

Supplementary Online Content

Kurian AW, Ward KC, Abrahamse P, et al. Association of germline genetic testing results with locoregional and systemic therapy in patients with breast cancer. *JAMA Oncol*. doi:10.1001/jamaoncol.2019.6400. Published online February 6, 2020.

eTable. Characteristics of patients according to treatment eligibility

eFigure. Decay diagram of patient exclusion from analytic sample

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

| eTable. Characteristics of patients according to treatment eligibility*† | | | | | | |
|---|----------------------------------|------|------------------------------|------|----------------------------------|------|
| | Bilateral Mastectomy n=15,126 | | Radiation Therapy n=7,248 | | Chemotherapy Omission n=8,509 | |
| | n | % | n | % | n | % |
| Germline genetic testing result | | | | | | |
| Negative | 11,562 | 76.4 | 5,808 | 80.1 | 6,621 | 77.8 |
| Variant of uncertain significance (VUS) only | 2,411 | 15.9 | 1,202 | 16.6 | 1,355 | 15.9 |
| Pathogenic variant (PV) in <i>BRCA1</i> or <i>BRCA2</i> | 823 | 5.4 | 106 | 1.5 | 336 | 3.9 |
| <i>BRCA1</i> | 438 | 2.9 | 49 | 0.7 | 112 | 1.3 |
| <i>BRCA2</i> | 439 | 2.9 | 57 | 0.8 | 225 | 2.6 |
| PV in other breast cancer-associated gene ^{†, **} | 330 | 2.2 | 132 | 1.8 | 197 | 2.3 |
| <i>ATM</i> | 71 | 0.5 | 27 | 0.4 | 46 | 0.5 |
| <i>CDH1</i> | 7 | 0 | 1 | 0 | 8 | 0.1 |
| <i>CHEK2</i> | 148 | 1 | 69 | 1 | 90 | 1.1 |
| <i>NBN</i> | 15 | 0.1 | 5 | 0.1 | 8 | 0.1 |
| <i>NF1</i> | 1 | 0 | 0 | 0 | 1 | 0 |
| <i>PALB2</i> | 66 | 0.4 | 20 | 0.3 | 39 | 0.5 |
| <i>PTEN</i> | 5 | 0 | 2 | 0 | 2 | 0 |
| <i>TP53</i> | 23 | 0.2 | 10 | 0.1 | 7 | 0.1 |
| Age in years (mean, standard deviation) | 51.7 | 12.2 | 52.8 | 11.1 | 53.3 | 12.2 |
| Cancer stage | | | | | | |
| 0 | 2,196 | 14.5 | 1,236 | 17.1 | - | - |
| I | 6,417 | 42.4 | 3,472 | 47.9 | 5,448 | 64 |
| II | 4,993 | 33 | 2,239 | 30.9 | 3,061 | 36 |
| III | 1,520 | 10 | 301 | 4.2 | - | - |
| Tumor grade | | | | | | |
| 1 | 2,790 | 18.4 | 1,591 | 22 | 2,613 | 30.7 |
| 2 | 6,443 | 42.6 | 3,093 | 42.7 | 4,286 | 50.4 |
| 3 | 5,893 | 39 | 2,564 | 35.4 | 1,610 | 18.9 |
| 21-gene recurrence score | | | | | | |
| Not performed | 13,544 | 89.5 | 6,455 | 89.1 | 6,989 | 82.1 |
| 0-10 | 351 | 2.3 | 172 | 2.4 | 390 | 4.6 |
| 11-18 | 683 | 4.5 | 346 | 4.8 | 718 | 8.4 |
| 19-30 | 439 | 2.9 | 234 | 3.2 | 412 | 4.8 |
| ≥31 | 109 | 0.7 | 41 | 0.6 | - | - |

*Treatment-eligible subgroups: for unilateral surgery, stages 0-III, unilateral tumor; for radiation therapy, all stage 0-III lumpectomy recipients except age ≥70 years with stage I, ER/PR-positive and HER2-negative disease; for chemotherapy omission, stages I-II, ER/PR-positive and HER2-negative, 21-gene recurrence score <30 if performed. All patients underwent germline genetic testing within three months of their breast cancer diagnosis.

†As designated by practice guidelines of the National Comprehensive Cancer Network (NCCN). *STK11* is also designated as a breast cancer-associated gene by NCCN, but no patients in the sample had *STK11* PVs so it was not included in the analysis.

**Excludes patients who also had *BRCA1/2* PV

eFigure. Decay diagram of patient exclusion from analytic sample

