# Supplementary Information

**Proteomics-derived basal biomarker DNA-PKcs is associated with intrinsic subtype and long-term clinical outcomes in breast cancer**

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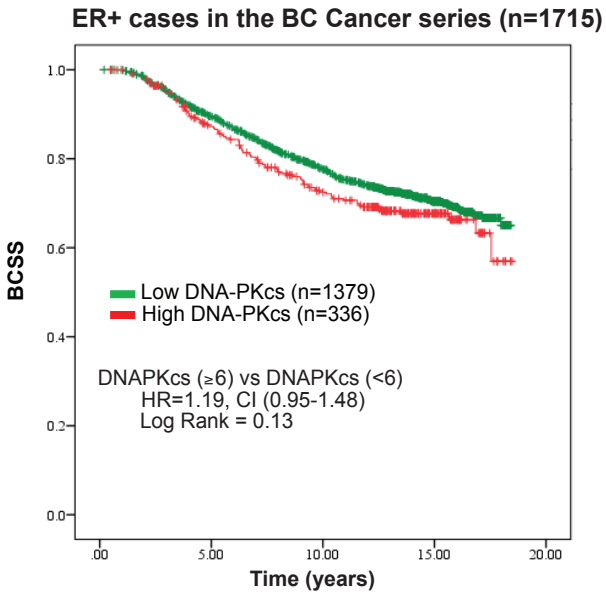
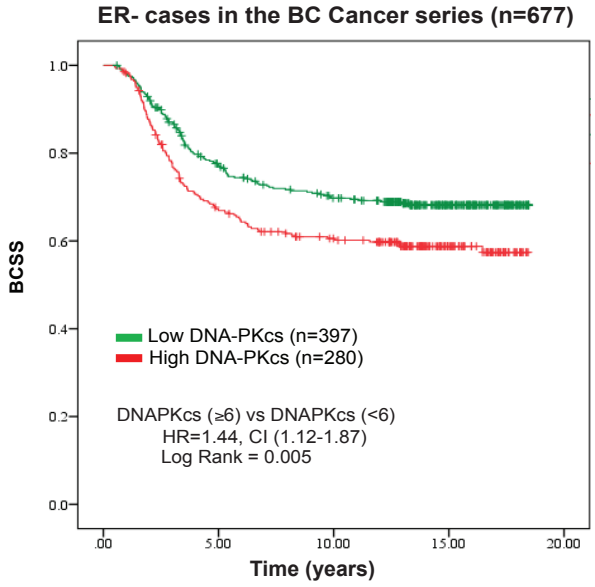
## Supplementary Information includes:

## Supplementary Figure 1

**a**



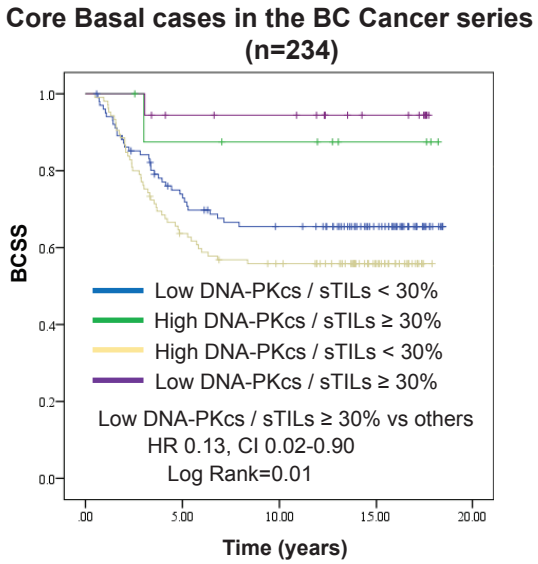

**b**




**Supplementary Fig. 1: Prognostic significance of DNA-PKcs expression by immunohistochemistry in different ER subgroups of the BC Cancer series.** Kaplan Meier

