Supplementary Table S1. The sequences of primers used in the study

Gene	Forward primer (5'→3')	Reverse primer (5'→3')
TFEB	GCGGCAGAAGAAAGACAATC	CTGCATCCTCCGGATGTAAT
PPARγ	TTTTCAAGGGTGCCAGTTTC	AATCCTTGGCCCTCTGAGAT
Arg1	TTTTTCCAGCAGACCAGCTT	GGAACCCAGAGAGAGCATGA
IL-10	GGACAACATACTGCTAACCGAC	TGGATCATTTCCGATAAGGCTTG
COX2	CAGCCAGGCAGCAAATCCTT	AGTCCGGGTACAGTCACACT
MMP9	CATTCGCGTGGATAAGGAGT	ACCTGGTTCACCTCATGGTC
LC3	CGTCCTGGACAAGACCAAGT	ATTGCTGTCCCGAATGTCTC
Lamp1	ACATCAGCCCAAATGACACA	GGCTAGAGCTGGCATTCATC
p62	GATAGCCTTGGAGTCGGTGG	CCGGGGATCAGCCTCTGTAG
ATG5	ACCCCTGAAATGAGTTTTCCAGA	CATCCAGAGCTGCTTGTGGT
NLRP3	CAAGGCTGCTATCTGGAGGAA	TGCAACGGACACTCGTCATC
IL-1β	GCCCATCCTCTGTGACTCAT	AGGCCACAGGTATTTTGTCG
IL-6	AGTTGCCTTCTTGGGACTGA	TCCACGATTTCCCAGAGAAC
HIF-1α	TCAAGTCACTCAACGTGGAAG	TATCGAGGCTGTGTCGACTG
MIF	GTGCCAGAGGGGTTTCTGT	AGGCCACACAGCAGCTTACT
cPLA2	GCTTAAGGCAGGAGCTAACCT	TGGCACGTAGAACCACAACA
18s	CGCGGTTCTATTTTGTTGGT	AGTCGGCATCGTTTATGGTC

Supplementary Figure Legends

Supplementary Figure S1. Flow cytometry analysis for T cells and dendritic cells (DCs) in the cells isolated from the resected orthotopic breast tumors in C57Bl/6 mice transplanted with bone marrow cells from $TFEB^{fl/fl}$ (BM-WT) or MΦ-$TFEB^{-/-}$ (BM-$TFEB^{-/-}$) mice. Data are shown as Mean±SEM, n=3, *p<0.05, two-tailed Student *t*-test.

Supplementary Figure S2. A. Heatmap of microarray data showing differentially expressed genes between WT and TFEBtg BMDMs treated with EO771 cell conditioned medium (ECM). Biologically triplicate samples were depicted in columns. B. Most significantly affected pathways by TFEB overexpression determined by Ingenuity pathway analysis. The stacked bar chart represents the percentage (%) of genes that were upregulated (red), no change (gray), or downregulated (green), and genes not overlapped with dataset (white) in each canonical pathway. The numerical value at the top of each bar represents the total number of genes in the considered pathway. The secondary y-axis (down) shows the –log of P-value calculated by right-tailed Fisher's exact test, which indicates the significance of each pathway. The ratio (orange dots connected by a line) indicates the ratio of genes from the dataset that map to the pathway divided by the total number of genes that map to the same pathway.

