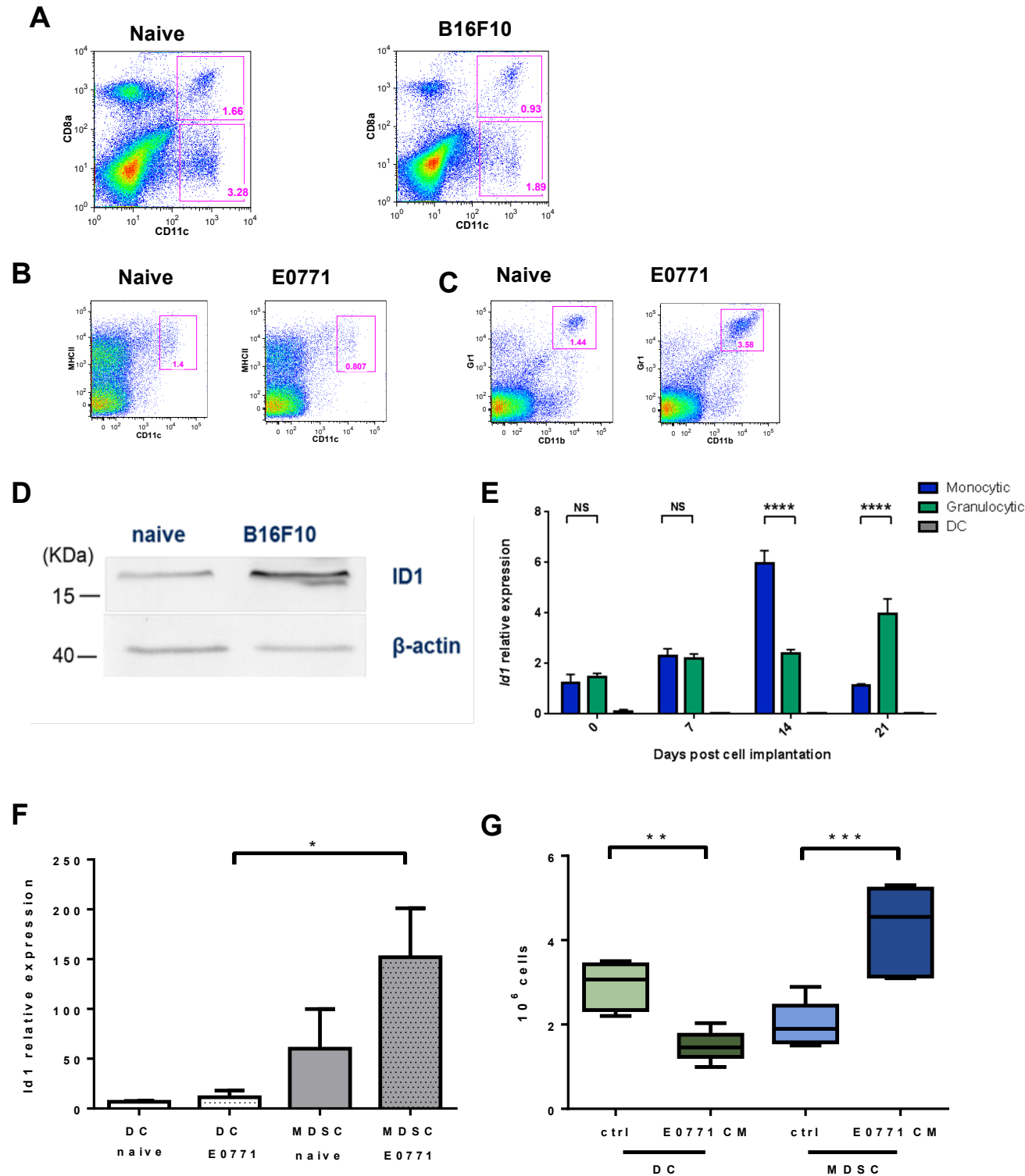


Supplementary Figures

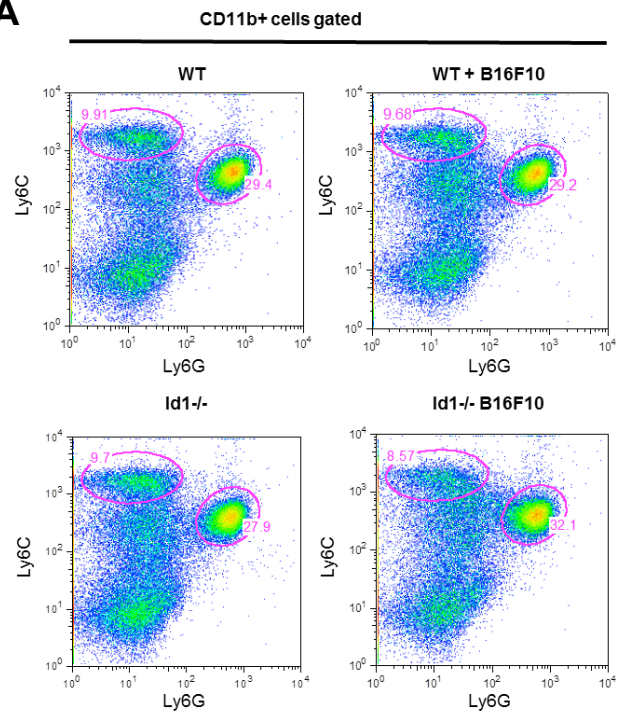


Supplementary Figure 1. Tumour-secreted factors favour bone marrow-derived cell differentiation towards high Id1-expressing MDSCs but not DC differentiation *in vivo* and *in vitro*

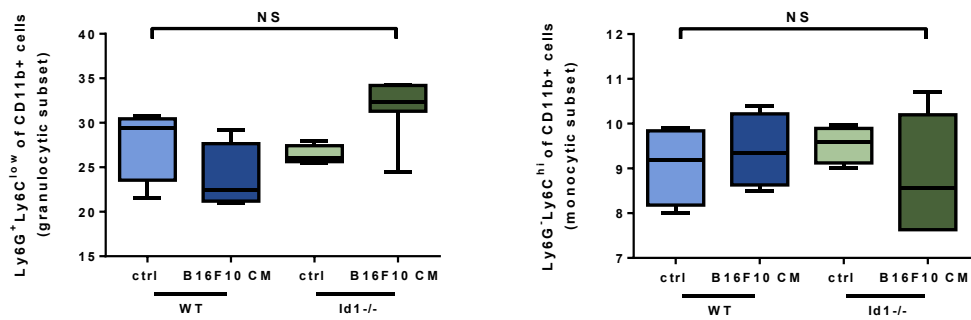
(A) Representative frequencies of CD8⁺ and CD8⁻ DCs by flow cytometry analysis of spleens from naïve and B16F10 melanoma-implanted and control mice (Day 21 post implantation). Representative plots of flow cytometry analysis of spleens from E0771 mammary adenocarcinoma -implanted mice (Day 21 post implantation) for (B) DC frequencies and (C) MDSC frequencies compared to control mice. (D) Id1 protein levels in lysates from naïve and B16F10 bearing CD11b⁺ bead sorted splenocytes as determined by western blot (Representative results from three independent experiments). (E) Id1 mRNA expression levels of FACS-sorted splenic DC (CD11c⁺), monocytic (CD11b⁺Ly6C⁺) and granulocytic (CD11b⁺Ly6G⁺) MDSC populations from spleens from naïve and B16F10 melanoma-bearing mice, on days 7, 14 and 21 following implantation as determined by qPCR analysis (means ± SEM, n = 5, One-way ANOVA, **** p<0.001). (F) Id1 mRNA expression levels of FACS-sorted splenic DC and MDSC populations from spleens from E0771 mammary adenocarcinoma-implanted mice, as determined by qPCR analysis (means ± SEM, n = 6, One-way ANOVA, p < 0.05). (G) *In vitro* differentiation of lin⁻ cells, cultured for 6 days in the presence of E0771 mammary adenocarcinoma TCM (25% v/v) and analyzed for DC and MDSC content by flow cytometry (means ± SEM, n = 6, Unpaired t-tests, ** p < 0.01, *** p < 0.001).

