A Breast Cancer Risk Model Incorporating Tyrer-Cuzick Version 8 and a Polygenic Risk Score for Diverse Ancestries

Elisha Hughes, PhD¹; Braden Probst, MStat¹; Holly J. Pederson, MD²; Timothy Simmons, MStat¹; Brian Morris, BS¹; Susan M. Domchek, MD³; Charis Eng, MD, PhD²; Monique Gary, MD⁴; Ora Gordon, MD⁵; Jennifer R. Klemp, PhD, MPH⁶; Semanti Mukherjee, PhD⁷; Kenneth Offitt, MD⁷; Olufunmilayo I. Olopade, MD⁶; Mark E. Robson, MD⁷; Joseph Vijai, PhD⁷; Pat W. Whitworth, MD, FACS, FSSO⁶; Susanne Wagner, PhD¹; Jerry S. Lanchbury, PhD¹; Thomas P. Slavin, MD¹; Alexander Gutin, PhD¹



Abstract # 557

1. Myriad Genetics, Inc., Salt Lake City, UT USA 2. Cleveland Clinic, Cleveland, OH, USA 3. University of Pennsylvania School of Medicine, Philadelphia, PA, USA 4. Grand View Health, Sellersville, PA, USA 5. Providence Health and Services, Renton, WA, USA 6. The University of Kansas Medical Center, Kansas City, KS, USA 7. Memorial Sloan Kettering Cancer Center, New York, NY, USA 8. University of Chicago, IL, USA 9. Nashville Breast Center, Nashville, TN, USA

BACKGROUND

- Breast cancer (BC) risk assessment is important for guiding personalized screening and preventive interventions.
- In clinical practice, Tyrer-Cuzick Version 8 (TCv8) is used to estimate BC risk based on age, breast density, family cancer history, and other clinical factors.
- Accuracy may be improved by combining TCv8 with a polygenic risk score (PRS).
- We recently developed and validated a PRS for diverse ancestries based on 149 common genetic variants (PRS-149).
- PRS-149 incorporates 56 ancestry-informative and 93 BCassociated variants.
- Here, we describe a BC risk model that combines PRS-149 with TCv8 (CRS).

