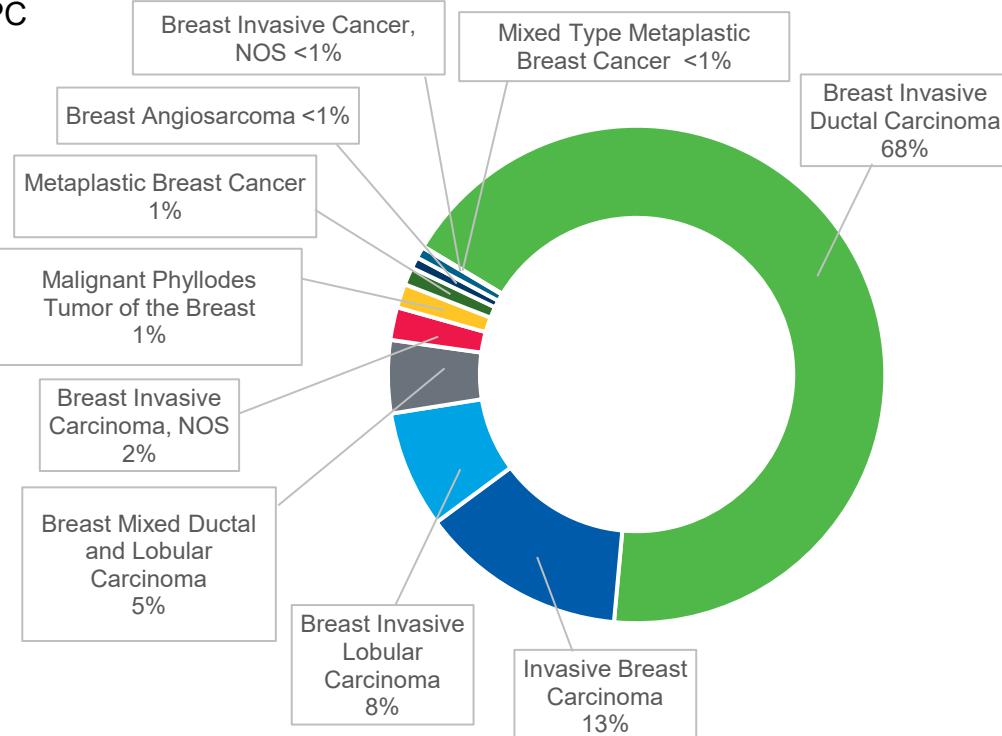


PRISMM™ is licensed from the Dana-Farber Cancer Institute.

# BPC BrCa 1.0-public Cohort Preview



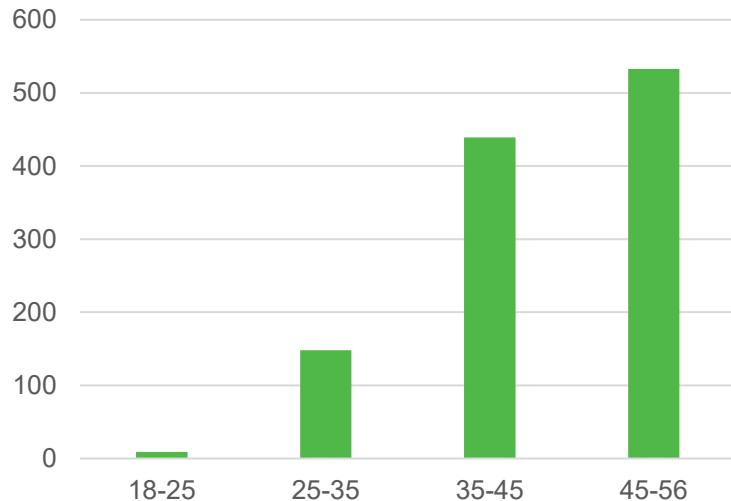
■ Breast Invasive Ductal Carcinoma	□ 830	67.9%
■ Invasive Breast Carcinoma	□ 164	13.4%
■ Breast Invasive Lobular Carcinoma	□ 93	7.6%
■ Breast Mixed Ductal and Lobular ...	□ 58	4.7%
■ Breast Invasive Carcinoma, NOS	□ 26	2.1%
■ Malignant Phyllodes Tumor of the ...	□ 19	1.6%
■ Metaplastic Breast Cancer	□ 14	1.1%
■ Breast Angiosarcoma	□ 9	0.7%
■ Breast Invasive Cancer, NOS	□ 9	0.7%
■ Mixed Type Metaplastic Breast C...	□ 1	<0.1%



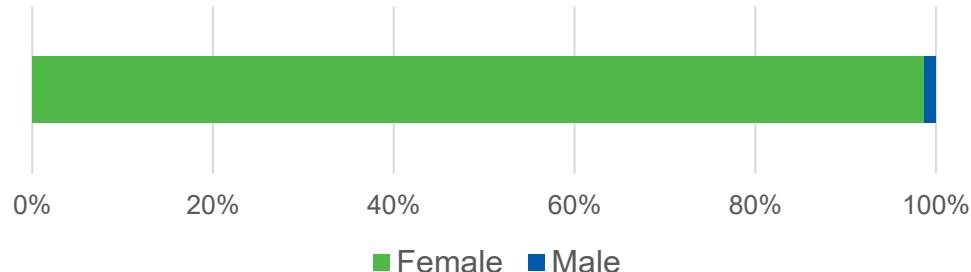
\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE®