Supplementary Figure 2

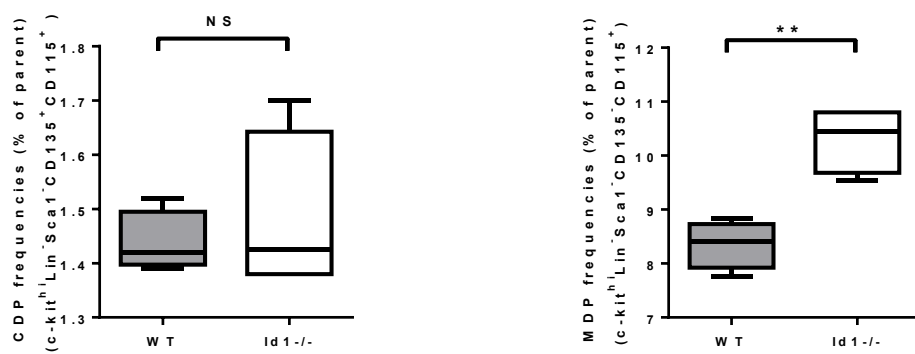
A



B



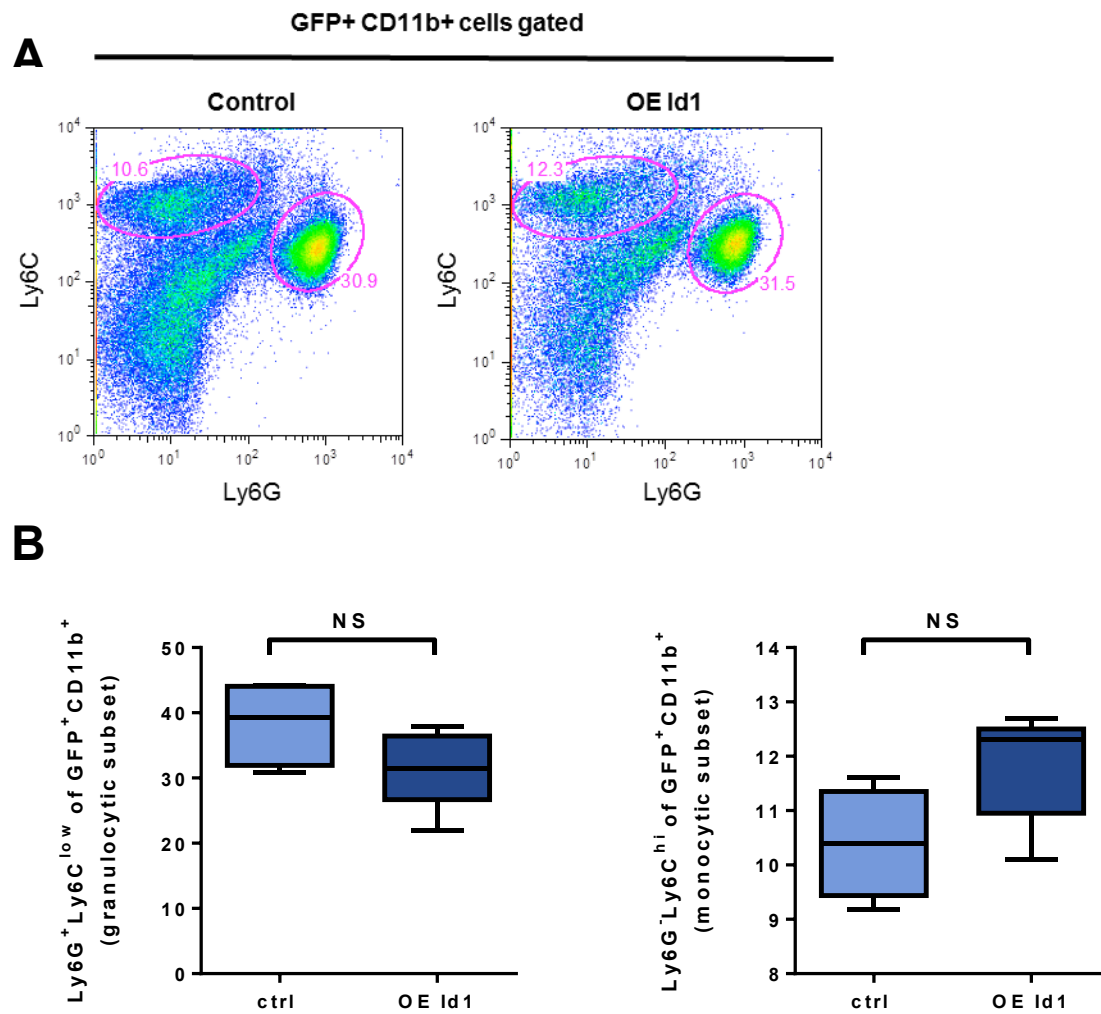
C



Supplementary Figure 2. Analysis of MDSC subsets.

