

Figure 1 displays immunofluorescence images of cells stained for DAPI (blue), CK (green), and PARP-1 (red). The images are arranged in two rows, A and B, and four columns. Row A shows cells with DAPI, CK, PARP-1, and an overlay. Row B shows cells with DAPI, CK, PARP-1, and an overlay. Scale bars are present in the bottom left of each image.

1

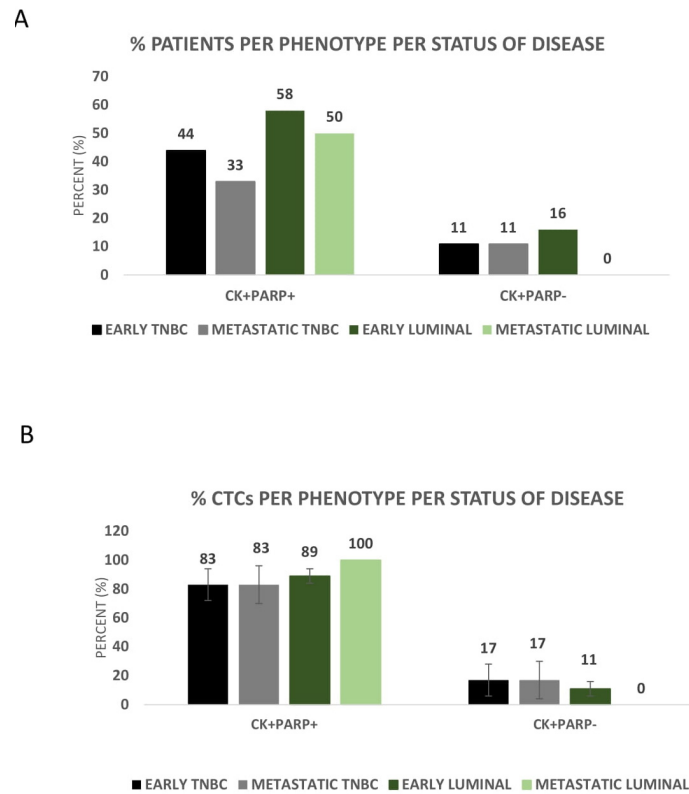


Figure S3. PARP-1 expression in TNBC and luminal BC patients' CTCs. (A) Percentage of early and metastatic TNBC and luminal patients with CK+PARP+ or CK+PARP- phenotypes; (B) Percentage of CTCs with CK+PARP+ or CK+PARP- phenotypes in early and metastatic TNBC and luminal patients.

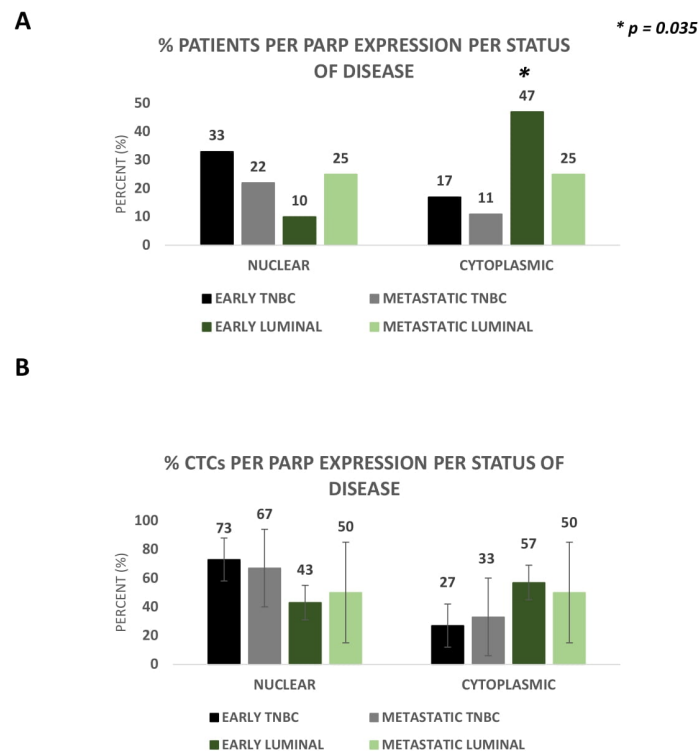


Figure S4. PARP-1 subcellular distribution in TNBC and luminal BC patients' CTCs. (A) Percentage of early and metastatic TNBC and luminal patients with either nuclear or cytoplasmic expression of PARP-1 in their CTCs; (B) Percentage of CTCs with cytoplasmic or nuclear PARP-1 localization in early and metastatic TNBC and luminal patients.