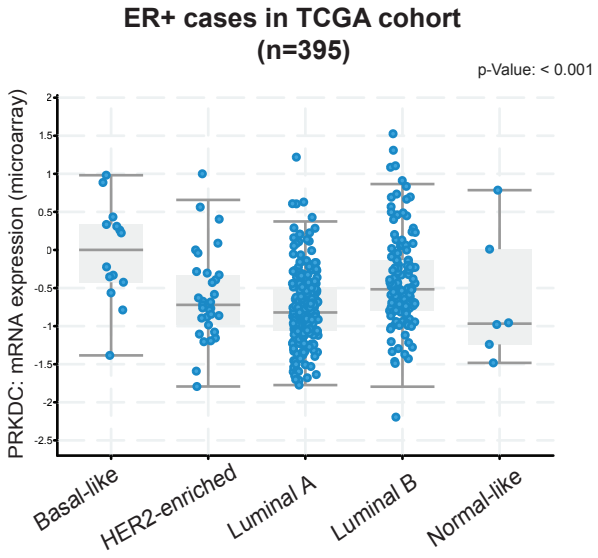
curves for BCSS in ER+ cases (a), and ER- cases (b). Abbreviations: BCSS, breast cancer specific survival; ER, estrogen receptor.

## Supplementary Figure 2



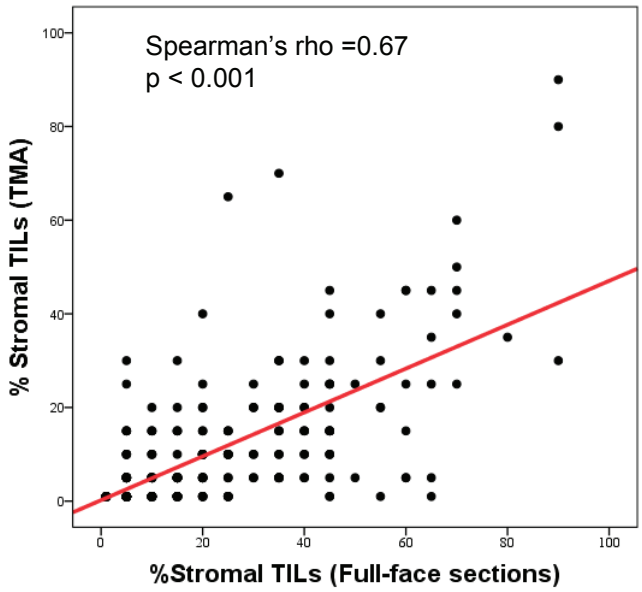

**Supplementary Fig. 2: Prognostic stratification of core basal cases by DNA-PKcs and stromal TILs in the BC Cancer series using a higher (30%) cutpoint.** Within core basal tumors, presence of sTILs (≥30% vs < 30%) in combination with low DNA-PKcs expression is associated with better BCSS. Abbreviations: BCSS, breast cancer specific survival; HR, hazard ratio, TIL, tumor infiltrating lymphocytes.

## Supplementary Figure 3




**Supplementary Fig. 3:** Boxplots showing that expression levels of *PRKDC,* as derived from the 395 ER+ breast cancers in TCGA are significantly associated with basal-like PAM50 intrinsic subtype. Centre bar denotes median, and the upper and lower box boundaries delineate the third and first quartiles.

## Supplementary Figure 4




**Supplementary Fig. 4:** Scatter plot showing correlation between morphologically assessed stromal TILs on full-face sections and tissue microarrays in BC Cancer series (n=317). Each data point represents one case. The Spearman correlation coefficient (*rho*) and p-values are displayed. Abbreviations: TILs, tumor infiltrating lymphocytes; TMA, tissue microarray.