(A) Flow cytometry analysis of granulocytic and monocytic MDSC subsets from WT and *Id1*^{-/-} splenocytes of mice injected daily with B16F10 TCM or control media over 21 days **(B)** Summary graphs of granulocytic and monocytic subset levels across all animal groups (One-way ANOVA, not significant). **(C)** Flow cytometry analysis of common dendritic cell progenitor (CDP) and myeloid dendritic cell progenitor (MDP) frequencies in bone marrow samples from WT and *Id1*^{-/-} animals (Unpaired t-tests, NS: not significant, ** $p < 0.01$).

Supplementary Figure 3

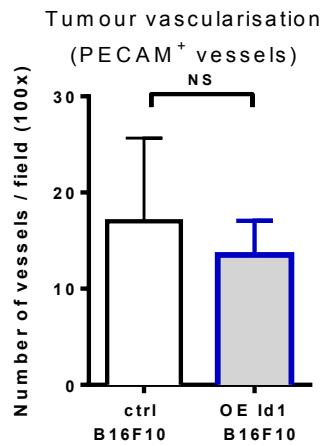


Supplementary Figure 3. Analysis of MDSC subsets.

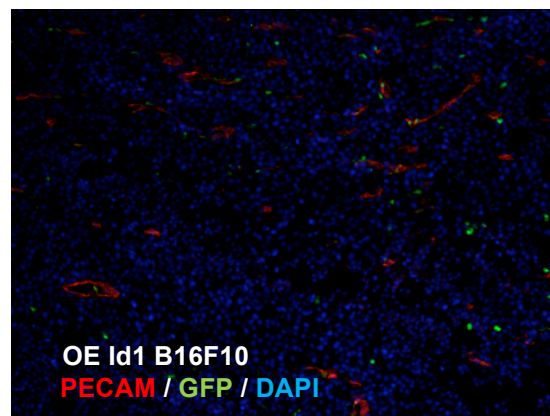
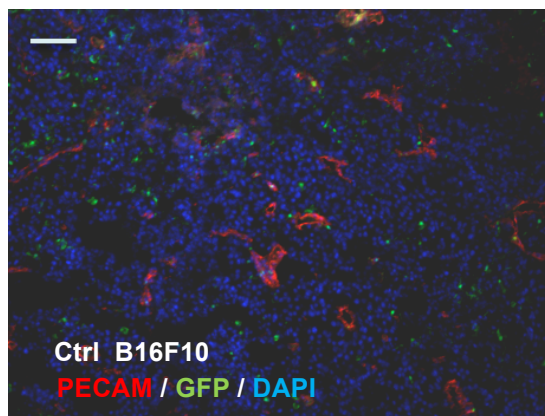
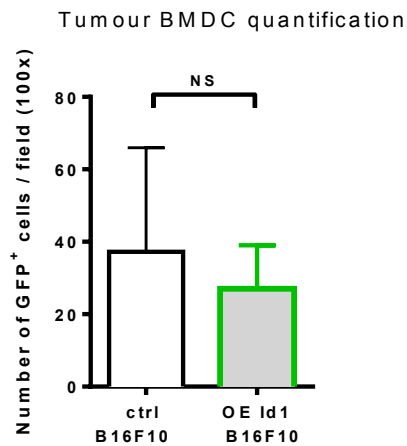
(A) Flow cytometry analysis of granulocytic and monocytic MDSC subsets from mice transplanted with control-vector and Id1-overexpressing-vector transduced lin⁻ bone-marrow cells **(B)** Summary graphs of granulocytic and monocytic subset levels (Unpaired t-test, NS: not significant).

Supplementary Figure 4

A



B

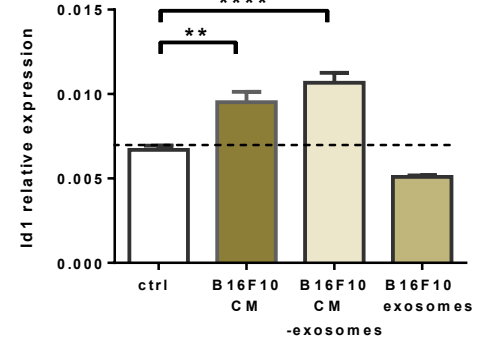


Supplementary Figure 4. Primary tumour analysis by immunofluorescence (A)

