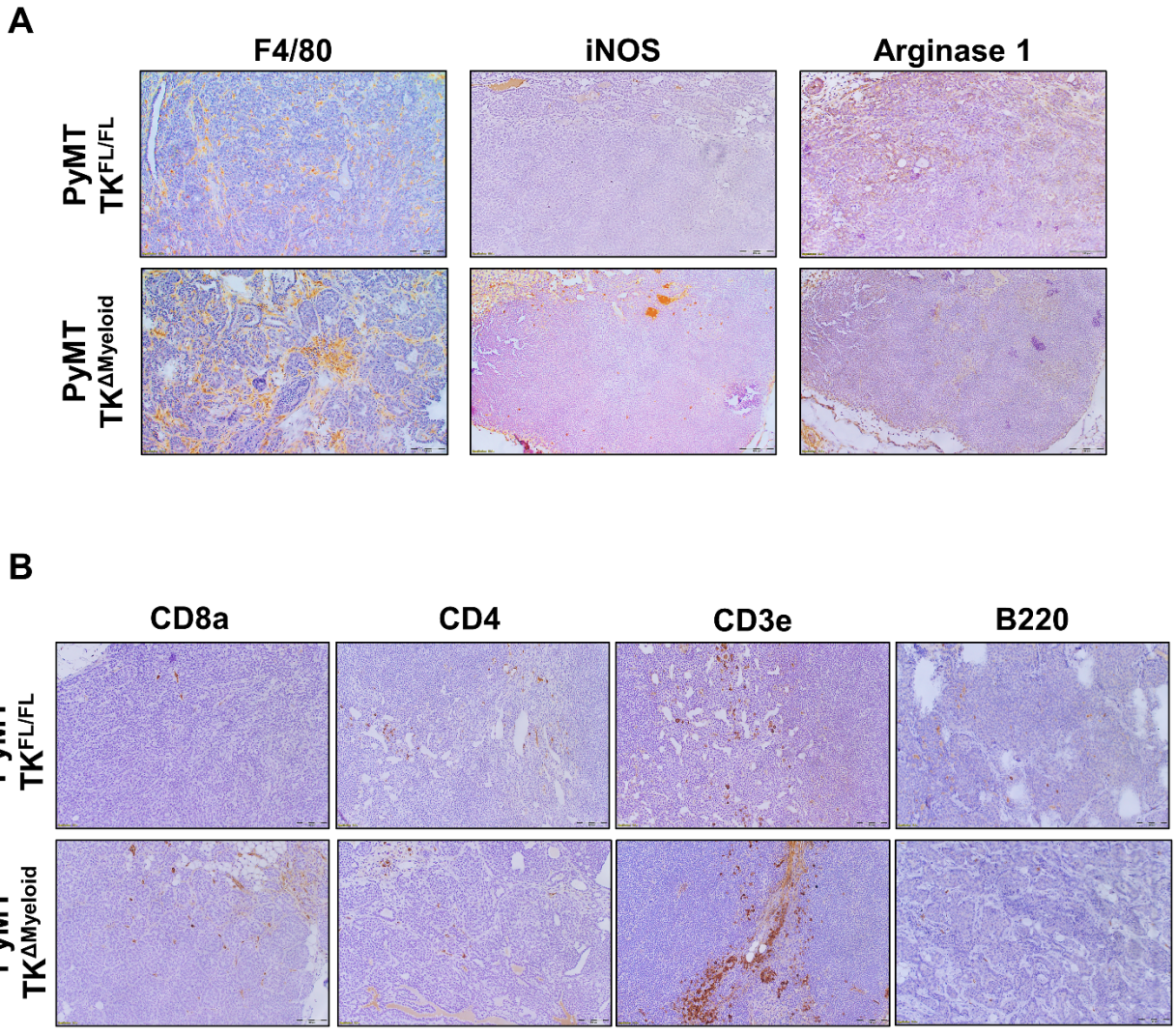
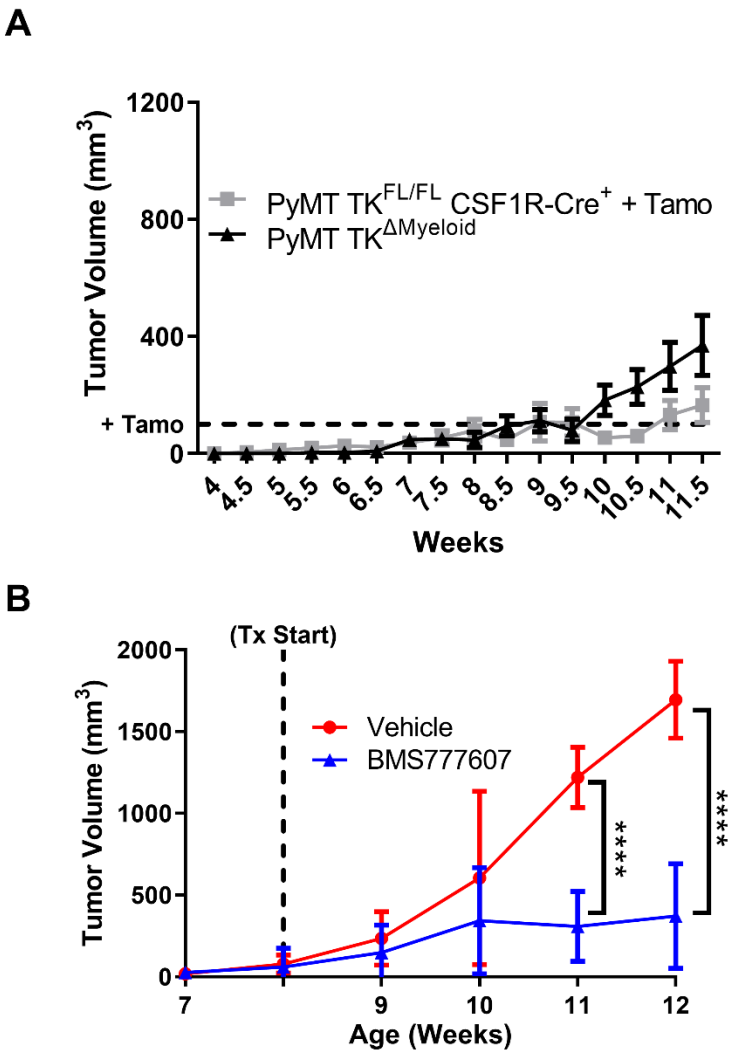