# BPC BrCa 1.0-public Demographics

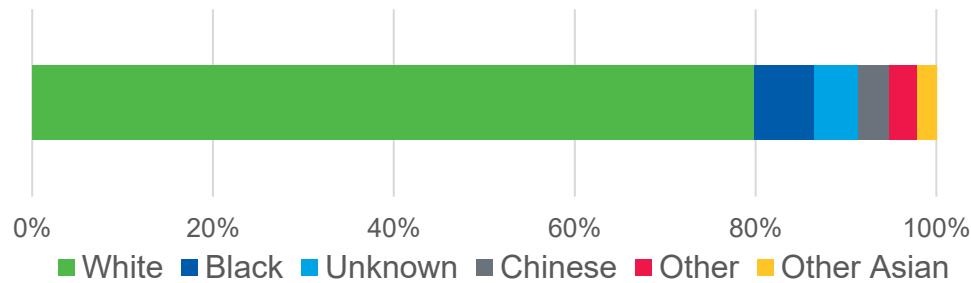
## Age at Diagnosis



## Sex

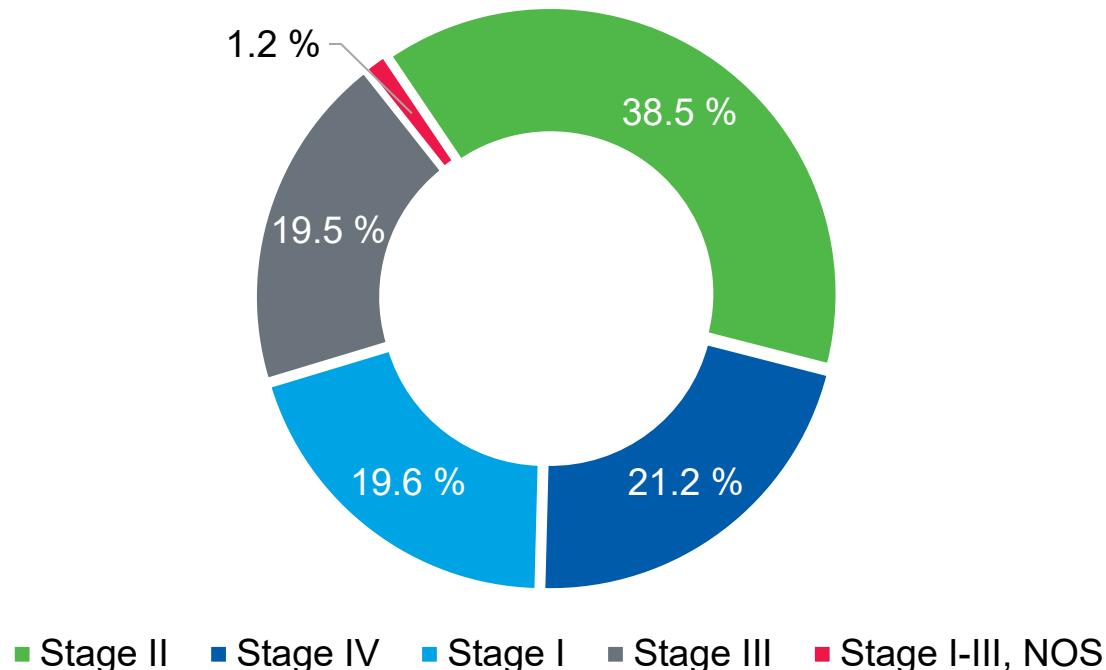


## Primary Race



\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE ®

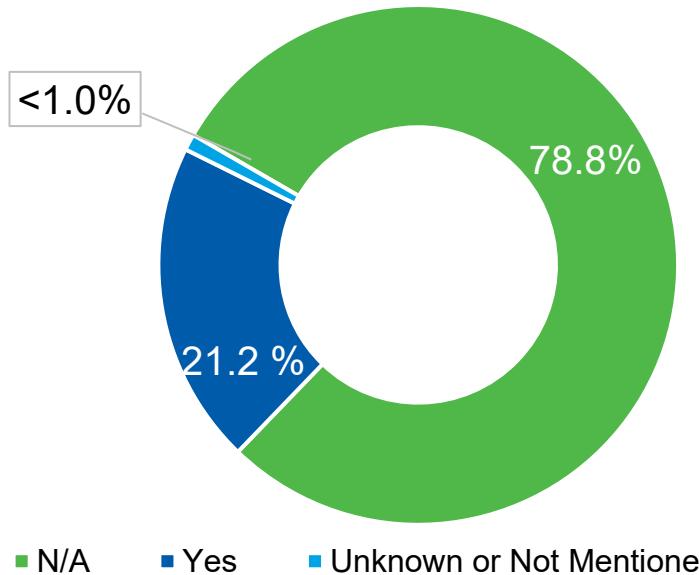
# BPC BrCa 1.0-public: Stage at Diagnosis



