**Supplemental Table 1. DASL NanoString correlations**

| DASL probe ID | Nanostrong Gene ID | Correlation[1] | P-value | P<0.05 | P<0.0006 |
|---|---|---|---|---|---|
| ILMN_1656593 | AK5 | 0.480 | 8.00E-10 | 1 | 1 |
| ILMN_2283473 | AK5 | 0.280 | 5.40E-04 | 1 | 1 |
| ILMN_2387712 | AK5 | 0.660 | 2.70E-19 | 1 | 1 |
| ILMN_1721391 | ATP6V0B | 0.330 | 5.20E-05 | 1 | 1 |
| ILMN_2353642 | ATP6V0B | 0.180 | 2.90E-02 | 1 | 0 |
| ILMN_1674670 | BTBD11 | -0.300 | 2.30E-04 | 1 | 1 |
| ILMN_1696582 | BTBD11 | -0.056 | 5.00E-01 | 0 | 0 |
| ILMN_1705066 | BTBD11 | 0.130 | 1.10E-01 | 0 | 0 |
| ILMN_1812262 | DDR1 | 0.099 | 2.30E-01 | 0 | 0 |
| ILMN_2360054 | DDR1 | -0.240 | 4.00E-03 | 1 | 0 |
| ILMN_2290547 | DDR1 | 0.031 | 7.10E-01 | 0 | 0 |
| ILMN_1662010 | DLK2 | -0.180 | 2.70E-02 | 1 | 0 |
| ILMN_1676728 | DLK2 | 0.180 | 3.10E-02 | 1 | 0 |
| ILMN_1702943 | DLK2 | 0.088 | 2.90E-01 | 0 | 0 |
| ILMN_1743199 | EGR2 | 0.056 | 5.00E-01 | 0 | 0 |
| ILMN_1667686 | EXOC6 | -0.400 | 8.80E-07 | 1 | 1 |
| ILMN_1651628 | EXOC6 | -0.300 | 2.90E-04 | 1 | 1 |
| ILMN_1679687 | EXOC6 | 0.076 | 3.60E-01 | 0 | 0 |
| ILMN_1732182 | FBXO44 | 0.210 | 9.60E-03 | 1 | 0 |
| ILMN_2325625 | FBXO44 | 0.120 | 1.40E-01 | 0 | 0 |
| ILMN_1651597 | FBXO44 | 0.100 | 2.20E-01 | 0 | 0 |
| ILMN_2344002 | GEMIN2 | 0.300 | 2.80E-04 | 1 | 1 |
| ILMN_2344007 | GEMIN2 | 0.190 | 2.00E-02 | 1 | 0 |
| ILMN_1659990 | HILPDA | -0.130 | 1.10E-01 | 0 | 0 |
| ILMN_1693560 | HMGA1 | 0.430 | 8.30E-08 | 1 | 1 |
| ILMN_1742699 | HMGA1 | 0.420 | 2.60E-07 | 1 | 1 |
| ILMN_2311537 | HMGA1 | 0.070 | 4.10E-01 | 0 | 0 |
| ILMN_2359287 | ITGA6 | -0.180 | 2.90E-02 | 1 | 0 |
| ILMN_2267488 | ITGA6 | 0.450 | 1.60E-08 | 1 | 1 |
| ILMN_1798373 | ITPRIPL1 | 0.170 | 3.80E-02 | 1 | 0 |
| ILMN_1788240 | ITPRIPL1 | 0.048 | 5.70E-01 | 0 | 0 |
| ILMN_1772383 | ITPRIPL1 | -0.089 | 2.90E-01 | 0 | 0 |
| ILMN_1809708 | KCTD21 | 0.090 | 2.80E-01 | 0 | 0 |
| ILMN_1790160 | KIT | 0.640 | 0.00E+00 | 1 | 1 |
| ILMN_2229379 | KIT | 0.430 | 1.00E-07 | 1 | 1 |
| ILMN_1752810 | LARP6 | 0.180 | 2.60E-02 | 1 | 0 |
| ILMN_1663401 | LARP6 | 0.360 | 7.00E-06 | 1 | 1 |
| ILMN_1770479 | LMO7 | 0.290 | 4.50E-04 | 1 | 1 |
| ILMN_2297196 | LRRC4B | 0.300 | 2.00E-04 | 1 | 1 |
| ILMN_1768510 | MAN2B2 | 0.170 | 4.70E-02 | 1 | 0 |
| ILMN_1774739 | MMP14 | -0.290 | 5.30E-04 | 1 | 1 |
| ILMN_1801146 | MMP17 | 0.064 | 4.50E-01 | 0 | 0 |
| ILMN_1674706 | MTHFD2 | 0.420 | 1.80E-07 | 1 | 1 |
| ILMN_2293322 | MTHFD2 | -0.200 | 1.70E-02 | 1 | 0 |
| ILMN_2405521 | MTHFD2 | 0.410 | 5.50E-07 | 1 | 1 |
| ILMN_1788268 | NAPG | -0.290 | 3.80E-04 | 1 | 1 |
| ILMN_1738229 | NDRG3 | -0.170 | 3.90E-02 | 1 | 0 |
| ILMN_2385097 | NDRG3 | -0.300 | 3.00E-04 | 1 | 1 |