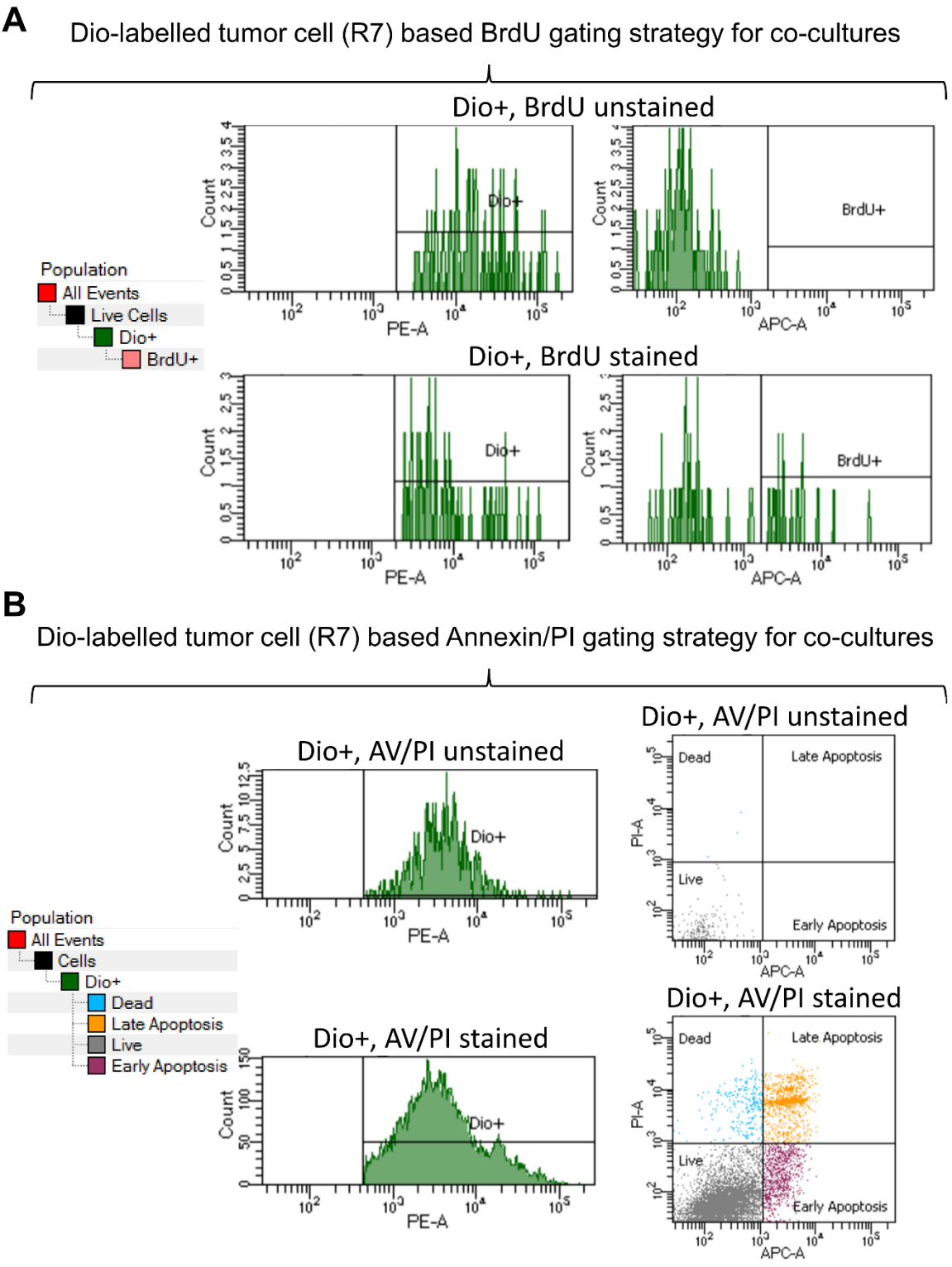
Supplemental Material