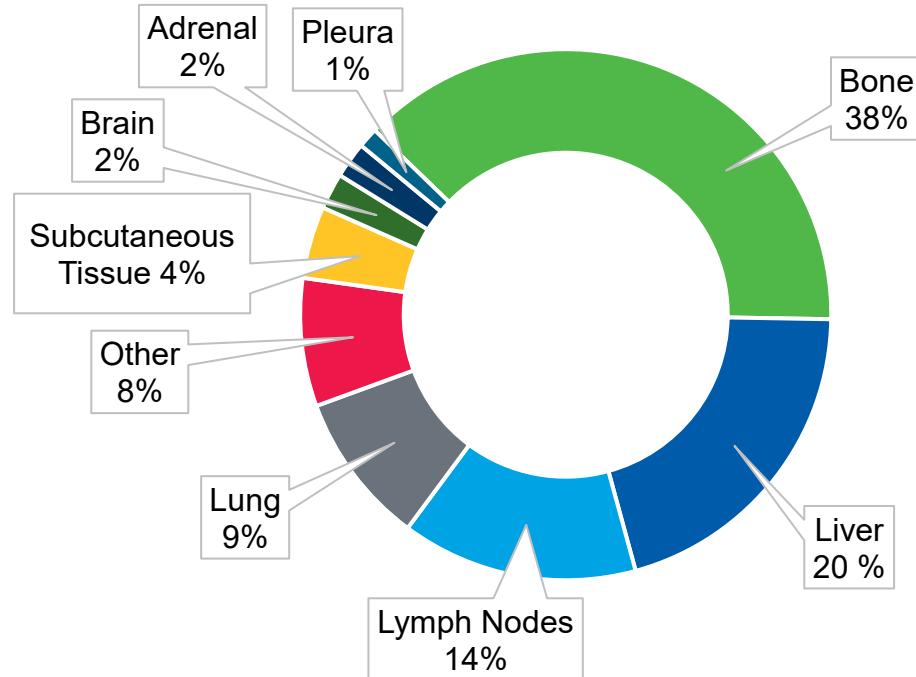
\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE®

# BPC BrCa 1.0-public: Sites of Metastases at Diagnosis

Patients with Distant Metastases at Diagnosis



Distribution of Sites of Distant Metastasis



\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE®

# BPC BrCa 1.0-public: Detailed Clinical Genomics

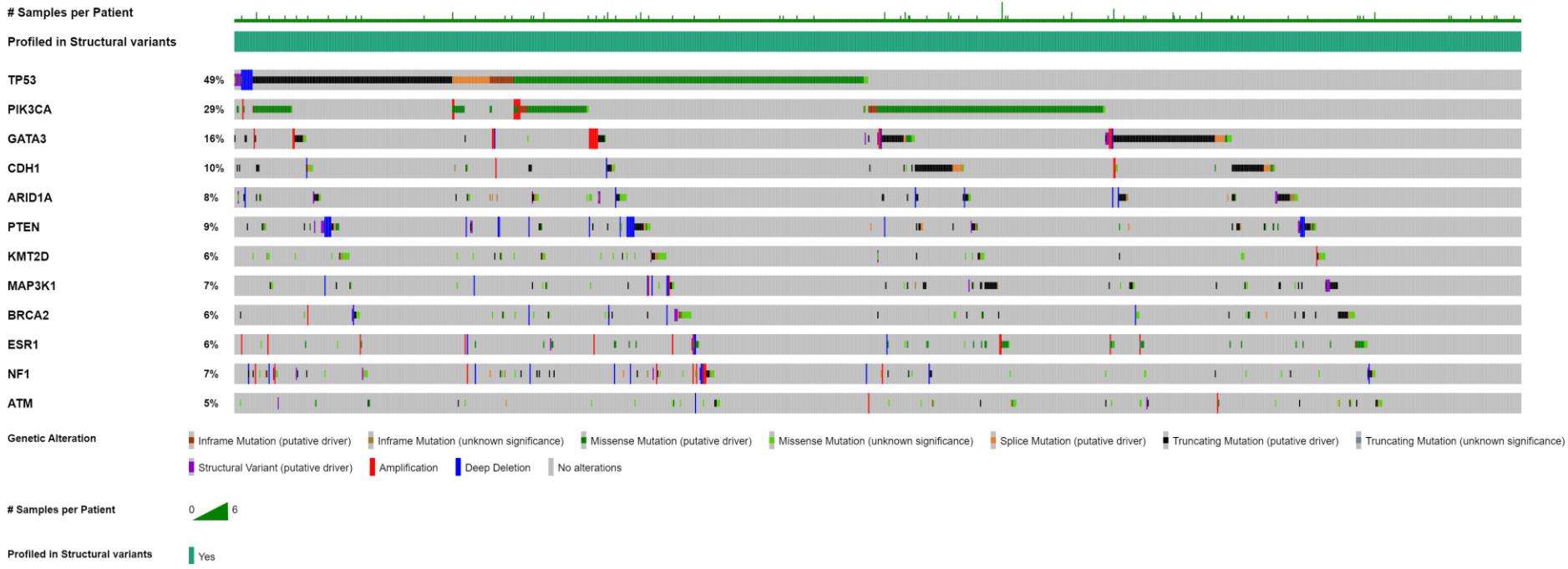
Mutated Genes (1223 profiled samples)				
Gene	# Mut	#	Freq	
TP53	584	<input type="checkbox"/> 565	46.2%	
PIK3CA	397	<input type="checkbox"/> 350	28.6%	
GATA3	187	<input type="checkbox"/> 176	14.4%	
CDH1	125	<input type="checkbox"/> 122	10.0%	
ARID1A	90	<input type="checkbox"/> 84	6.9%	
KMT2D	84	<input type="checkbox"/> 77	6.3%	
MAP3K1	91	<input type="checkbox"/> 74	6.1%	
PTEN	86	<input type="checkbox"/> 73	6.0%	
BRCA2	72	<input type="checkbox"/> 68	5.6%	
ESR1	66	<input type="checkbox"/> 63	5.2%	
NF1	65	<input type="checkbox"/> 62	5.1%	