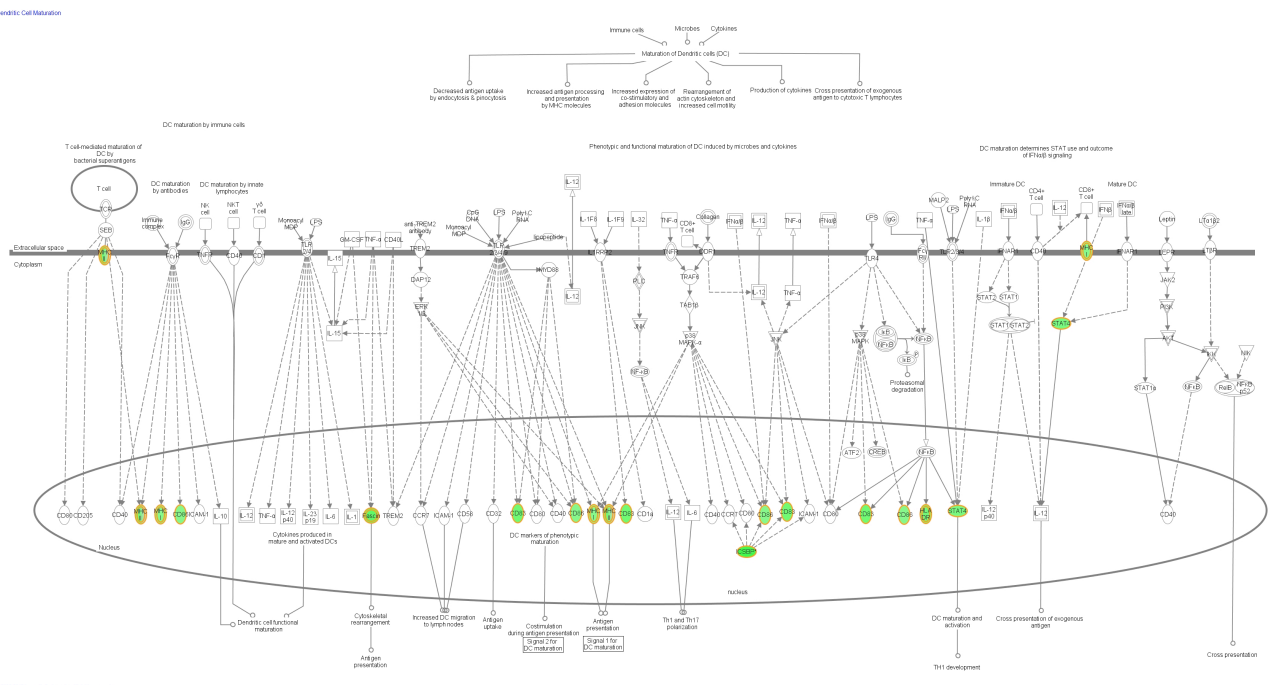
Immunofluorescence analysis of vascularization of platelet/endothelial cell adhesion molecule-1 (PECAM-1) (Texas Red staining quantification) and (B) bone marrow cell infiltration (GFP⁺ quantification) in primary B16F10 tumours from mice transplanted with control-vector and Id1-overexpressing-vector transduced lin⁻ bone-marrow cells. Scale bar: 50 μ m (Unpaired t-tests, NS: not significant).

Supplementary Figure 5

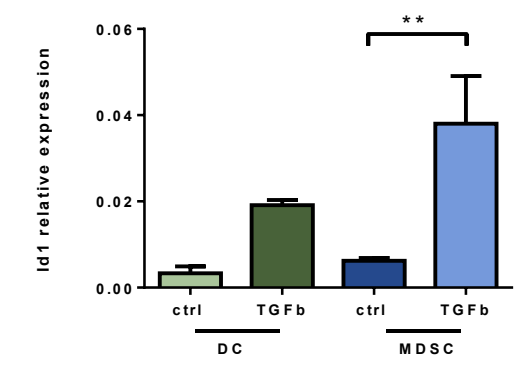
A



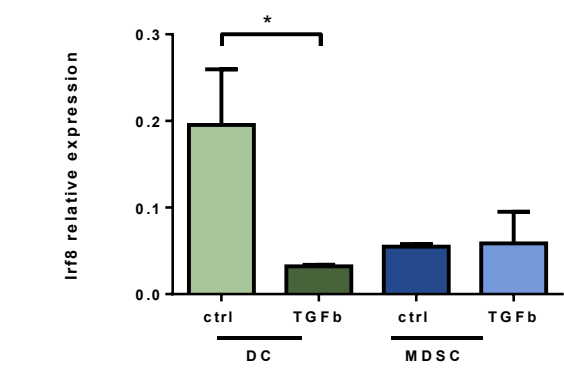
B



C



D



Supplementary Figure 5.