| | | | | | |
|---|---|---|---|---|---|
| ILMN_1682503 | NPFF | -0.062 | 4.60E-01 | 0 | 0 |
| ILMN_1735762 | NPNT | -0.028 | 7.40E-01 | 0 | 0 |
| ILMN_1780132 | PELI2 | 0.380 | 2.70E-06 | 1 | 1 |
| ILMN_1789176 | PSMB1 | -0.310 | 1.60E-04 | 1 | 1 |
| ILMN_2359789 | RAC1 | -0.072 | 3.90E-01 | 0 | 0 |
| ILMN_1652445 | RAC1 | -0.200 | 1.50E-02 | 1 | 0 |
| ILMN_3251085 | RBBP4 | 0.420 | 2.30E-07 | 1 | 1 |
| ILMN_2062524 | RBBP4 | 0.340 | 3.20E-05 | 1 | 1 |
| ILMN_1751141 | RGS12 | 0.230 | 4.90E-03 | 1 | 0 |
| ILMN_1722834 | RGS12 | 0.640 | 3.70E-18 | 1 | 1 |
| ILMN_2384629 | RGS12 | -0.110 | 1.80E-01 | 0 | 0 |
| ILMN_1691843 | RNPS1 | -0.410 | 3.90E-07 | 1 | 1 |
| ILMN_2375386 | RNPS1 | -0.310 | 1.30E-04 | 1 | 1 |
| ILMN_1685661 | RRP15 | 0.260 | 1.60E-03 | 1 | 0 |
| ILMN_1778294 | SENP7 | 0.390 | 1.70E-06 | 1 | 1 |
| ILMN_2382354 | SENP7 | 0.420 | 2.20E-07 | 1 | 1 |
| ILMN_2102069 | SLC16A4 | 0.290 | 3.80E-04 | 1 | 1 |
| ILMN_1804673 | SLC16A4 | 0.460 | 7.50E-09 | 1 | 1 |
| ILMN_1693183 | SORBS2 | 0.089 | 2.90E-01 | 0 | 0 |
| ILMN_1716407 | SORBS2 | 0.530 | 0.00E+00 | 1 | 1 |
| ILMN_2407879 | SORBS2 | 0.480 | 1.20E-09 | 1 | 1 |
| ILMN_1674098 | SORBS2 | -0.130 | 1.20E-01 | 0 | 0 |
| ILMN_1726805 | STX2 | -0.200 | 1.50E-02 | 1 | 0 |
| ILMN_1747775 | STX2 | 0.170 | 4.00E-02 | 1 | 0 |
| ILMN_2344216 | STX2 | 0.450 | 2.90E-08 | 1 | 1 |
| ILMN_1726928 | TCEA3 | 0.570 | 9.50E-14 | 1 | 1 |
| ILMN_1754102 | TGIF1 | 0.130 | 1.30E-01 | 0 | 0 |
| ILMN_2247842 | TGIF1 | -0.013 | 8.80E-01 | 0 | 0 |
| ILMN_2318643 | TGIF1 | 0.310 | 1.40E-04 | 1 | 1 |
| ILMN_1702211 | TGIF1 | 0.043 | 6.10E-01 | 0 | 0 |
| ILMN_2318638 | TGIF1 | 0.680 | 0.00E+00 | 1 | 1 |
| ILMN_2245292 | TGIF1 | -0.210 | 1.00E-02 | 1 | 0 |
| ILMN_1656761 | TGIF1 | -0.470 | 3.40E-09 | 1 | 1 |
| ILMN_1724096 | TNK1 | 0.320 | 1.10E-04 | 1 | 1 |
| ILMN_1726873 | TPCN2 | 0.065 | 4.40E-01 | 0 | 0 |
| ILMN_1745079 | TRIM2 | 0.079 | 3.50E-01 | 0 | 0 |
| ILMN_2058975 | UFL1 | -0.110 | 1.80E-01 | 0 | 0 |
| ILMN_1691188 | UIMC1 | 0.009 | 9.20E-01 | 0 | 0 |
| ILMN_2311826 | USP6NL | 0.075 | 3.70E-01 | 0 | 0 |
| ILMN_1659696 | USP6NL | 0.150 | 7.00E-02 | 1 | 0 |
| ILMN_1681846 | ZNF540 | 0.400 | 6.50E-07 | 1 | 1 |

