

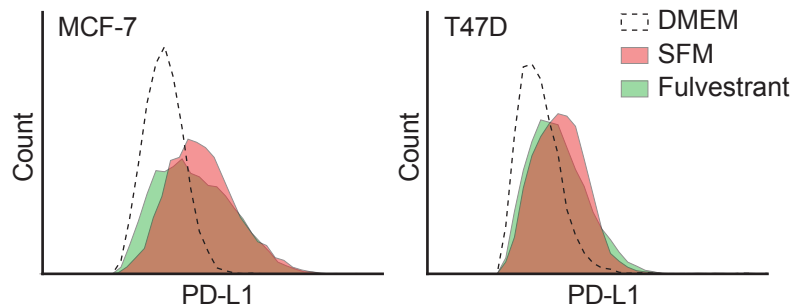
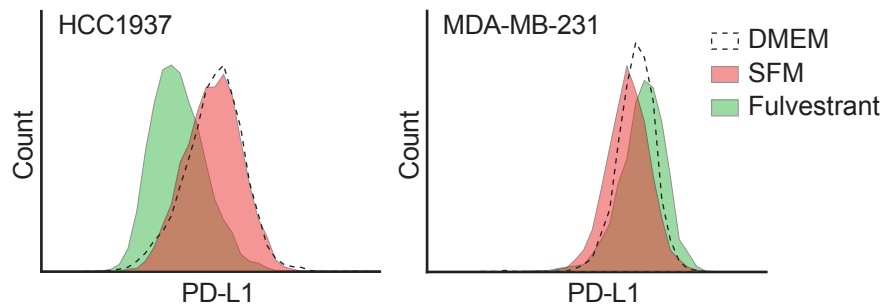
A

B


Figure S1. Estrogen-deprivation induces PD-L1 expression in ER+ BC cells **A**, Flow cytometry-mediated quantification of PD-L1 surface levels in ER α ⁺ BC cell lines (MCF7 and T47D), grown in DMEM, SFM or DMEM supplemented with fulvestrant (1 μ M) for 18 days. **B**, Flow cytometry-mediated quantification of PD-L1 surface levels in ER α ⁻ BC cell lines (HCC1937 and MDA-MB-231), grown in normal medium (DMEM for MDA-MB-231 and RPMI 1640 for HCC1937), SFM or medium supplemented with fulvestrant (1 μ M) for 18 days.