Structural Variant Genes (1221 profiled samples)				
Gene	# SV	#	Freq	
CDK12	11	<input type="checkbox"/> 11	1.2%	
PTEN	10	<input type="checkbox"/> 10	0.8%	
ERBB2	10	<input type="checkbox"/> 10	0.8%	
BRIP1	8	<input type="checkbox"/> 8	0.7%	
NOTCH2	8	<input type="checkbox"/> 8	0.7%	
FGFR2	11	<input type="checkbox"/> 8	0.7%	
FGFR1	8	<input type="checkbox"/> 8	0.7%	
RARA	7	<input type="checkbox"/> 7	0.6%	
ARID1A	7	<input type="checkbox"/> 7	0.6%	
RB1	6	<input type="checkbox"/> 6	0.5%	
MYC	6	<input type="checkbox"/> 6	0.5%	

CNA Genes (1223 profiled samples)				
Gene	Cytoband	CNA	#	Freq
CCND1	11q13.3	<b>AMP</b>	<input type="checkbox"/> 209	17.1%
ERBB2	17q12	<b>AMP</b>	<input type="checkbox"/> 180	14.7%
MYC	8q24.21	<b>AMP</b>	<input type="checkbox"/> 153	12.5%
FGFR1	8p11.23	<b>AMP</b>	<input type="checkbox"/> 145	11.9%
FGF19	11q13.3	<b>AMP</b>	<input type="checkbox"/> 143	18.1%
FGF4	11q13.3	<b>AMP</b>	<input type="checkbox"/> 137	17.3%
FGF3	11q13.3	<b>AMP</b>	<input type="checkbox"/> 135	17.1%
CDK12	17q12	<b>AMP</b>	<input type="checkbox"/> 107	11.3%
RAD21	8q24.11	<b>AMP</b>	<input type="checkbox"/> 83	8.5%
NSD3	8p11.23	<b>AMP</b>	<input type="checkbox"/> 61	11.3%
BRIP1	17q23.2	<b>AMP</b>	<input type="checkbox"/> 59	4.8%

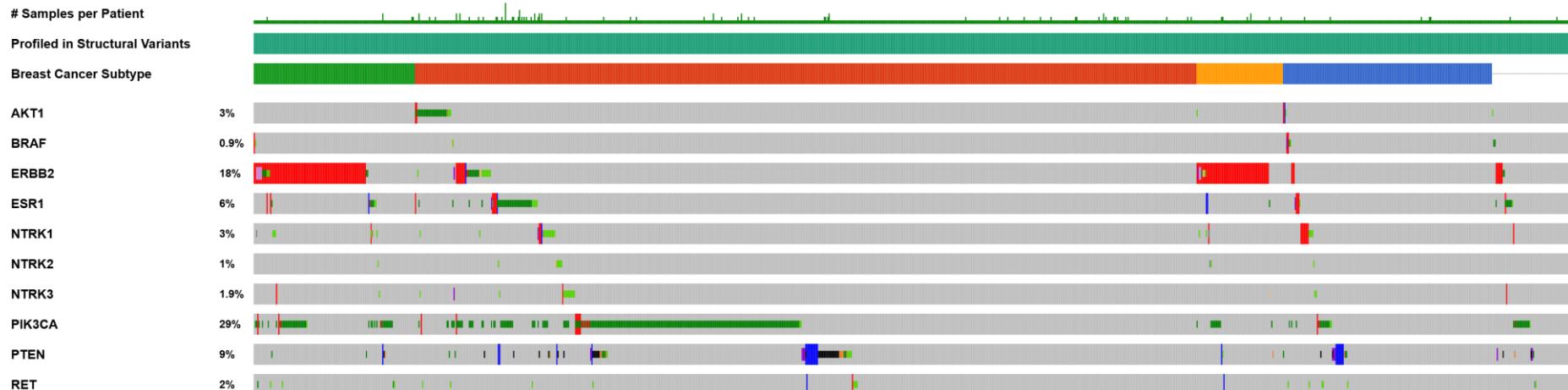
\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE®