Supplementary Figure S3. Quantification of the relative protein levels in Figure 3B. The intensities of the indicated protein bands were normalized to the corresponding β-actin bands. The intensity of phosphorylated p65 was normalized relative to corresponding total p65. Data are shown as mean±SEM of triplicates and are

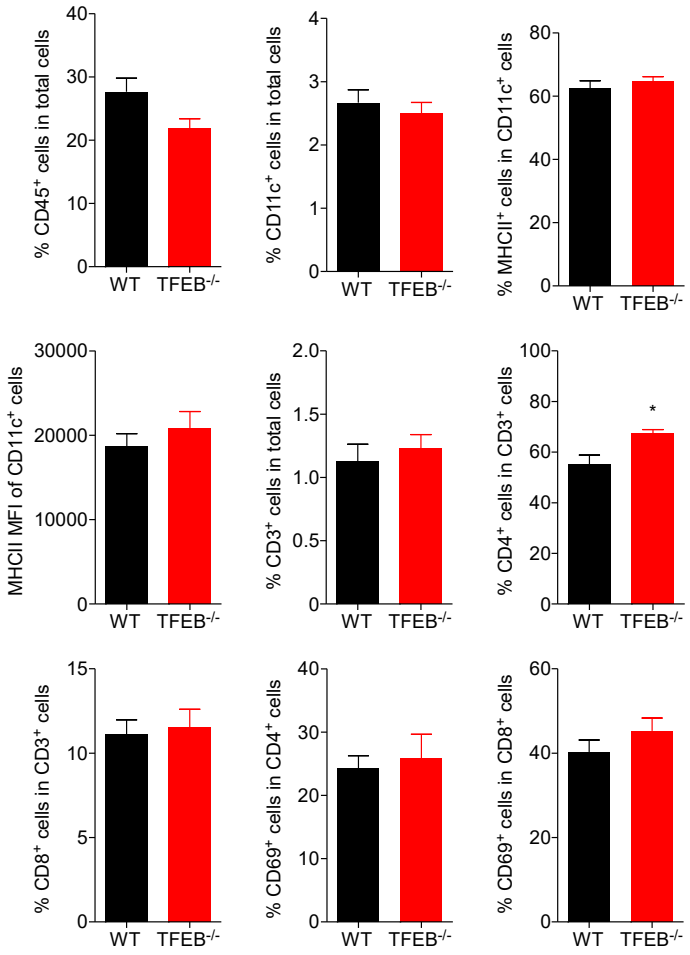
representative of three independent experiments. N=3; two-tailed Student *t*-test; *p<0.05, **p<0.01, ***p<0.001.

Supplementary Figure S4. Quantification of the relative protein levels in Figure 4A. The intensities of the indicated protein bands were normalized to corresponding β-actin bands. The intensity of phosphorylated p65 was normalized relative to corresponding total p65. Data are shown as mean±SEM of triplicates and are representative of three independent experiments. N=3; two-tailed Student *t*-test; *p<0.05, **p<0.01, ***p<0.001.

