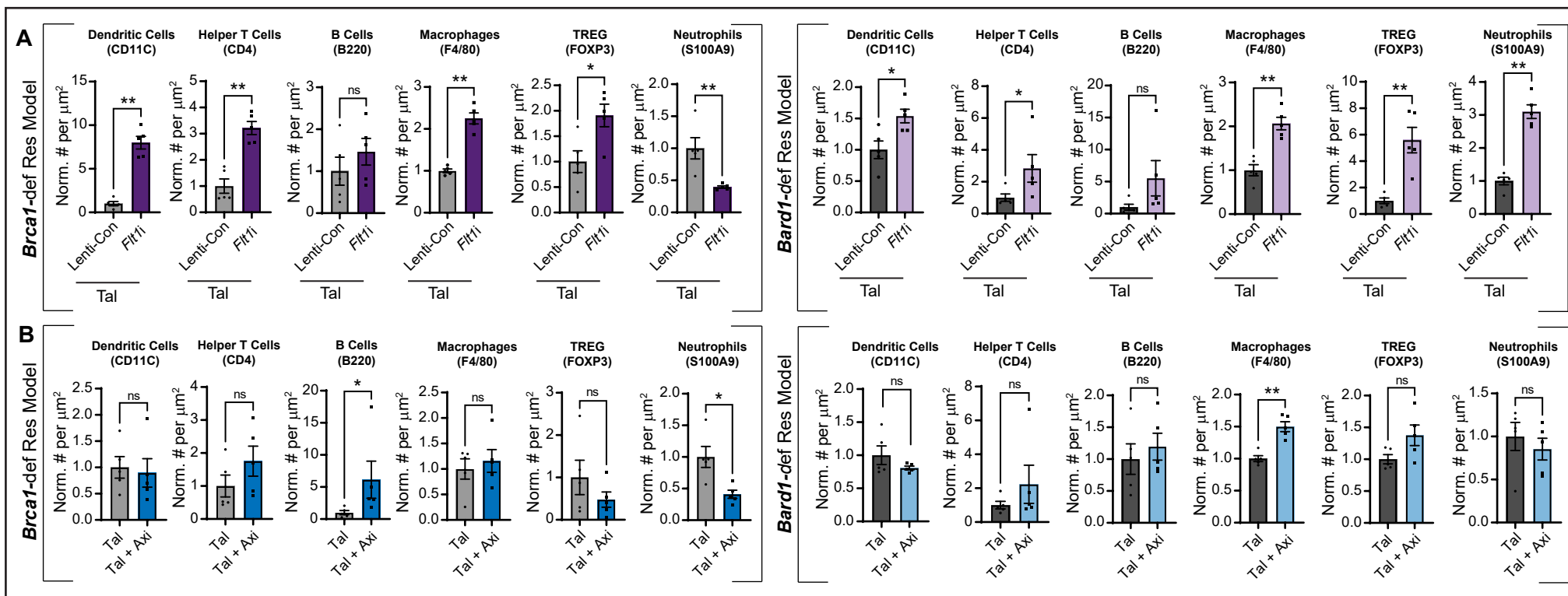
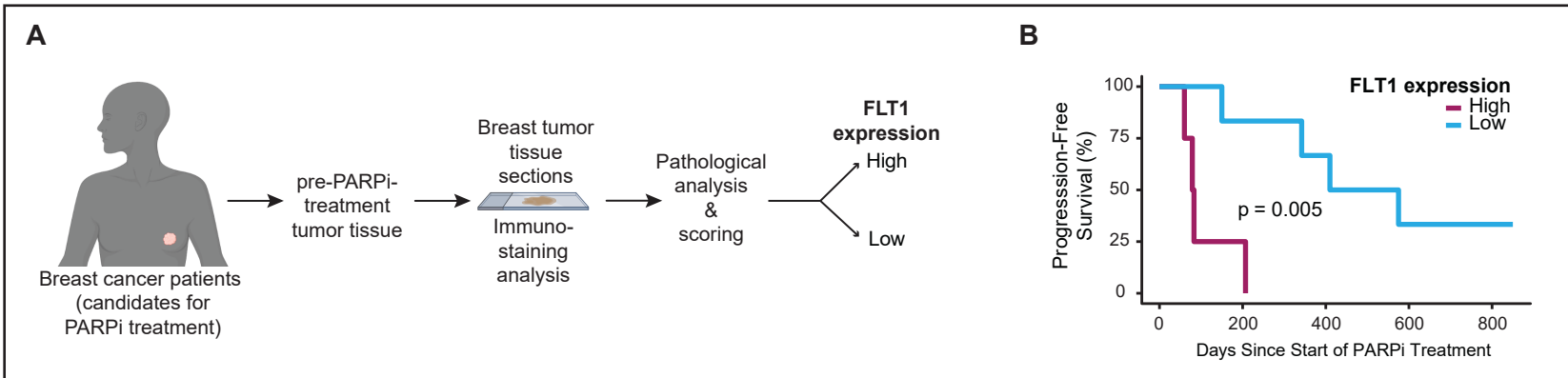