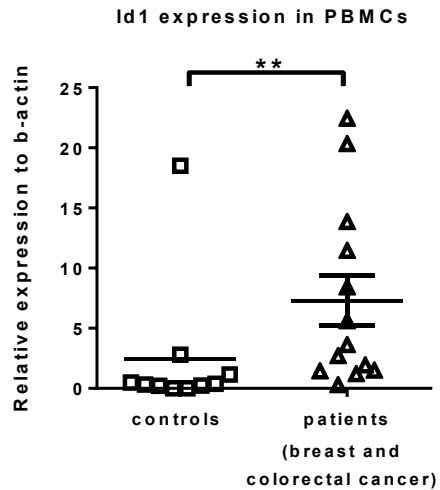
(A) Id1 relative mRNA expression levels of in vitro differentiation of lin^- hematopoietic progenitors isolated from C57Bl/6 mice, cultured for 6 days in the presence of B16F10 CM, B16F10 CM depleted from exosomes and B16F10 exosomes, as determined by qPCR analysis (means $\pm$ SEM, $n = 6$, One-way ANOVA, $** p < 0.001$).

(B) Id1 downstream mediators. Pathway analysis of differentially expressed genes in Id1 overexpressing BMDC. DC maturation is one of the top pathways affected by Id1 overexpression as determined using Ingenuity Pathway Analysis software. Relevant downregulated genes are shown in green.

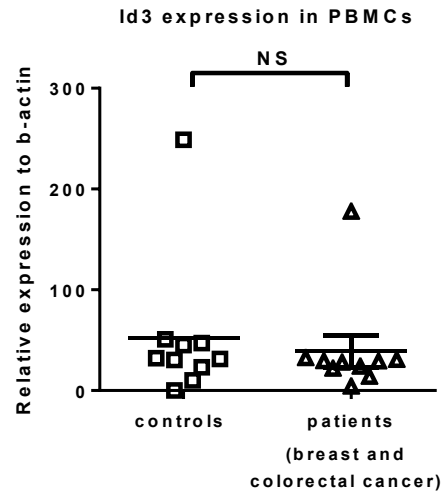
(C) Id1 and **(D)** Irf8 mRNA expression levels of FACS-sorted DC and MDSC populations following in vitro differentiation of lin^- cells, cultured for 6 days in the presence of recombinant TGF β , as determined by qPCR analysis (means $\pm$ SEM, $n = 5$, One-way ANOVA, $**p < 0.01$, $*p < 0.05$).

Supplementary Figure 6

A



B



Supplementary Figure 6. PBMCs from patients with metastatic breast and colorectal cancer express higher levels of Id1 compared with PBMC from controls.

(A) qPCR analysis of Id1 (Mann Whitney test, $^{**}p < 0.01$) and **(B)** Id3 mRNA expression levels following isolation of PBMCs from metastatic colorectal and breast cancer patient blood samples (n=13) compared to healthy age-matched controls (n=10).

Supplementary table

Supplementary Table 1. DC maturation gene signature. List of DC maturation-associated differentially expressed genes following Id1 overexpression compared to control BMDC

Symbol	Entrez Gene Name	Affymetrix	Fold Change	Entrez Gene ID for Mouse
IRF8	interferon regulatory factor 8	1416714_at	-2.048	15900
FSCN1	fascin homolog 1, actin-bundling protein	1416514_a_at	-1.786	14086
HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	1452431_s_at	-1.669	14960
CD83	CD83 molecule	1416111_at	-1.669	12522
HLA-DRB1	major histocompatibility complex, class II, DR beta 1	1417025_at	-1.642	14969
STAT4	signal transducer and activator of transcription 4	1448713_at	-1.557	20849
HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	1451721_a_at	-1.465	14961
HLA-A	major histocompatibility complex, class I, A	1425137_a_at	-1.425	15007
CD86	CD86 molecule	1420404_at	-1.408	12524