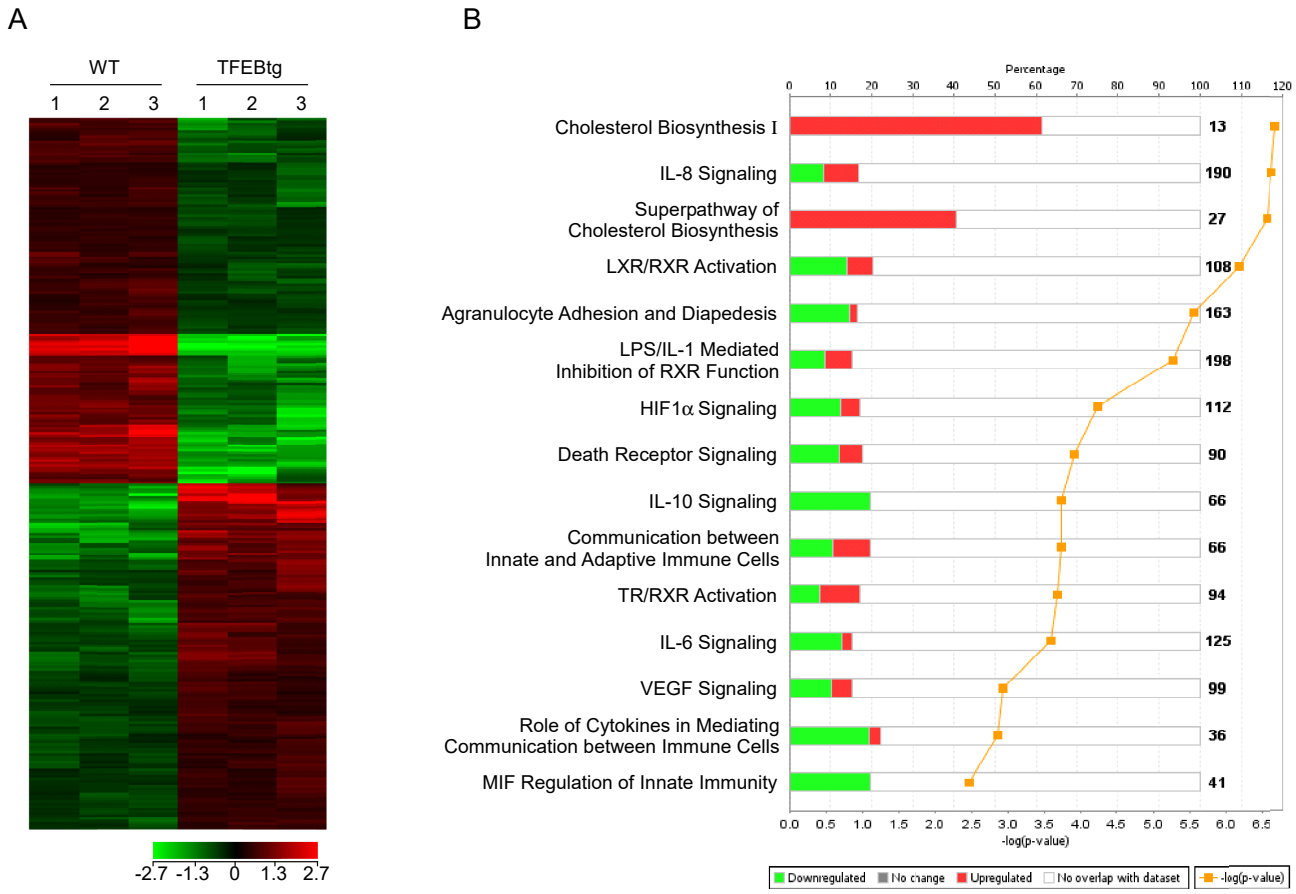
Supplementary Figure S5. A and B. Western blot analysis of TFEB protein levels in cytosolic or nuclear subcellular fraction and whole cells of pMΦs treated with Trehalose (1 mM), HPβCD (1 mM), CQ (10 μM) and ECM. Histone H3 and GAPDH represent control proteins for the nuclear and cytosolic fraction, respectively. Quantification of relative intensity of the protein bands is shown under the lanes. C. Band intensities of proteins in Figure 5B were quantified by Gel-Pro Analyzer software and normalized by β-actin protein, and the intensity of phosphorylated p65 was normalized relative to total p65. D. Bone marrow-derived MΦs from WT or MΦs-specific Atg5 KO mice were treated with DMEM or trehalose for 12 h and the expression of ATG5 and PPARγ was measured by qPCR. Data are shown as mean±SEM of triplicates and are representative of three independent experiments. N=3; two-tailed Student *t*-test; *p<0.05, **p<0.01, ***p<0.001.

Supplementary Figure S6. A. qPCR measurement of Arg1 and IFNγ expression in the tumors of mice treated with vehicle or trehalose. N=5. B. Tumor number and weight per mouse as well as the ratio of tumor weight to body weight were measured in the C3(1)/SV40Tag spontaneous breast tumor mouse treated with Trehalose (2 g/kg, three times a week) or vehicle from 6 weeks of age to 17 weeks of age.