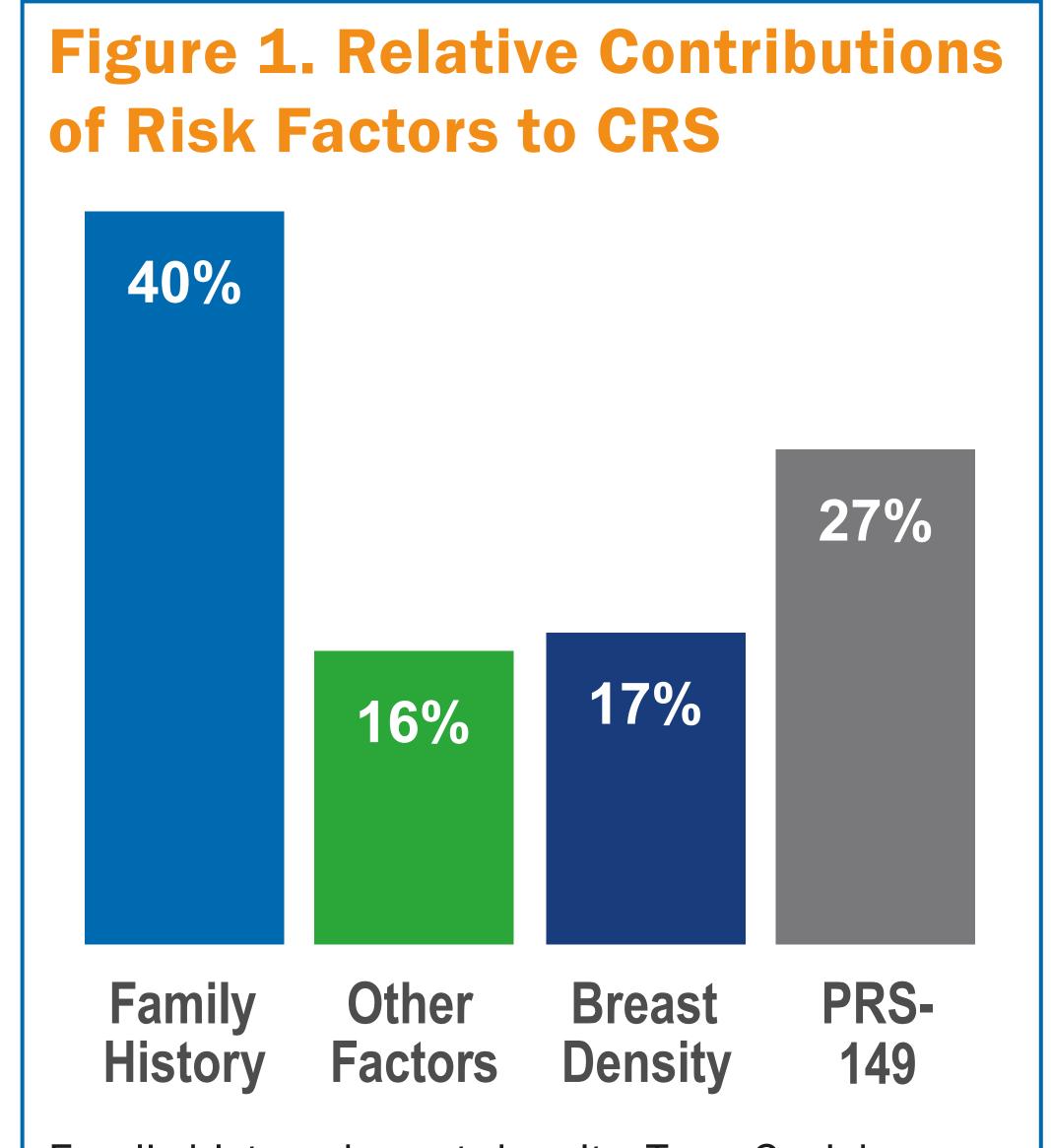
METHODS

- Study subjects were referred for hereditary cancer testing and negative for pathogenic variants in BC susceptibility genes.
- A development cohort of 12,363 women with Breast Imaging Reporting and Data System (BI-RADS) breast density measurements was used to test the extent to which breast density and PRS-149 improve BC risk stratification over family history and other clinical factors.
- Even though PRS-149 uses ancestry-specific SNPs to guide the reported risk value, sub-cohorts herein were grouped for analyses based on self-reported ethnicity.
- We used multivariable logistic regression to test breast density and PRS-149 for association with risk of BC.
- An independent test cohort of 6,030 women with BI-RADS assessment was used to evaluate risk stratification.
- Relative contributions of family history, breast density, other clinical factors in TCv8, and PRS-149 were examined by adding terms sequentially to an ANOVA model.
- We compared differences in classification of women as high (>20%) versus low/moderate (≤20%) remaining lifetime risk according to TCv8 versus CRS.