[1] Spearman’s rank correlation coefficients (rho).

[2] Indicator if p-value is less than the uncorrected threshold.

[3] Indicator if p-value is less than the Bonferroni corrected threshold for 46 probes.

**Supplemental Table 2. Univariate associations of gene expression values by breast cancer status at 10 years.**

| Gene | Mean Expression Cases | Mean Expression Controls | Wilcoxon P-value | OR | Age-adjusted OR | In SATTC10? |
|---|---|---|---|---|---|---|
| AK5 | 7.843 | 7.252 | 0.008 | 1.714 | 1.426 | Yes |
| ATP6V0B | 8.534 | 8.581 | 0.578 | 0.867 | 0.707 | Yes |
| BTBD11 | 4.795 | 4.453 | 0.119 | 1.674 | 1.749 | No |
| DDR1 | 7.840 | 7.613 | 0.013 | 2.941 | 2.220 | No |
| DLK2 | 5.367 | 4.831 | 0.002 | 2.331 | 2.136 | No |
| EGR2 | 6.393 | 6.310 | 0.895 | 1.074 | 1.211 | No |
| EXOC6 | 5.554 | 5.121 | 0.001 | 1.675 | 1.565 | Yes |
| FBXO44 | 7.715 | 7.585 | 0.235 | 1.653 | 1.265 | No |
| GEMIN2 | 4.956 | 4.821 | 0.504 | 1.125 | 1.064 | Yes |
| HILPDA | 6.735 | 6.635 | 0.427 | 1.158 | 1.037 | Yes |
| HMGA1 | 8.111 | 8.111 | 0.526 | 1.000 | 0.992 | No |
| ITGA6 | 7.969 | 7.755 | 0.015 | 3.616 | 3.854 | No |
| ITPRIPL1 | 4.357 | 3.962 | 0.091 | 1.584 | 1.449 | Yes |
| KCTD21 | 5.854 | 5.567 | 0.098 | 1.684 | 1.269 | Yes |
| KIT | 7.564 | 6.968 | 0.001 | 2.261 | 2.278 | No |
| LARP6 | 5.598 | 5.204 | 0.188 | 1.503 | 1.426 | Yes |
| LMO7 | 7.084 | 6.984 | 0.648 | 1.266 | 1.265 | No |
| LRRC4B | 3.905 | 4.460 | 0.006 | 0.621 | 0.618 | Yes |
| MAN2B2 | 7.520 | 7.447 | 0.546 | 1.334 | 0.975 | Yes |
| MMP14 | 7.568 | 7.258 | 0.201 | 1.360 | 1.515 | No |
| MMP17 | 5.074 | 5.061 | 0.314 | 1.019 | 0.918 | No |
| MTHFD2 | 6.858 | 6.629 | 0.358 | 1.335 | 1.256 | Yes |
| NAPG | 6.064 | 5.799 | 0.117 | 1.474 | 1.354 | Yes |
| NDRG3 | 7.171 | 7.086 | 0.817 | 1.296 | 1.283 | Yes |
| NPFF | 5.379 | 5.518 | 0.168 | 0.721 | 0.706 | Yes |
| NPNT | 6.643 | 6.221 | 0.103 | 1.402 | 1.208 | Yes |
| PELI2 | 5.455 | 5.264 | 0.626 | 1.207 | 1.327 | Yes |
| PSMB1 | 6.881 | 6.458 | 0.026 | 1.797 | 1.528 | Yes |
| RAC1 | 9.108 | 9.043 | 0.810 | 1.250 | 0.966 | No |
| RBBP4 | 7.132 | 6.867 | 0.137 | 1.744 | 1.635 | No |