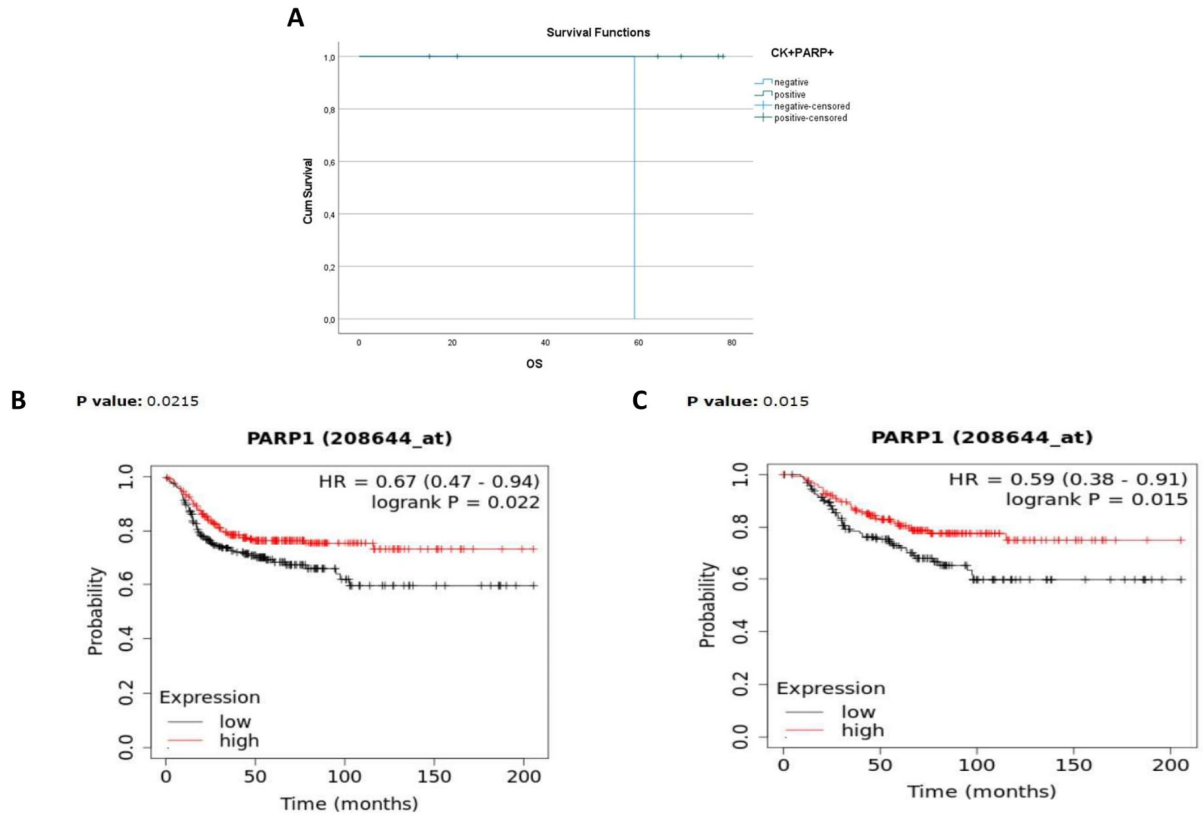


Figure S5. PARP-1 expression and clinical outcome. (A) Kaplan–Meier survival curve for CK-positive BC patients in respect to the CK+PARP+ phenotype (log-rank $p = 0.046$). (B) Correlation of PARP-1 expression with Disease Free Interval (DFI) in patients with basal-like BC using KMplot (<https://kmplot.com/analysis/>). (C) Correlation of PARP-1 expression with OS in patients with basal-like BC using KMplot (<https://kmplot.com/analysis/>, accessed on 27 September 2021).

Table S1. Statistical analysis and p values for the different PARP-1 phenotypes and localizations identified in the corresponding graphs.

Figure	PARP expression	Test	p Values
1a	CK+PARP+	Chi-square	0.156
1a	CK+PARP-	Chi-square	0.834
1b	CK+PARP+	Chi-square	0.175
1b	CK+PARP-	Chi-square	0.491
1c	CK+PARP+	Mann-Whitney	0.701
1c	CK+PARP-	Mann-Whitney	0.701
1d	CK+PARP+	Mann-Whitney	0.860
1d	CK+PARP-	Mann-Whitney	0.860
S3a	CK+PARP+	Chi-square	0.232
S3a	CK+PARP-	Chi-square	0.755
S3b	CK+PARP+	Kruskal-Wallis	0.853
3a	Nuclear	Chi-square	0.951
3a	Cytoplasmic	Chi-square	0.024
3b	Nuclear	Mann-Whitney	0.230
3b	Cytoplasmic	Mann-Whitney	0.093
S4a	Nuclear	Chi-square	0.929
S4a	Cytoplasmic	Chi-square	0.035
S4b	Nuclear	Kruskal-Wallis	0.661
S4b	Cytoplasmic	Kruskal-Wallis	0.397

Table S2. Statistical analysis and p values for the identified mutations in the corresponding graphs.

Figure	Mutations	Test	p Values
4a	M1	Chi-square	0.321
4a	M2	Chi-square	0.363
4a	M3	Chi-square	0.054
4a	M4	Chi-square	0.857
4a	M5	Chi-square	0.507
4a	M6	Chi-square	0.908
4a	M7	Chi-square	0.030
4a	M8	Chi-square	0.507
4a	M9	Chi-square	0.777
4b	M1	Chi-square	0.363
4b	M2	Chi-square	0.725
4b	M3	Chi-square	0.209
4b	M4	Chi-square	0.945
4b	M5	Chi-square	0.159
4b	M6	Chi-square	0.521
4b	M7	Chi-square	0.014
4b	M8	Chi-square	0.002
4b	M9	Chi-square	0.483