Fig. S1. Flow sorting of human and mouse TAMs.

Tumor associated macrophages were isolated from human breast cancer and mouse mammary cancer from the PyMT model as described in the Materials and Methods. For human TAMs, CD45 positive cells (A) were also sorted for expression of CD11b, CD14, and CD163 (B, C). The CD11b+ CD14+ CD163 cells were isolated and used for transcript analysis (Fig. 1C). For mouse tumors, CD11b+ cells were analyzed for their expression of Gr1 (D). A $CD11b^{hi}$ and $Gr1^{hi}$ population was shown to be F4/80 negative (E) and represents neutrophils and myeloid derived suppressor cells (MDSC). The $CD11b^{lo}$ population was $Gr1^{+}$ (D) while the $CD11b^{hi}$ population was $Gr1^{-}$ (D) and both populations were F4/80 positive (F, G). They represent monocytes and TAMs respectively. The $CD11b^{lo}$ $Gr1^{+}$ $F4/80^{+}$ population was $Tie2^{lo}$ (H) while the $CD11b^{hi}$, $Gr1^{-}$ $F4/80^{+}$ population was $Tie2^{hi}$ (I). The latter population was analyzed for *Wnt7b* expression and gene deletion (Fig. 1D, E).

Fig. S2. Assessment of Vegfa and Notch target gene expression in flow sorted VECs.

Vascular endothelial cells were isolated from mouse MMTV-PyMT mammary tumors by flow-sorting for CD45 negative (A) CD31+ cells (C, D). VECs were isolated from both control tumors (B) and myeloid conditional *Wnt7d* deletion tumors (C) and then QPCR performed on the RNA isolated from those cells. An assessment of *Vegfa* expression in control and mutant showed that *Wnt7b* deletion from myeloid cells resulted in reduced *Vegfa* expression in VECs (D). No significant change was observed in the transcripts for the two Notch pathway target genes *Dll4* and *Hey1* (D). By contrast the level of the transcripts for both *Vegfr2* and *Vegfr3* were significantly elevated (D). p values calculated using Student's T-test.