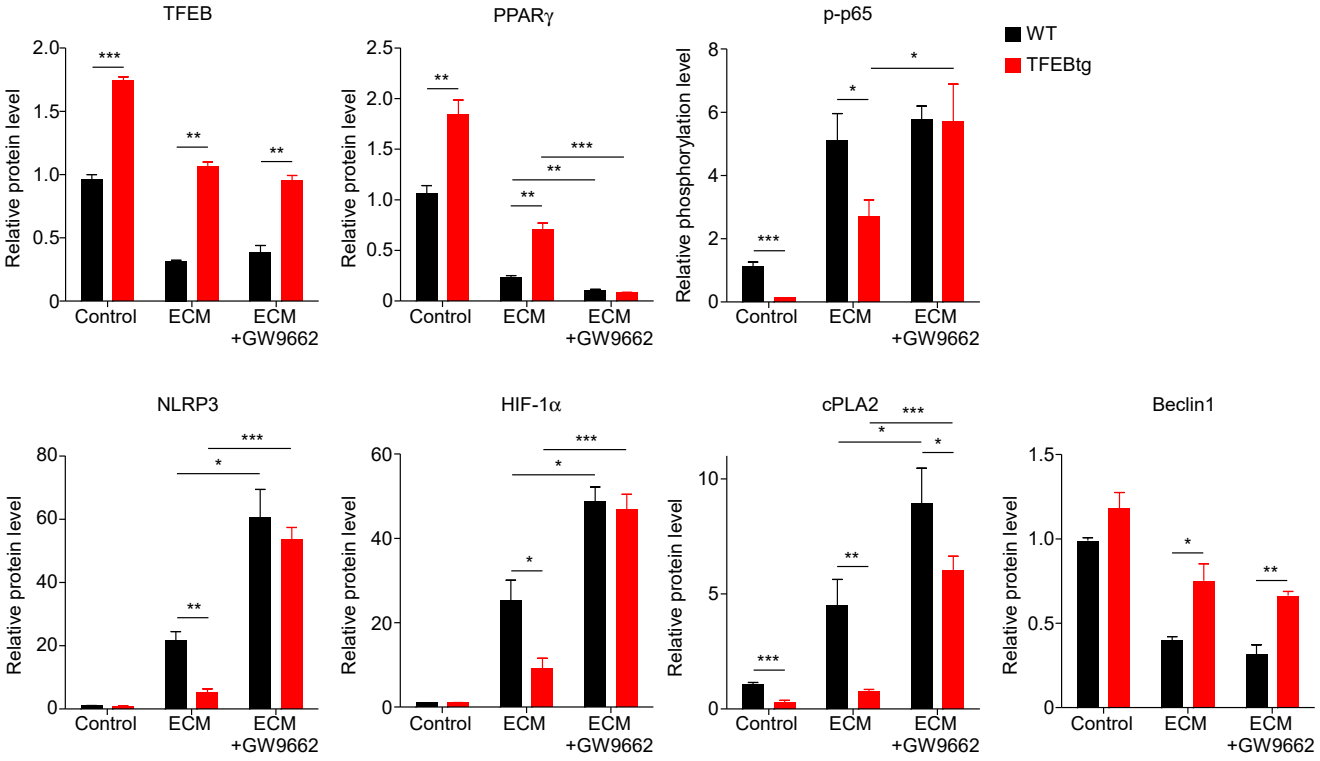
Supplementary Figure S7. **TFEB expression is reduced in tumor-associated MΦs in human breast cancer.** Formalin fixed paraffin embedded human breast cancer tumor and peri-tumor tissues were immunofluorescent stained for MΦs (CD68) and TFEB; nuclei were counterstained using DAPI. Five pairs of tissues were used for quantification of TFEB positive MΦs (Graph at lower panel). Four representative MΦs were enlarged (Lower panel; 1 and 2: peritumor tissue cells; 3 and 4: tumor cells). Each data point represents the mean ± SEM. *$p<0.05$.