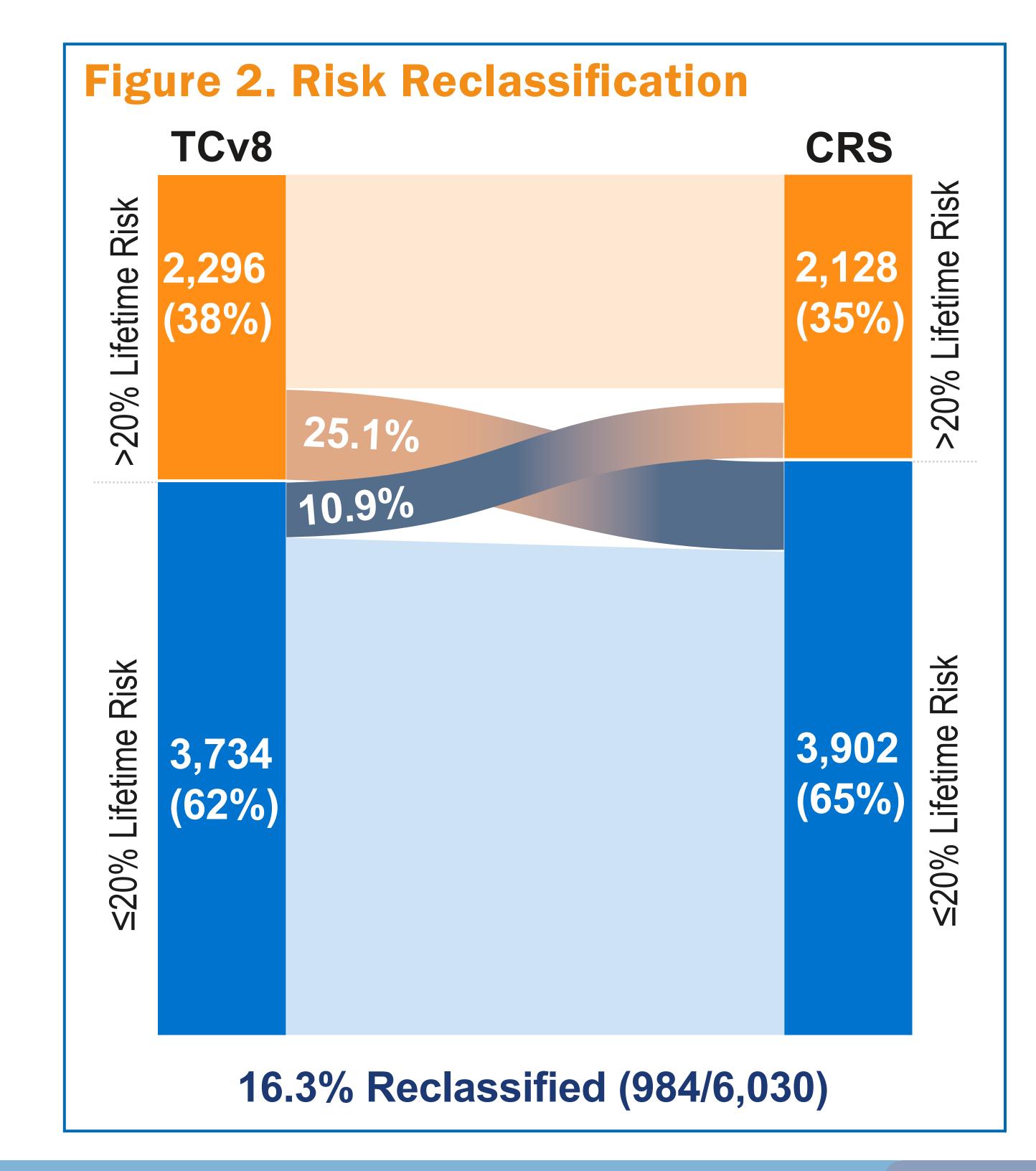
Table 1. Patient Demographics

| | | Development Cohort | | Independent Evaluation Cohort |
|--|----------------|------------------------------|----------------------------|-------------------------------|
| Characteristic | Variable | All Patients (N = 12,363) | BC Unaffected (N = 11,554) | BC Unaffected (N = 6,030) |
| First-Degree Relative(s) with BC | N | 5,029 | 4,812 | 2,490 |
| | (%) | 40.68% | 41.65% | 41.29% |
| Age at Testing (years) | Range | 18-84 | 18-84 | 19-83 |
| | Median | 49 | 49 | 48 |
| | %≤50 | 55.48% | 55.06% | 59.65% |
| Self-Reported Ancesty | Asian | 254 (2.05%) | 228 (1.97%) | 137 (2.27%) |
| | Black/ African | 856 (6.92%) | 782 (6.77%) | 420 (6.97%) |
| | European* | 9,481 (76.69%) | 8,920 (77.20%) | 4,635 (76.87%) |
| | Hispanic | 806 (6.52%) | 746 (6.46%) | 359 (5.95%) |
| | All Others | 966 (7.81%) | 878 (7.60%) | 479 (7.94%) |

*Includes White/Non-Hispanic, and/or Ashkenazi Jewish



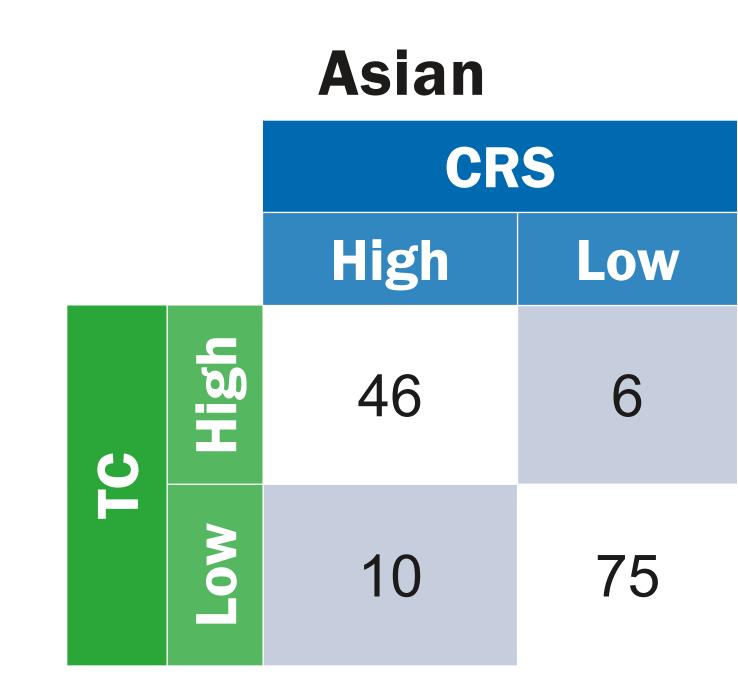
Family history, breast density, Tyrer-Cuzick clinical factors, and the PRS-149 scores were added sequentially to an ANOVA model. PRS-149 explained 27% of the CRS after accounting for family history, other clinical factors, and breast density.