Supplemental Figure S1. A) Representative images of PyMT $TK^{FL/FL}$ and PyMT $TK^{\Delta Myeloid}$ tumors stained for **A)** F4/80, iNOS, and Arginase 1; and **B)** CD8a, CD3e, CD4, and B220. Scale bars=100μm; n=3-8 tumors per group; n=3-5 fields per tumor were analyzed.

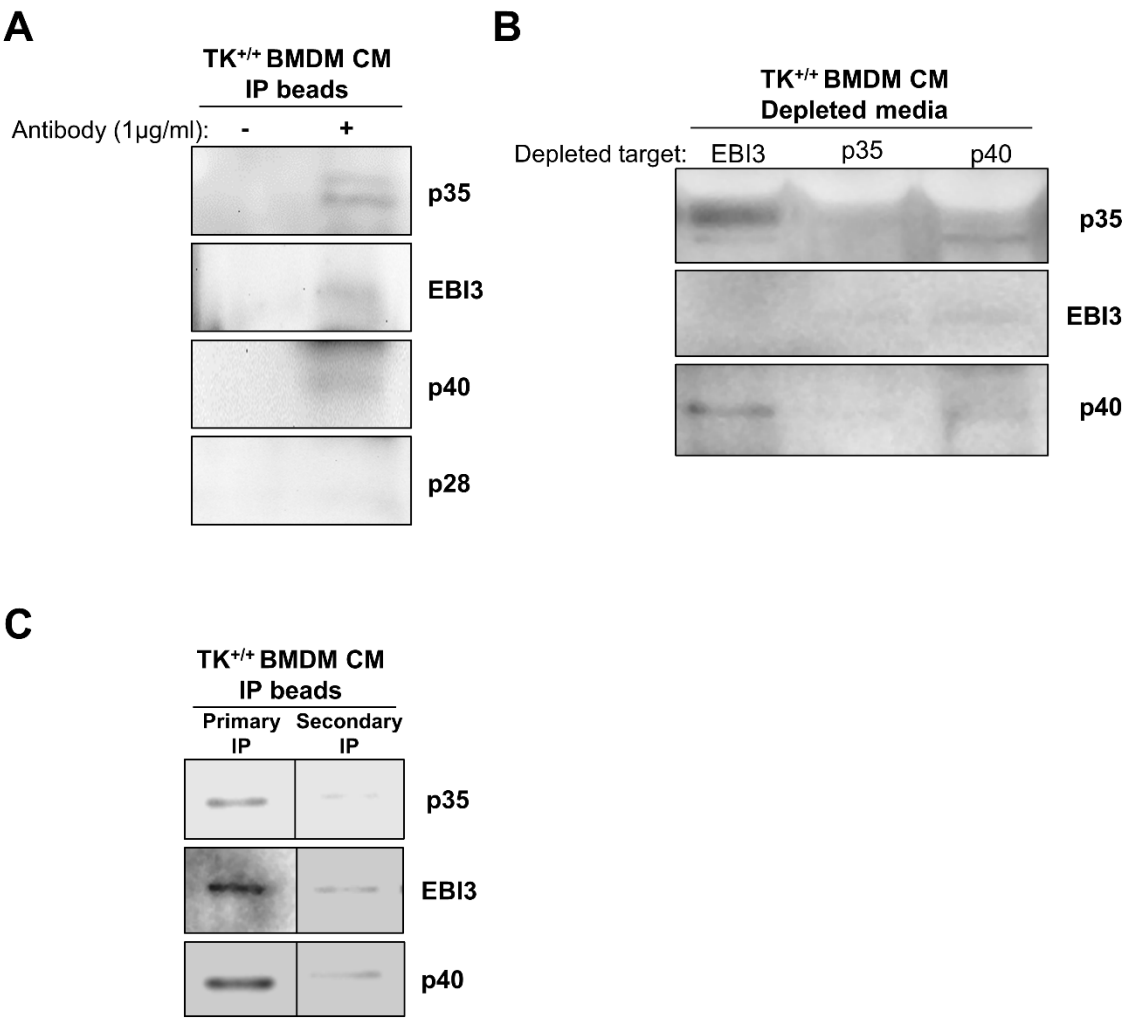


Supplemental Figure S2. A) Average tumor growth curves of PyMT TK$^{FL/FL}$ CSF1R-Cre^{+} (n=10) mice with tamoxifen (Tamo) treatment and PyMT TK$^{\Delta Myeloid}$ (n=27) mice. Tamoxifen treatment was initiated when tumors reached 100mm^3 (denoted by the dashed line). **B)** Average tumor growth curves of PyMT WT (n=27) and PyMT WT + BMS-777607 (n=5) mice. Statistical significance was determined using a two-way ANOVA with corrected multiple t tests. Data represent average values ± SD. *P<0.05. Chemical inhibition of RON in PyMT TK$^{+/+}$ mice was performed with 50 mg/kg/day BMS-777607 (Selleck Chemical) treatment via oral gauge, starting at 8 weeks of age (when palpable tumors reach a measurable size).



Supplemental Figure S3. Representative flow cytometry gating strategies for tumor cell/macrophage co-culture. Using Dio fluorescent labeling of tumor cells prior to macrophage co-

culture, tumor cells were resolved from the mixed culture by gating on Dio fluorescence to examine **A)** tumor cell proliferation via BrdU incorporation and **B)** tumor cell apoptosis/cell death via Annexin V/PI expression.



Supplemental Figure S4. A) Representative Western blot images showing the immunoprecipitation of p35, EBI3, p40, and p28 in $TK^{+/+}$ BMDM CM with (+) and without (-) antibody depletion (n=3). Depletion of p35, EBI3, p40, and p28 subunits from $TK^{+/+}$ BMDM CM was performed by rotating BMDM conditioned media with 1µg/ml antibody and protein A/G agarose beads (SCBT). Following incubations with antibody and beads, the depleted CM was used for treatment. Western blot