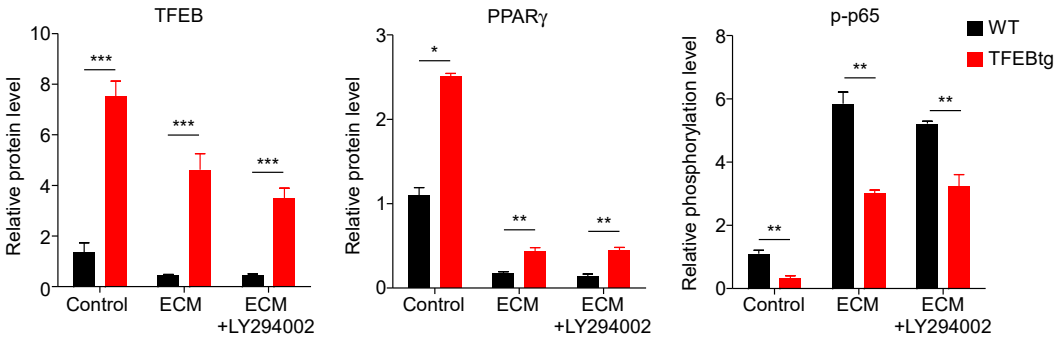
Supplementary Figure S1



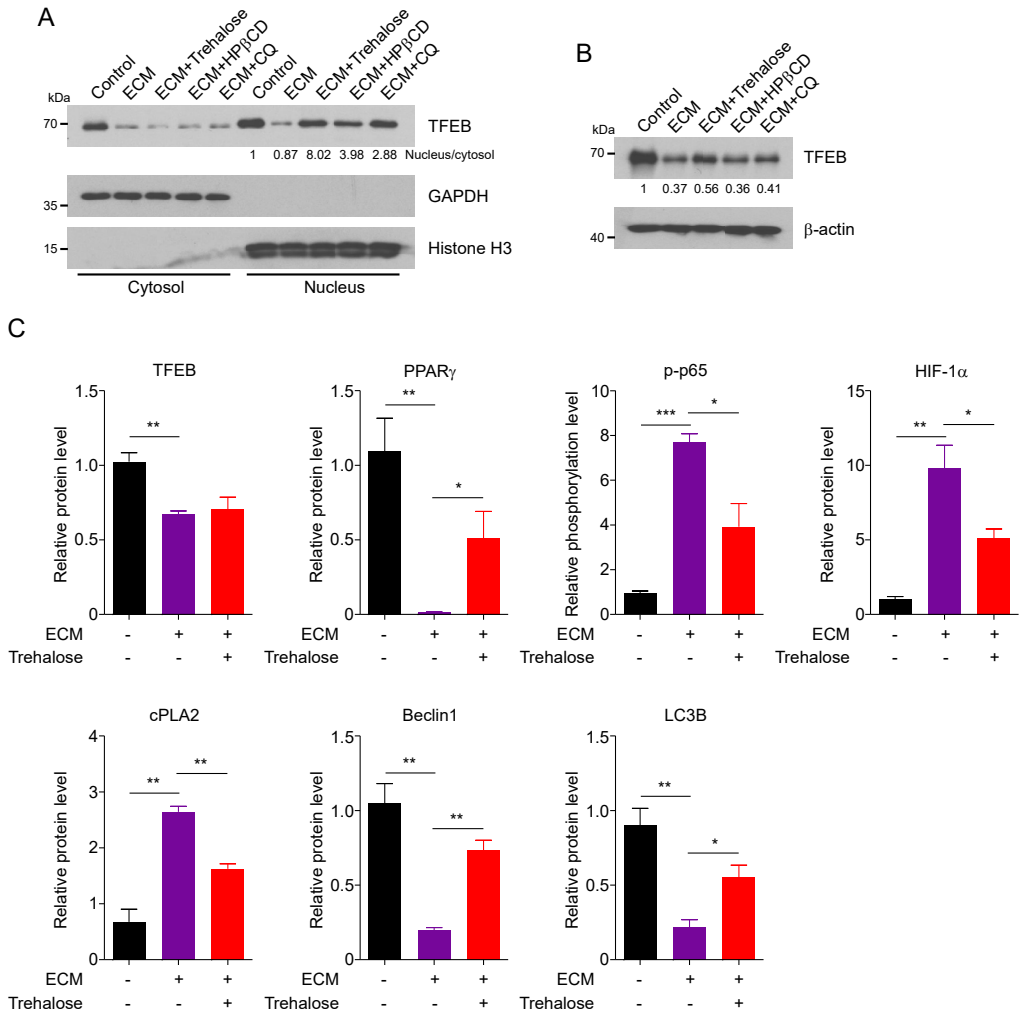
Supplementary Figure S2



Supplementary Figure S3



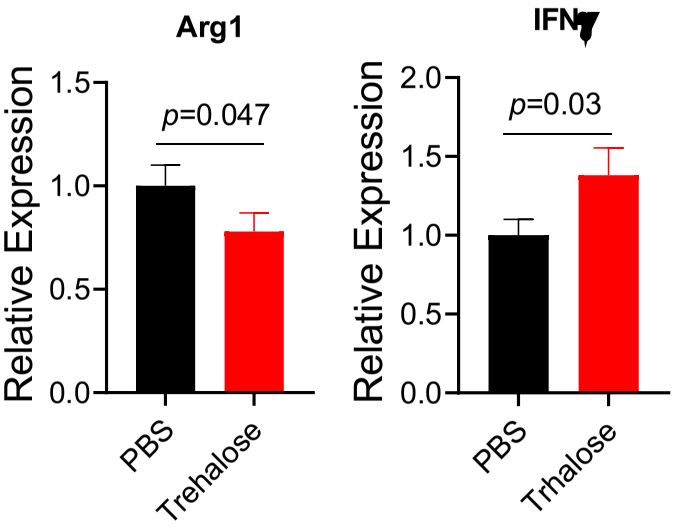
