

Supplemental Tables for:

Biomarkers in Breast Cancer: An Integrated Analysis of Comprehensive Genomic Profiling and PD-L1 Immunohistochemistry Biomarkers in 312 Breast Cancer Patients

Richard Sheng Poe Huang et al.

Supplemental Table 1. Prevalence of genomic alterations of top 20 genes in HR⁺/HER2⁻, TNBC, and HER2⁺ disease subsets with Bonferroni p-value adjustments for multiple comparisons

| Gene | Percent TNBC patients with mutation (n=121) | Percent HR ⁺ /HER2 ⁻ patients with mutation (n=159) | Percent HER2 ⁺ patients with mutation (n=32) | Fisher's Exact Test (adjusted p-value) TNBC and HR ⁺ /HER2 ⁻ | Fisher's Exact Test (adjusted p-value) HR ⁺ /HER2 ⁻ and HER2 ⁺ | Fisher's Exact Test (adjusted p-value) TNBC and HER2 ⁺ |
|---------------|---|---|---|---|--|--|
| TP53 | 86.8% (105) | 36.5% (58) | 71.9% (23) | < 0.001 | 1 | 1 |
| РІКЗСА | 18.2% (22) | 38.4% (61) | 46.9% (15) | 0.020 | 1 | 0.116 |
| RAD21 | 31.4% (38) | 30.2% (48) | 31.3% (10) | 1 | 1 | 1 |
| МҮС | 26.4% (32) | 19.5% (31) | 34.4% (11) | 1 | 1 | 1 |
| NBN | 17.4% (21) | 27% (43) | 15.6% (5) | 1 | 1 | 1 |
| WHSC1L1 | 9.9% (12) | 23.9% (38) | 15.6% (5) | 0.158 | 1 | 1 |
| CCND1 | 8.3% (10) | 25.2% (40) | 12.5% (4) | 0.015 | 1 | 1 |
| FGF19 | 8.3% (10) | 23.3% (37) | 12.5% (4) | 0.065 | 1 | 1 |
| FGF3 | 8.3% (10) | 23.3% (37) | 12.5% (4) | 0.065 | 1 | 1 |
| GATA3 | 10.7% (13) | 22.6% (36) | 9.4% (3) | 0.651 | 1 | 1 |
| ZNF703 | 6.6% (8) | 24.5% (39) | 9.4% (3) | 0.003 | 0.779 | 1 |
| FGF4 | 7.4% (9) | 20.8% (33) | 15.6% (5) | 0.129 | 1 | 1 |
| FGFR1 | 8.3% (10) | 20.8% (33) | 9.4% (3) | 0.257 | 1 | 1 |
| CDH1 | 9.1% (11) | 19.5% (31) | 3.1% (1) | 1 | 0.195 | 1 |
| ESR1 | 3.3% (4) | 22% (35) | 9.4% (3) | <0.001 | 1 | 1 |
| LYN | 14% (17) | 13.2% (21) | 12.5% (4) | 1 | 1 | 1 |
| DDR2 | 17.4% (21) | 11.3% (18) | 6.3% (2) | 1 | 1 | 1 |
| PTEN | 14.9% (18) | 15.7% (25) | 6.3% (2) | 1 | 1 | 1 |
| GNAS | 14.9% (18) | 11.9% (19) | 9.4% (3) | 1 | 1 | 1 |
| RB1 | 15.7% (19) | 10.7% (17) | 3.1% (1) | 1 | 1 | 1 |

| Gene | Percent PDL1 ⁺ patients with mutation (n=52) | Percent PDL1 ⁻ patients with mutation (n=69) | Fisher's Exact Test (p-value) |
|---------------|---|--|-------------------------------------|
| TP53 | 90.4% (47) | 84.1% (58) | 0.419 |
| RAD21 | 25% (13) | 37.7% (26) | 0.171 |
| МҮС | 25% (13) | 27.5% (19) | 0.836 |
| РІКЗСА | 15.4% (8) | 20.3% (14) | 0.635 |
| NBN | 9.6% (5) | 23.2% (16) | 0.057 |
| DDR2 | 21.2% (11) | 14.5% (10) | 0.346 |
| RB1 | 9.6% (5) | 20.3% (14) | 0.134 |
| GNAS | 13.5% (7) | 17.4% (12) | 0.621 |
| PTEN | 15.4% (8) | 14.5% (10) | 1 |
| MCL1 | 11.5% (6) | 15.9% (11) | 0.601 |
| LYN | 9.6% (5) | 17.4% (12) | 0.294 |
| MLL2 | 11.5% (6) | 11.6% (8) | 1 |
| NOTCH2 | 13.5% (7) | 10.1% (7) | 0.581 |
| GATA3 | 13.5% (7) | 8.7% (6) | 0.555 |
| FH | 17.3% (9) | 5.8% (4) | 0.072 |
| PARP1 | 9.6% (5) | 11.6% (8) | 0.776 |
| IKBKE | 11.5% (6) | 10.1% (7) | 1 |
| NTRK1 | 9.6% (5) | 11.6% (8) | 0.776 |
| BRCA2 | 9.6% (5) | 10.1% (7) | 1 |
| WHSC1L1 | 11.5% (6) | 8.7% (6) | 0.76 |

Supplemental Table 2. Prevalence of genomic alterations in the top 20 genes in TNBC/PD-L1⁺ and TNBC/PD-L1⁻ disease subsets