| RGS12 | 5.376 | 4.966 | 0.011 | 2.273 | 2.085 | Yes |
| RNPS1 | 8.644 | 8.497 | 0.073 | 2.314 | 1.717 | Yes |
| RRP15 | 5.429 | 5.144 | 0.189 | 1.748 | 1.807 | Yes |
| SENP7 | 7.685 | 7.474 | 0.271 | 1.486 | 1.433 | No |
| SLC16A4 | 5.156 | 4.847 | 0.173 | 1.549 | 1.359 | Yes |
| SORBS2 | 7.816 | 7.391 | 0.002 | 3.130 | 2.409 | Yes |
| STX2 | 6.129 | 6.161 | 0.310 | 0.964 | 0.875 | No |
| TCEA3 | 7.221 | 6.868 | 0.106 | 1.610 | 1.321 | Yes |
| TGIF1 | 7.863 | 7.629 | 0.049 | 1.979 | 1.726 | Yes |
| TNK1 | 6.210 | 5.947 | 0.060 | 1.777 | 1.395 | No |
| TPCN2 | 7.167 | 7.028 | 0.437 | 1.410 | 1.290 | Yes |
| TRIM2 | 5.756 | 5.897 | 0.273 | 0.695 | 0.605 | No |
| UFL1 | 8.627 | 8.640 | 0.741 | 0.871 | 0.846 | Yes |
| UIMC1 | 6.888 | 6.955 | 0.163 | 0.822 | 0.683 | No |
| USP6NL | 7.483 | 7.434 | 0.981 | 1.240 | 1.134 | No |
| ZNF540 | 5.598 | 5.368 | 0.443 | 1.312 | 1.138 | Yes |

Mean Expression Cases, mean of gene expression across case samples; Mean Expression Controls, mean of gene expression across control samples; Wilcoxon P-value, p-value from a Wilcoxon Rank Sum Test comparing mean gene expression in cases vs. controls; OR, odds ratio from a logistic regression model predicting case-control status; age-adjusted OR, odds ratio from a logistic regression model adjusting for age; In SA-TTC10, indicator of whether the probe was part of the previously derived SA-TTC10 model or selected based on biological insight.

**Supplemental Table 3.** ROC AUC values from the 5-fold cross-validation using the genes in the SATTC10 gene set

| | | **Training** | | | | | |
|---|---|---|---|---|---|---|---|
| **fold** | **# probes** | **cases:controls** | **Gene expression only** | **Gail model only** | **Gene expression and Gail model** | **BBD-BC model only** | **Gene expression and BBD-BC model** |
| 1 | 27 | 29:92 | 0.67 | 0.57 | 0.68 | 0.67 | 0.70 |
| 2 | 27 | 29:91 | 0.65 | 0.52 | 0.65 | 0.62 | 0.66 |
| 3 | 27 | 30:91 | 0.67 | 0.60 | 0.68 | 0.69 | 0.70 |
| 4 | 27 | 30:91 | 0.71 | 0.57 | 0.71 | 0.63 | 0.72 |
| 5 | 27 | 30:91 | 0.72 | 0.59 | 0.72 | 0.67 | 0.73 |
| | | **average** | **0.69** | **0.57** | **0.69** | **0.65** | **0.70** |