Supplementary Figure S4



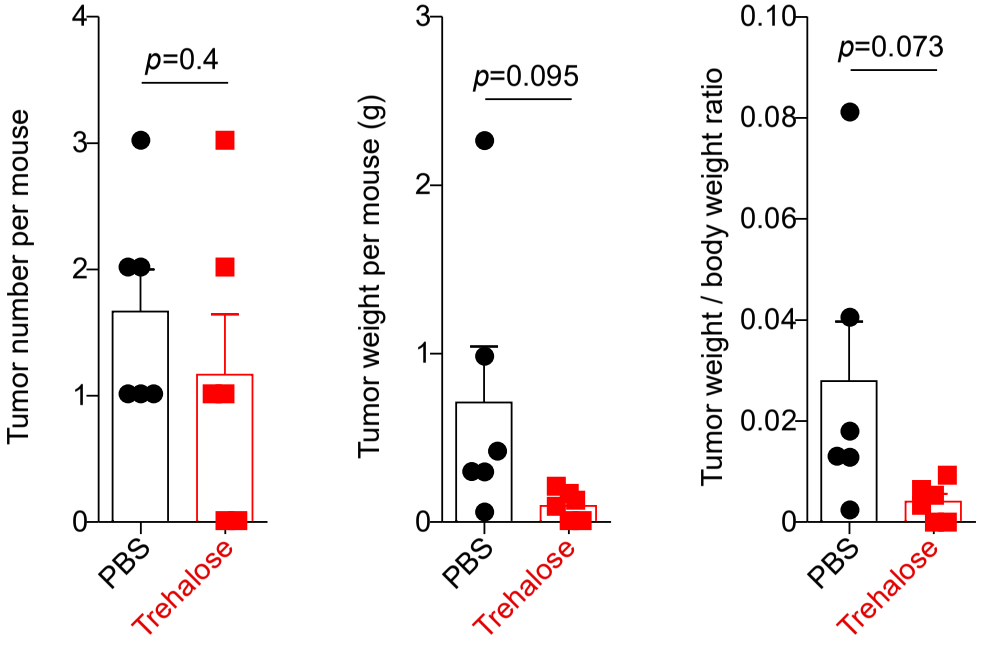
Supplementary Figure S5

Li Y, *et al. J Immunother Cancer* 2020; 8:e000543. doi: 10.1136/jitc-2020-000543