shown using proteins eluted from beads. Incubation with beads without antibody served as the control. **B)** Representative Western blot images showing p35, p40, and EBI3 expression from concentrated $TK^{+/+}$ CM that was depleted for EBI3, p35, or p40. CM samples were concentrated (approximately 10 fold) using Amicon Ultra-4 Ultracel 3K Centrifugal filters (Millipore Sigma) as per manufacturer's recommendations. **C)** Representative Western blot

images of pulled down target protein showing p35, p40, and EBI3 levels following primary IP pull down and a second sequential IP pull down in respective lanes.

Supplemental Table S1. Primers for Genotyping

	Gene	Primers
Genotyping	*PyMT*	5'-GGAAGCAAGTACTTCACAAGGG-3' 5'-GGAAAGTCACTAGGAGCAGGG-3'
	Ron Flox	5'-TCATTTGAATCAGTCCCCTCACTTTTCTCC-3' 5'-GGAACCAGTACACAGATGAGTAAACTGAGC-3' 5'-TCGCTCAAGCCCAGGCAGGGCCTCACAGAG-3'
	Lys-Cre	5'-TTACAGTCGGCCAGGCTGAC-3' 5'-CTTGGGCTGCCAGAATTTCTC-3' 5'-CCCAGAAATGCCAGATTACG-3'
	CSF1R-Cre	5'-AGATGCCAGGACATCAGGAACCTG-3' 5'-ATCAGCCACACCAGACACAGAGATC-3'

Supplemental Methods

RNA-Sequencing (RNA-Seq)

RNA-Seq analysis was performed in GeneSpring NGS software (Agilent Technologies). First, sequences were aligned to the mouse reference genome (mm9), which aligns reads spanning known or novel splice junctions. The reference annotations were produced by the Ensembl project1. Multiple mapping reads were removed and aligned reads were filtered on base quality, with a quality threshold >=30 and zero 'Ns' allowed in each read. The aligned gene read counts were quantified and used to compute reads per kilobase per million reads (RPKMs) for each transcript in each sample. Raw counts were normalized using the DESeq algorithm, threshold set to 1, and base lined to the median of control samples. Further filtration was applied, requiring at least 3 RPKM in each sample of at least one experimental condition, yielding 13,949 transcripts.