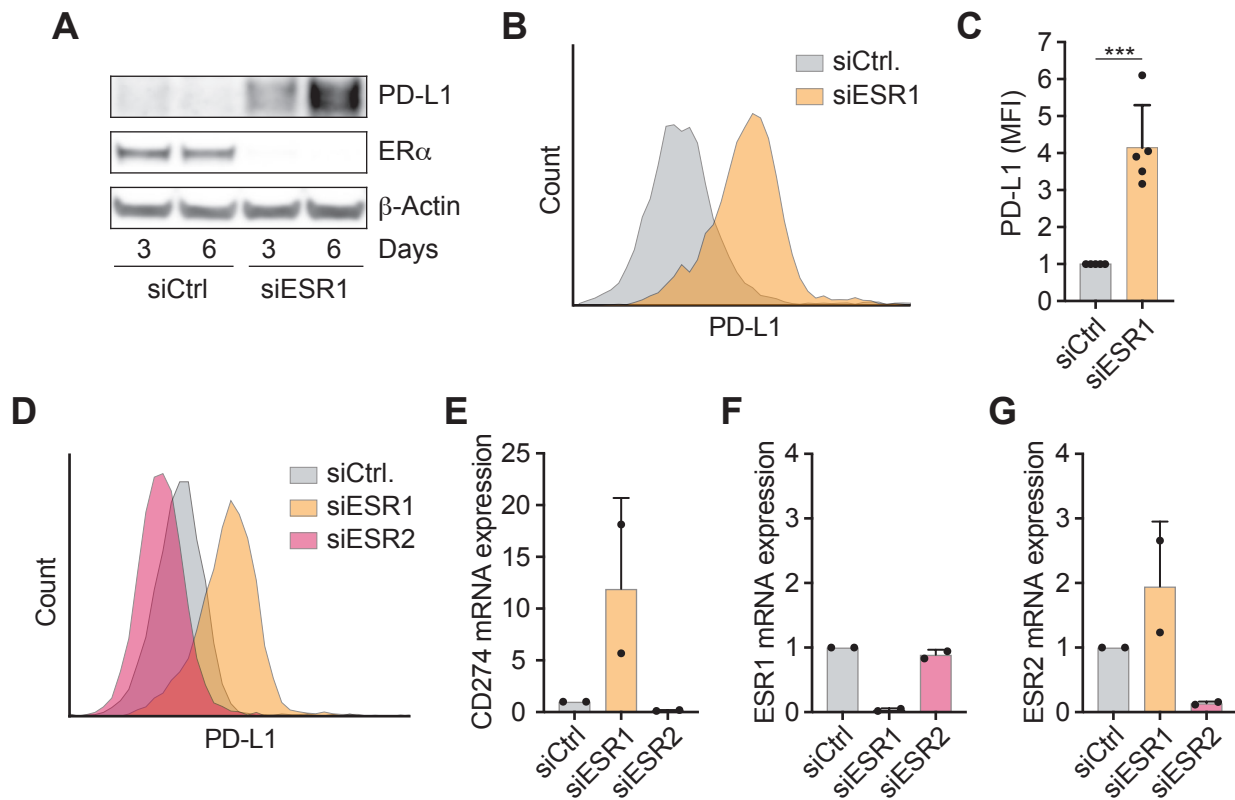


Figure S2. ER α , and not ER β , suppresses PD-L1 expression in MCF7 cells

A, Western blot analysis of the indicated proteins in MCF7 cells treated with either 20 nM control or ER α -targeting (*ESR1*) siRNA for 3 or 6 days. β -Actin is shown as a loading control. **B**, PD-L1 membrane levels analysed by flow cytometry after treatment of MCF7 cells with the indicated siRNAs for 6 days. **C**, Quantification of 3 independent experiments as the one shown in (**B**). Data are presented as mean +SD (n=5). *** $p < 0.001$. **D**, PD-L1 membrane levels as analysed by flow cytometry in MCF7 cells transfected twice with 20nM of the indicated siRNAs for 6 days. **E-G** qRT-PCR analysis of *CD274* (**E**), *ESR1* (**F**) and *ESR2* (**G**) mRNA levels in MCF7 cells transfected as in (**D**). Levels of the *18S* rRNA served as an internal control.