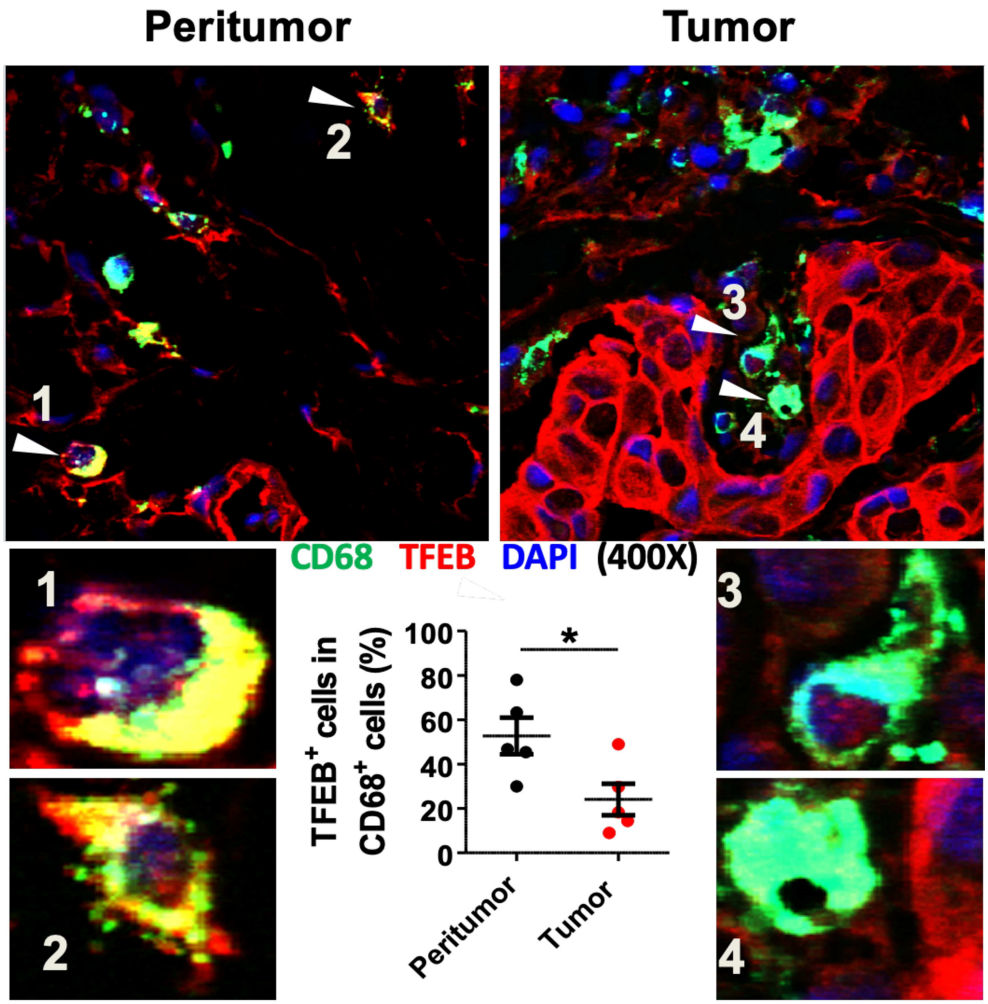
A



B



Supplementary Figure S6



Supplementary Figure S7