| | | **Validation** | | | | | |
|---|---|---|---|---|---|---|---|
| **fold** | **# probes** | **cases:controls** | **Gene expression only** | **Gail model only** | **Gene expression and Gail model** | **BBD-BC model only** | **Gene expression and BBD-BC model** |
| 1 | 27 | 8:22 | 0.74 | 0.57 | 0.74 | 0.60 | 0.76 |
| 2 | 27 | 8:23 | 0.86 | 0.82 | 0.86 | 0.81 | 0.88 |
| 3 | 27 | 7:23 | 0.79 | 0.42 | 0.77 | 0.54 | 0.76 |
| 4 | 27 | 7:23 | 0.53 | 0.60 | 0.54 | 0.76 | 0.56 |
| 5 | 27 | 7:23 | 0.39 | 0.45 | 0.39 | 0.57 | 0.40 |
| | | **average** | **0.66** | **0.57** | **0.66** | **0.66** | **0.67** |

Genes expression only, model contains only the selected probes; Gail model only, model includes only the the BCRAT (Gail) Model predicted risk, Gene expression and Gail model, model includes selected probes plus the BCRAT model predicted risk; BBD-BC model only, model includes only the BBD-BC model predicted risk; Gene expression and BBD-BC model, models includes selected probes plus the BBD-BC model predicted risk.

**Supplemental Table 4.** ROC AUC values from the 5-fold cross-validation using all genes in the Nanostring codeset

| | | Training | | | | | |
|---|---|---|---|---|---|---|---|
| **fold** | **# probes** | **cases: controls** | **Gene expression only** | **Gail model only** | **Gene expression and Gail model** | **BBD-BC model only** | **Gene expression and BBD-BC model** |
| 1 | 46 | 29:92 | 0.76 | 0.56 | 0.76 | 0.67 | 0.76 |
| 2 | 46 | 29:91 | 0.68 | 0.59 | 0.69 | 0.69 | 0.70 |
| 3 | 46 | 30:91 | 0.73 | 0.61 | 0.73 | 0.66 | 0.73 |
| 4 | 46 | 30:91 | 0.73 | 0.52 | 0.73 | 0.60 | 0.73 |
| 5 | 46 | 30:91 | 0.72 | 0.59 | 0.71 | 0.67 | 0.72 |
| | | **average** | **0.72** | **0.57** | **0.72** | **0.66** | **0.73** |

| | | Validation | | | | | |
|---|---|---|---|---|---|---|---|
| **fold** | **# probes** | **cases: controls** | **Gene expression only** | **Gail model only** | **Gene expression and Gail model** | **BBD-BC model only** | **Gene expression and BBD-BC model** |
| 1 | 46 | 8:22 | 0.59 | 0.63 | 0.59 | 0.64 | 0.60 |
| 2 | 46 | 8:23 | 0.92 | 0.54 | 0.89 | 0.53 | 0.90 |
| 3 | 46 | 7:23 | 0.53 | 0.42 | 0.55 | 0.69 | 0.57 |
| 4 | 46 | 7:23 | 0.69 | 0.76 | 0.69 | 0.86 | 0.70 |
| 5 | 46 | 7:23 | 0.77 | 0.49 | 0.77 | 0.61 | 0.77 |
| | | **average** | **0.70** | **0.57** | **0.70** | **0.66** | **0.71** |

Gene expression only, model contains only the selected probes; Gail model only, model includes only the BCRAT (Gail) Model predicted risk, Gene expression and Gail model, model includes selected probes plus the BCRAT model predicted risk; BBD-BC model only, model includes only the BBD-BC model predicted risk; Gene expression and BBD-BC model, models includes selected probes plus the BBD-BC model predicted risk.