# BPC BrCa 1.0-public: Top 12 Mutated Genes



\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE ®

# BPC BrCa 1.0-public: Top Clinically Actionable Genes



**Genetic Alteration**

- Inframe Mutation (putative driver)
- Inframe Mutation (unknown significance)
- Missense Mutation (putative driver)
- Missense Mutation (unknown significance)
- Splice Mutation (putative driver)
- Splice Mutation (unknown significance)
- Truncating Mutation (putative driver)
- Truncating Mutation (unknown significance)
- Structural Variant (putative driver)
- Structural Variant (unknown significance)

# Samples per Patient 0 6

Profiled in Structural Variants Yes

Breast Cancer Subtype HR-, HER2- HR+, HER2- HR+, HER2+ Triple Negative No data

Click here for more  
information on:  
Actionable Genes

**Oncokb™**  
Chakravarty et al., JCO PO 2017

\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE®

# BPC BrCa 1.0-public: HER2 Receptor Status Summary

**HER2 Summary Result:** Overall human epidermal growth factor receptor 2 (HER2) status at diagnosis. This variable accounts for both IHC and ISH results at diagnosis.

**HER2 IHC Lab Value:** Breast cancer human epidermal growth factor receptor 2 (HER2) immunohistochemistry lab value at diagnosis (Collaborative Stage Site Specific Factor 8)

**HER2 IHC Lab Interpretation at Diagnosis:** Breast cancer human epidermal growth factor receptor 2 (HER2) immunohistochemistry lab interpretation at diagnosis (Collaborative Stage Site Specific Factor 9)

HER2 Summary Result		
	#	Freq ▾
Negative/normal within normal limits	<input type="checkbox"/> 849	75.1%
Positive/elevated/amplified	<input type="checkbox"/> 215	19.0%
Unknown or no information	<input type="checkbox"/> 34	3.0%
Borderline-equivocal/indeterminant	<input type="checkbox"/> 14	1.2%
NA	<input type="checkbox"/> 10	0.9%
Tests not done	<input type="checkbox"/> 7	0.6%
Test ordered/results not in chart	<input type="checkbox"/> 1	<0.1%

HER2 IHC Lab Value		
	#	Freq ▾
Score 0	<input type="checkbox"/> 302	26.7%
Score of 1+	<input type="checkbox"/> 301	26.6%
Unknown or no information	<input type="checkbox"/> 171	15.1%
Score of 3+	<input type="checkbox"/> 143	12.7%
Score of 2+	<input type="checkbox"/> 125	11.1%
Test not done	<input type="checkbox"/> 74	6.5%
NA	<input type="checkbox"/> 10	0.9%
Test ordered/results not in chart	<input type="checkbox"/> 4	0.4%

HER2 IHC Lab Interpretation at Diagnosis		
	#	Freq ▾
Negative/normal	<input type="checkbox"/> 692	61.2%
Positive/elevated	<input type="checkbox"/> 156	13.8%
Borderline; equivocal; indetermin...	<input type="checkbox"/> 131	11.6%
Test not done	<input type="checkbox"/> 73	6.5%
Unknown or no information	<input type="checkbox"/> 64	5.7%
NA	<input type="checkbox"/> 12	1.1%
Test ordered/results not in chart	<input type="checkbox"/> 2	0.2%

# BPC BrCa 1.0-public: Hormone Receptor Status Summary



**ER Summary Status:** Breast cancer estrogen receptor (ER) summary  
(Collaborative Stage Site Specific Factor 1)

ER Summary Status		
	#	Freq ▾
Positive/elevated	<input type="checkbox"/> 804	71.2%
Negative/normal	<input type="checkbox"/> 293	25.9%
Unknown or no information	<input type="checkbox"/> 17	1.5%
NA	<input type="checkbox"/> 9	0.8%
Test not done	<input type="checkbox"/> 4	0.4%
Test ordered/results not interpretable	<input type="checkbox"/> 2	0.2%
Borderline	<input type="checkbox"/> 1	<0.1%

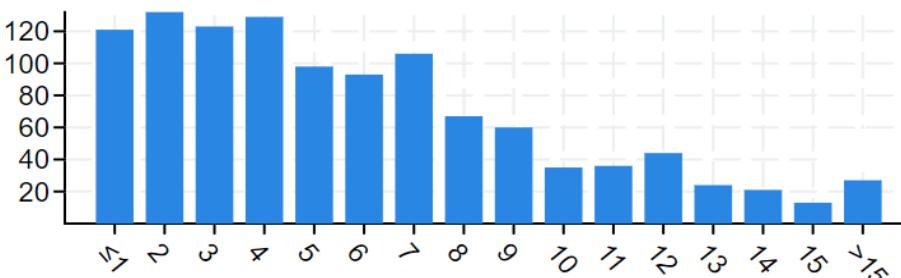
**PR Summary Status:** Breast cancer progesterone receptor (PR) summary  
(Collaborative Stage Site Specific Factor 2)