**Supplementary Tables:**

**Supplementary Table 1: Association of DNA-PKcs expression with clinicopathological features in the UBC series**

| Clinicopathological Features | DNA-PKcs Expression (IHC score) | | *P*-value |
|---|---|---|---|
| | Low (< 6) n = 233 | High (≥ 6) n = 67 | |
| Age at diagnosis | | | 0.51 |
| < 50 | 87 (37.3) | 28 (41.8) | |
| ≥ 50 | 146 (62.7) | 39 (58.2) | |
| Tumor size (cm) | | | 0.97 |
| ≤ 2 cm | 135 (57.9) | 39 (58.2) | |
| >2 cm | 98 (42.1) | 28 (41.8) | |
| Tumor grade | | | <0.001 |
| Grade 1 or 2 | 145 (63) | 22 (32.8) | |
| Grade 3 | 85 (37) | 45 (67.2) | |
| Axillary lymph node status | | | 0.10 |
| Positive | 76 (35.5) | 31 (48.4) | |
| Negative | 138 (64.5) | 33 (51.6) | |
| Lymphovascular invasion | | | 0.01 |
| Positive | 46 (20.6) | 24 (35.8) | |
| Negative | 177 (79.4) | 43 (64.2) | |
| Ki-67 (%) | | | <0.001 |
| < 14 | 147 (64.5) | 24 (36.4) | |
| ≥ 14% | 81 (35.5) | 42 (63.6) | |
| ER expression | | | 0.007 |
| Negative | 41 (17.8) | 22 (33.3) | |
| Positive | 189 (82.2) | 44 (66.7) | |
| Progesterone receptor expression | | | 0.06 |
| Negative | 69 (30.1) | 28 (42.4) | |
| Positive | 160 (69.9) | 38 (57.6) | |
| HER2 expression | | | 0.14 |
| Negative | 217 (95.6) | 54 (87.1) | |
| Positive | 10 (4.4) | 8 (12.9) | |
| EGFR expression | | | 0.004 |
| Negative | 211 (91.3) | 51 (78.5) | |
| Positive | 20 (8.7) | 14 (21.5) | |

| | | | |
|---|---|---|---|
| CK5/6 expression | | | 0.05 |
| Negative | 217 (94.8) | 57 (87.7) | |
| Positive | 12 (5.2) | 8 (12.3) | |
| IHC subtype | | | <0.001 |
| Luminal A ([ER+ or PR+], HER2-, low Ki67) | 132 (59.2) | 18 (29.5) | |
| Luminal B ([ER+ or PR+], HER2-, high Ki67) | 51 (22.9) | 20 (32.8) | |
| Luminal B ([ER+ or PR+], HER2+) | 5 (2.2) | 2 (3.3) | |
| ER-, PR-, HER2+ | 5 (2.2) | 6 (9.8) | |
| ER-, PR-, HER2- | 30 (13.5) | 15 (24.6) | |
| Triple negative phenotype | | | 0.03 |
| Yes | 30 (13.5) | 15 (24.6) | |
| No | 193 (86.5) | 46 (75.4) | |
| Core basal subtype | | | 0.02 |
| Yes | 17 (7.3) | 11 (16.4) | |
| No | 216 (92.7) | 56 (83.6) | |
| Stromal TILs (H&E) | | | 0.11 |
| < 10% | 191 (82) | 49 (73.1) | |
| ≥ 10% | 42 (18) | 18 (26.9) | |
| CD8 iTIL count | | | 0.006 |
| < 1 | 93 (49.2) | 14 (27.5) | |
| ≥ 1 | 96 (50.8) | 37 (72.5) | |

Abbreviations: IHC, immunohistochemistry; ER, estrogen receptor; PR, progesterone receptor; HER2, human epidermal growth factor receptor 2; EGFR, epidermal growth factor receptor; CK, cytokeratin; H&E, hematoxylin and eosin; CD, cluster of differentiation.

**Supplementary Data 1 (appears as an Excel file):** Characteristics of the BC Cancer series including pathological features for the whole cohort and genomic *PRKDC* mutation data for the ER+ subset.