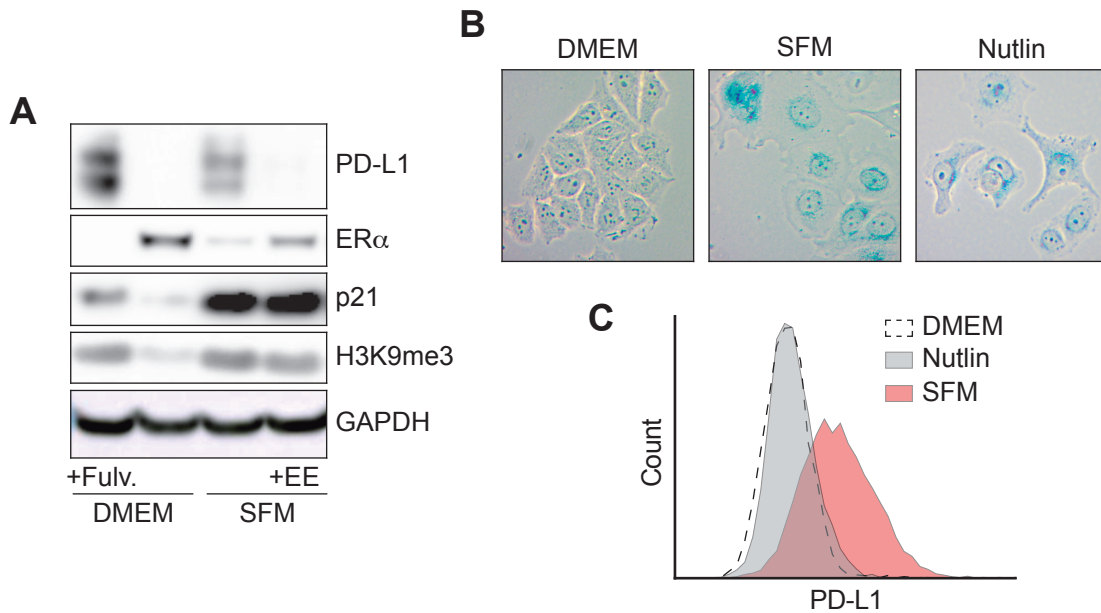


Figure S3. Senescence fails to upregulate PD-L1 expression in MCF7 cells

A, MCF7 cells were grown in DMEM, SFM or DMEM with fulvestrant (1 μ M) for 17 days. Where indicated, EE (10 nM) was added for the last 3 days. Whole-cell extracts were subjected to western blot analysis of the indicated proteins. **B**, SA- β -Galactosidase assay of MCF7 cells cultured in DMEM, SFM (19 days) or Nutlin-3 (5 μ M, 5 days). Representative images for each condition are shown. **C**, FACS analysis of PD-L1 membrane levels in MCF7 cells cultivated as in (**B**).

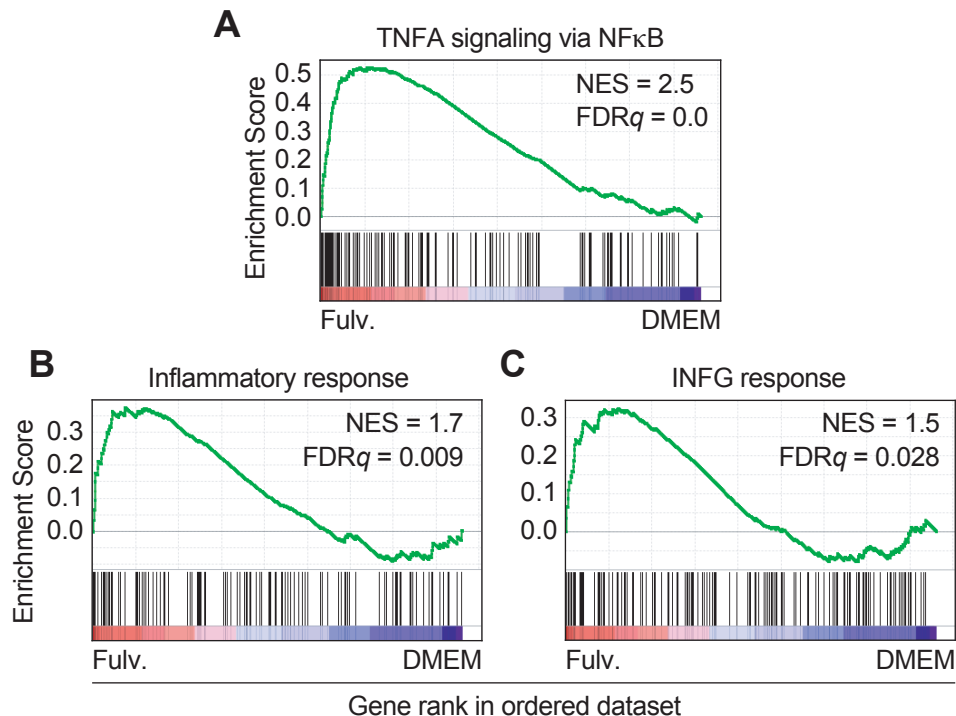


Figure S4. Fulvestrant triggers an inflammatory transcriptional program in MCF7 cells A-C, Pre-ranked GSEA on the genes from the hallmarks "TNFA signaling via NF- κ B" (**A**), "Inflammatory response" (**B**) and "IFNG response" (**C**) obtained from RNAseq analysis comparing the transcriptome of MCF7 cells grown in DMEM or fulvestrant (1 μ M) for 3 weeks. The heatmap representation illustrates the overall upregulation of these pathways in fulvestrant-treated MCF7 cells.