PR Summary Status		
	#	Freq ▾
Positive/elevated	<input type="checkbox"/> 722	63.9%
Negative/normal	<input type="checkbox"/> 370	32.7%
Unknown or no information	<input type="checkbox"/> 18	1.6%
NA	<input type="checkbox"/> 9	0.8%
Test not done	<input type="checkbox"/> 7	0.6%
Borderline	<input type="checkbox"/> 3	0.3%
Test ordered/results not in chart	<input type="checkbox"/> 1	<0.1%

\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE ®

# BPC BrCa 1.0-public : Complete Treatment Histories

Number of Cancer-Directed Drug Regimens Curated  
for Each Patient



Treatment by Sample (pre- and post-NGS): useful to identify treatment induced mutations

Treatment	Pre / Post	# ▾
Capecitabine	Pre	435
Capecitabine	Post	99
Cyclophosphamide	Pre	355
Cyclophosphamide	Post	428
Paclitaxel	Pre	402
Paclitaxel	Post	355
Doxorubicin HCL	Pre	318
Doxorubicin HCL	Post	381
Tamoxifen	Pre	355
Tamoxifen	Post	293
Investigational Drug	Pre	350

# BPC BrCa 1.0-public: Complete Treatment Histories



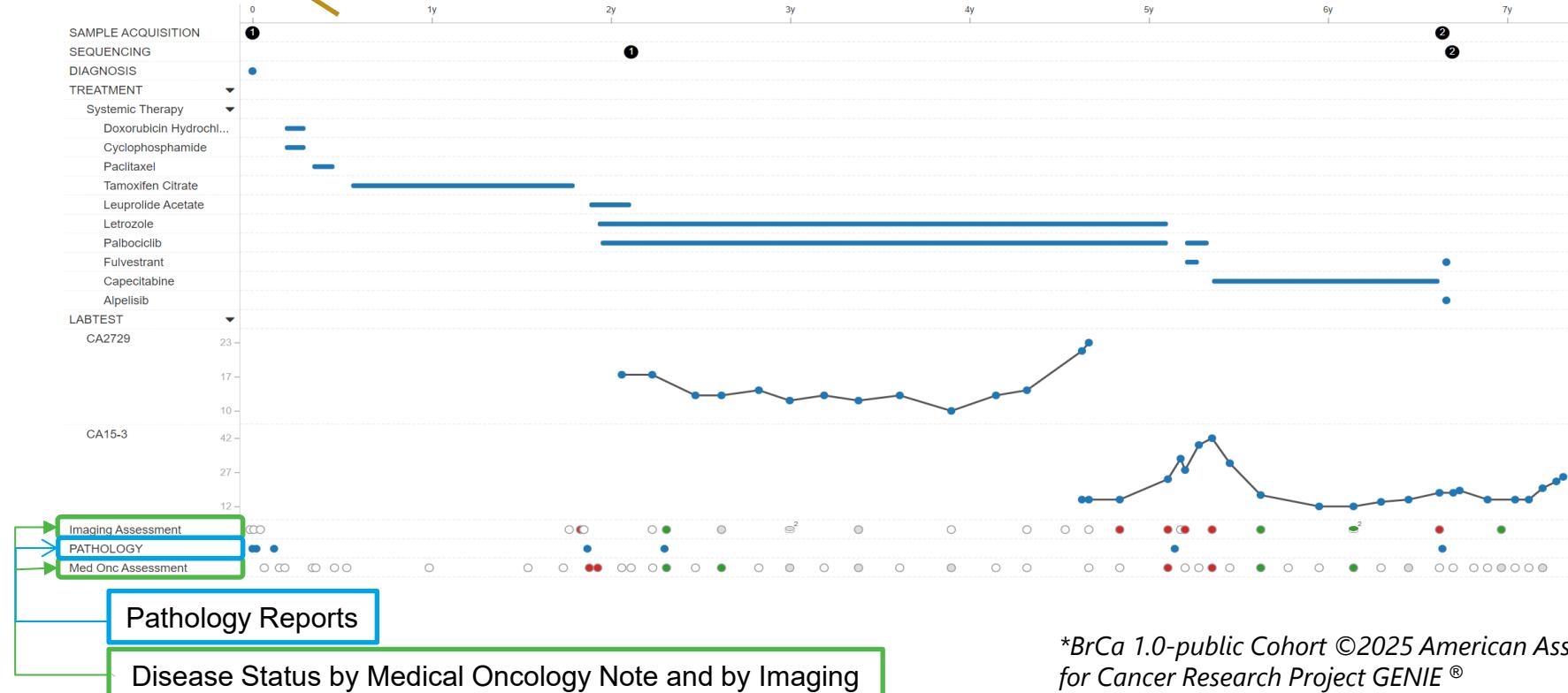
Cancer-directed Drug Regimens*	# of patients
Dose-Dense AC-T Chemotherapy (doxorubicin, cyclophosphamide, and paclitaxel)	532
TH Chemotherapy and Targeted Therapy (paclitaxel and trastuzumab)	191
TC Chemotherapy (docetaxel and cyclophosphamide)	171
CMF Chemotherapy (cyclophosphamide, methotrexate, and fluorouracil)	80