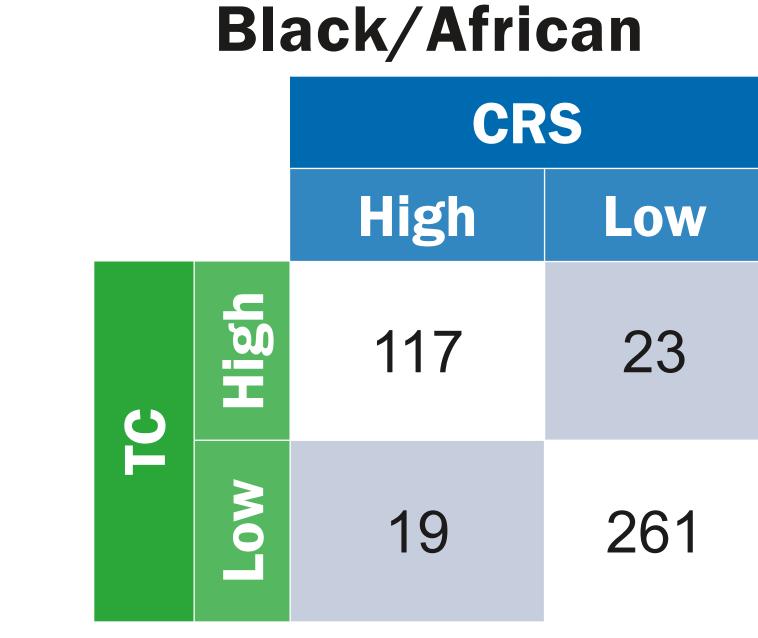


RESULTS

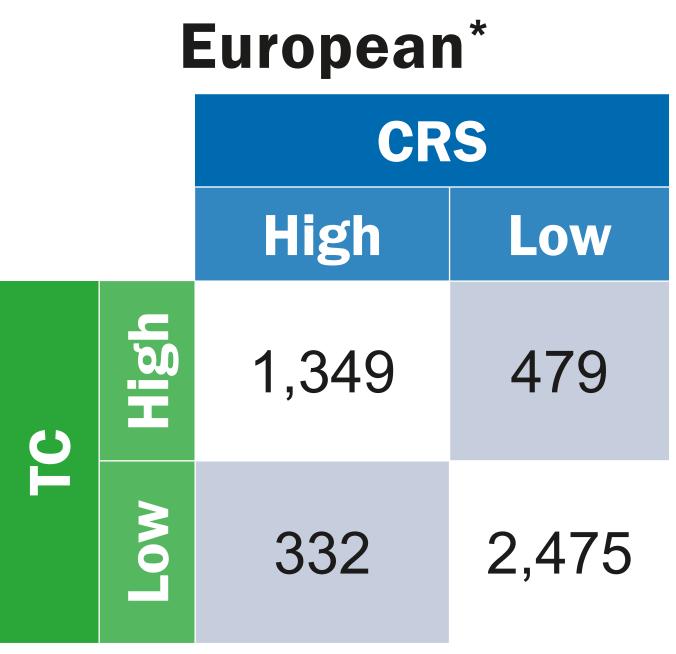
- In the development cohort, increased breast density was significantly associated with higher risk of BC (p=2.4x10⁻⁶) with an effect size consistent with its weighting in TCv8.
- PRS-149 improved BC risk stratification over age, breast density, and family history (OR per unit standard deviation: 1.40, 95% CI: 1.36–1.45; p: 3.7x10⁻⁶).
- PRS-149 was weakly but significantly correlated with both family history (r=0.08) and breast density (r=0.01).
- After adjusting for multiple testing, no other factors were significantly correlated with PRS-149.

Table 2. Risk Reclassification by Ancestry





Hispanic CRS High Low 48 60 32 81 16 251



*Includes White/Non-Hispanic, and/or Ashkenazi Jewish

- In the independent test cohort, PRS-149 explained 27% of CRS variability after accounting for family history, breast density, and other clinical factors (Figure 1).
- Adding PRS-149 to TCv8 significantly altered risk estimates for women of all ancestries, with 16.3% of patients classified differently by CRS versus TCv8 In the independent test cohort (Table 2).
- Among patients who were classified as high-risk by TCv8 in the independent test cohort, 25.1% were downgraded by CRS and, among patients classified as low/moderate by TCv8, 10.9% were upgraded by CRS (Figure 2).

CONCLUSIONS

- This is the first BC risk model that includes breast density, family history, and a PRS based on genetically determined ancestry that is validated for diverse populations.
- The addition of PRS-149 substantially improved risk stratification over TCv8 alone and may therefore lead to enhanced BC risk reduction and early detection strategies such as preventive medications and increased surveillance, respectively.