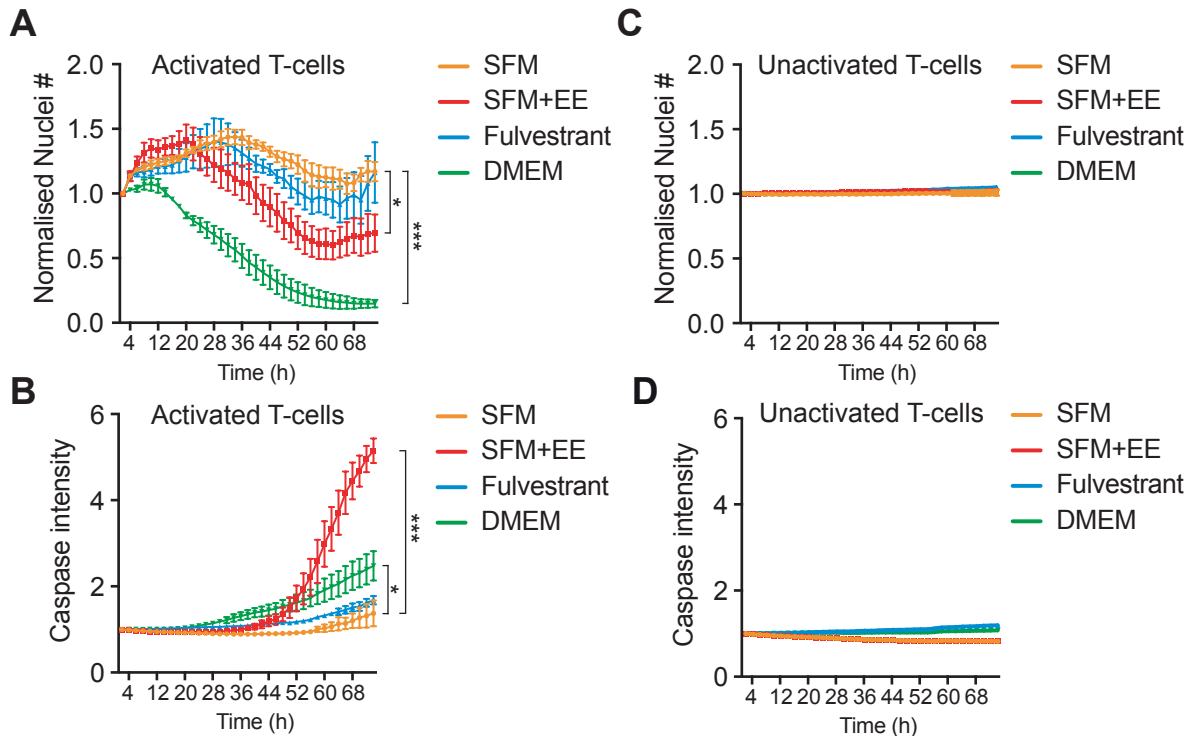


Figure S5. Estrogen-deprivation limits T-cell mediated killing of MCF7 cells **A**, Live cell imaging of MCF7 nuclei count after addition of activated primary T lymphocytes isolated from human peripheral blood. Nuclei counts were normalized to the value at T = 0 hrs for each condition and then each timepoint was subsequently normalized to the value of the control to which no T-cells were added. Values represent the mean \pm SEM. **B**, Time-lapse microscopy of the intensity of a fluorescently labelled caspase-3/7 substrate in MCF7 cells treated with activated primary T-cells. Values represent the mean \pm SEM. **C,D** Equivalent analyses as the ones shown in **(A)** and **(B)**, but where non-activated T-cells were used, illustrating that activation of the T-cells is a requisite for their cytotoxic activity against MCF7 cells.