HER2-Directed Treatment Histories*	# of patients
T-DM1: Trastuzumab-DM1 (Trastuzumab emtansine)	101
Pertuzumab & T-DM1: Pertuzumab & Trastuzumab-DM1 (Trastuzumab emtansine)	81
L+T: Lapatinib & Trastuzumab	69
Neratinib monotherapy	12

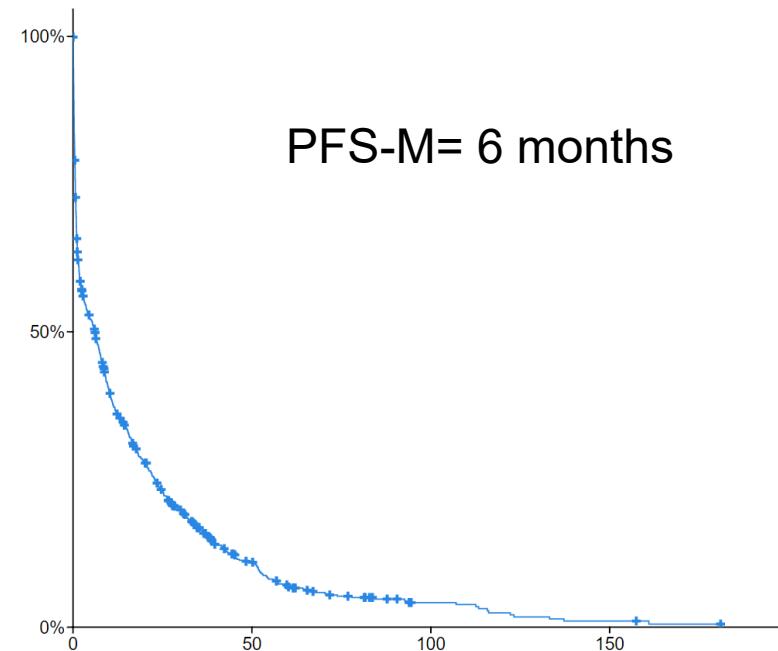
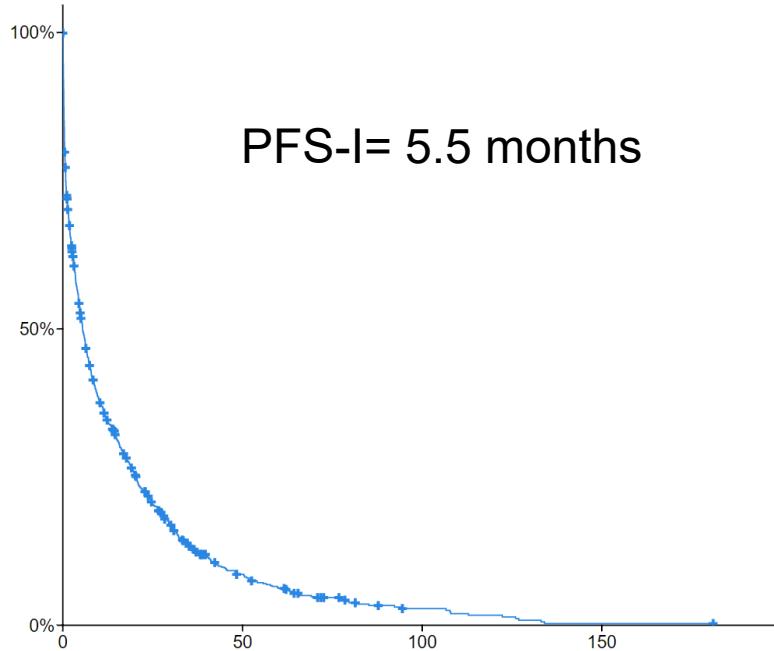
\*(includes regimens ever received for Breast cancer diagnosis irrespective of line or stage)