Table of Contents

Appendix Figure S1.....	2
Appendix Figure S2.....	3
Appendix Table S1.....	4



Appendix Figure S1. Immunohistochemical analysis of the immune cells in the tumor microenvironment following FLT1 blockade and talazoparib treatment in mouse models. **A**, Multiple immune markers were analyzed in talazoparib-resistant (“Res”) tumor sections from both *Brca1*-def and *Bard1*-def breast cancer models expressing either Lenti-Con or Flt1i and treated with talazoparib (“Tal”) (see Fig. 3C). $n = 5$ for both groups from each model. Data are presented as mean values \pm SEM. P values were determined by a two-tailed, unpaired, Mann–Whitney test and are listed in parentheses following the immunostains analyzed: for the *Brca1*-def model, CD11C (0.0079), CD4 (0.0079), B220 (ns), F4/80 (0.0079), FOXP3 (0.0317), and S100A9 (0.0079) and for the *Bard1*-def model, CD11C (0.0317), CD4 (0.0317), B220 (ns), F4/80 (0.0079), FOXP3 (0.0079), and S100A9 (0.0079). ns: not significant. **B**, Multiple immune markers were analyzed in Res tumors from both *Brca1*-def and *Bard1*-def breast cancer models treated with Tal or Tal + axitinib (“Axi”) (see Fig. 4A/E). $n = 5$ for both groups from each model. Data are presented as mean values \pm SEM. P values were determined by a two-tailed, unpaired, Mann–Whitney test. ns: not significant. For the *Brca1*-def model, * indicates $P = 0.0159$ for both quantitation for B220 and S100A9. For the *Bard1*-def model, ** indicates $P = 0.0079$ for F4/80. Remaining comparisons for other immune cells were not significant (ns).



Appendix Figure S2. High FLT1 expression in human tumor cells prior to PARPi treatment is associated with shorter progression-free survival in breast cancer patients. **A**, Schematic representation of the workflow for the pathological evaluation of the FLT1 expression in human tumor cells in breast tumor sections pre-PARPi treatment in breast cancer patients. FLT1 immunostainings were performed on tumor tissue specimens (biopsies/resected material) from 10 patients with breast cancer and were obtained prior to PARPi treatment. The immunostained samples were scored by a pathologist who was blinded to the sample details, as either FLT1-high or -low expression. **B**, Kaplan–Meier plots for the PFS of patients described in **A**. Data were analyzed using the log-rank test: $\chi^2 = 8.044$, degrees of freedom (d.f.) = 1; $P = 0.005$; $n = 10$ patients.

Appendix Table S1

Sample ID	Germline Variant	pFLT1
PARP 007	BRCA1	High
PARP 12	BRCA1	Low
PARP 21	BRCA1	Low
PARP 50	BRCA2	Low
S19-30556	PALB2	Low
S19-46410	BRCA2	High
S19-713	BRCA2	Low
S18-73798	BRCA2	High
S19-15838	BRCA1	High
S17-58773	BRCA2	High

Appendix Table S1.

De-identified list of tumor tissue samples from human breast cancer patients ($n = 10$) with confirmed *BRCA1/2* or *PALB2* germline mutations, along with high or low levels of pFLT1. Samples were collected prior to PARP inhibitor treatment.