**Supplemental Table 5. Sensitivity analysis models without atypia samples.**

| | | Training | | | | | |
|---|---|---|---|---|---|---|---|
| **fold** | **# probes** | **cases:controls** | **Gene expression only** | **Gail model only** | **Gene expression and Gail model** | **BBD-BC model only** | **Gene expression and BBD-BC model** |
| 1 | 46 | 26:81 | 0.71 | 0.53 | 0.71 | 0.63 | 0.72 |
| 2 | 46 | 26:81 | 0.78 | 0.53 | 0.78 | 0.60 | 0.78 |
| 3 | 46 | 26:81 | 0.75 | 0.55 | 0.75 | 0.62 | 0.75 |
| 4 | 46 | 26:81 | 0.72 | 0.54 | 0.72 | 0.60 | 0.73 |
| 5 | 46 | 26:81 | 0.75 | 0.49 | 0.75 | 0.61 | 0.75 |
| | | **average** | **0.74** | **0.53** | **0.74** | **0.61** | **0.74** |

| | | Validation | | | | | |
|---|---|---|---|---|---|---|---|
| **fold** | **# probes** | **cases:controls** | **Gene expression only** | **Gail model only** | **Gene expression and Gail model** | **BBD-BC model only** | **Gene expression and BBD-BC model** |
| 1 | 46 | 6:20 | 0.82 | 0.51 | 0.82 | 0.52 | 0.82 |
| 2 | 46 | 6:20 | 0.66 | 0.55 | 0.66 | 0.68 | 0.66 |
| 3 | 46 | 5:20 | 0.62 | 0.49 | 0.58 | 0.60 | 0.58 |
| 4 | 46 | 5:20 | 0.55 | 0.46 | 0.55 | 0.71 | 0.54 |
| 5 | 46 | 5:21 | 0.71 | 0.64 | 0.72 | 0.59 | 0.69 |
| | | **average** | **0.67** | **0.53** | **0.67** | **0.62** | **0.66** |

Genes expression only, model contains only the selected probes; Gail model only, model includes only the BCRAT (Gail) Model predicted risk, Gene expression and Gail model, model includes selected probes plus the BCRAT model predicted risk; BBD-BC model only, model includes only the BBD-BC model predicted risk; Gene expression and BBD-BC model, models includes selected probes plus the BBD-BC model predicted risk.

**Supplemental Table 6. ROC AUC values from the 5-fold cross-validation using the five genes present in all models**

|  |  | Training |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| fold | # probes | cases:controls | Gene expression only | Gail model only | Gene expression and Gail model | BBD-BC model only | Gene expression and BBD-BC model |
| 1 | 5 | 29:91 | 0.78 | 0.61 | 0.79 | 0.70 | 0.82 |
| 2 | 5 | 29:91 | 0.76 | 0.54 | 0.76 | 0.65 | 0.79 |
| 3 | 5 | 30:90 | 0.77 | 0.58 | 0.78 | 0.67 | 0.80 |
| 4 | 5 | 30:90 | 0.77 | 0.60 | 0.78 | 0.67 | 0.79 |
| 5 | 5 | 30:90 | 0.74 | 0.53 | 0.74 | 0.59 | 0.76 |
|  |  | **average** | **0.77** | **0.57** | **0.77** | **0.65** | **0.79** |

|  |  | Validation |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| fold | # probes | cases:controls | Gene expression only | Gail model only | Gene expression and Gail model | BBD-BC model only | Gene expression and BBD-BC model |
| 1 | 5 | 8:22 | 0.69 | 0.39 | 0.66 | 0.53 | 0.66 |
| 2 | 5 | 8:22 | 0.73 | 0.66 | 0.75 | 0.67 | 0.77 |
| 3 | 5 | 7:23 | 0.73 | 0.58 | 0.75 | 0.60 | 0.75 |
| 4 | 5 | 7:23 | 0.75 | 0.47 | 0.75 | 0.61 | 0.80 |
| 5 | 5 | 7:23 | 0.88 | 0.75 | 0.88 | 0.91 | 0.93 |
|  |  | **average** | **0.75** | **0.57** | **0.76** | **0.67** | **0.78** |

Genes expression only, model contains only the selected probes; Gail model only, model includes only the BCRAT (Gail) Model predicted risk, Gene expression and Gail model, model includes selected probes plus the BCRAT model predicted risk; BBD-BC model only, model includes only the BBD-BC model predicted risk; Gene expression and BBD-BC model, models includes selected probes plus the BBD-BC model predicted risk.