# BPC BrCa 1.0-public: Comprehensive Patient View

Sample Patient



# BPC BrCa 1.0-public: High Quality Clinical Data

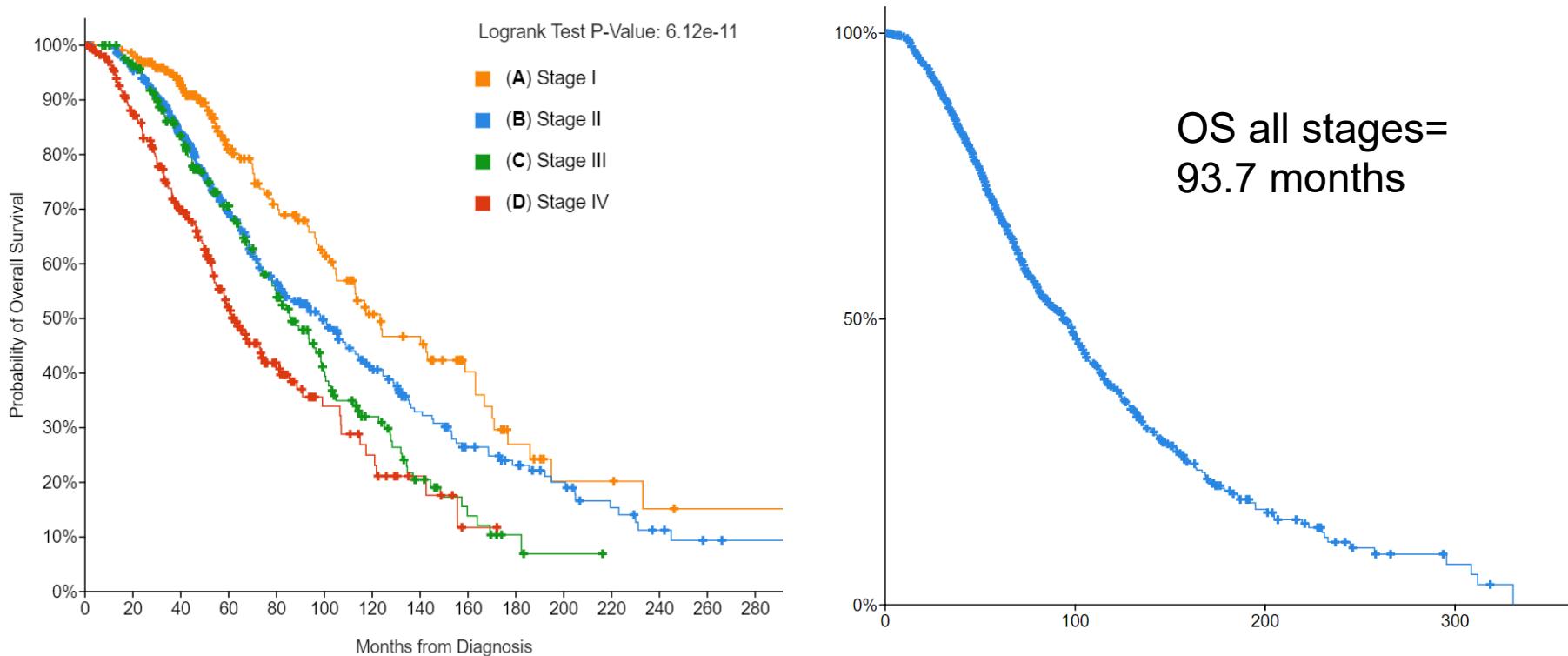


- PFS-M and PSF-I are available by regimen for those regimens containing greater than 10 patients as well as the entire cohort

\* Not adjusted  
for delayed entry

\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE®

# BPC BrCa 1.0-public: Overall Survival by Stage



\*BrCa 1.0-public Cohort ©2025 American Association for Cancer Research Project GENIE®

\*not adjusted for delayed entry

# GENIE BPC Acknowledgements



Shawn M. Sweeney  
Kelli Rasmussen  
Alyssa Acebedo  
Jennifer Hoppe



Niki Schultz  
Ben Gross  
Ritika Kundra  
Brooke Mastrogiacomo



Xindi Guo  
Thomas Yu  
Chelsea Nayan  
Alex Paynter



Memorial Sloan Kettering  
Cancer Center.™

Gregory Riely  
Deb Schrag  
Julia Rudolph  
Charles L. Sawyers  
Hira Rizvi  
John Phillip  
Julian Schwartz  
Marufur Bhuiya  
Stu Gardos  
Cynthia Chu  
Shirin Pillai

**Statistical Core**  
Kathy Panageas  
Jessica Lavery  
Samantha Brown  
Hannah Fuchs  
Axel Martin  
Michael Curry



**Dana-Farber**  
Cancer Institute

Ken Kehl  
Asha Postle  
Kevin Haigis  
John Orechia  
Daniel Quinn  
Simon Arango Baquero



Philippe Bedard  
Celeste Yu  
Samanta Del Rossi  
Nitthusha Singaravelan  
Demi Plagianakos  
Alisa Nguyen  
Nazish Qazi  
Gunjan Srivastava  
Sophie Cooke  
Alisha Rizvi



Christine Micheel  
Rhonda Potter  
Ben Ho Park  
Sanjay Mishra  
Daniel Fabbri  
Marilyn Holt  
Neha Jain  
Protiva Rahman  
Li Wen  
Yuanchu James Yang  
Kate Mittendorf

Former BPC Team Members  
can be found [here](#)