Legend to Supplementary Material:

Supp. Figure 1: A. BRAF regulates CD200 expression in melanoma cell lines. Taqman qRT-PCR of *CD200* expression after WM2664, SKMEL24, and SKMEL28 melanoma cell lines were transduced with a BRAF knockdown construct. *CD200* expression was normalized to a control transcript (18S). **B.** Immunoblot showing ERK inhibition in melanoma cell lines transduced with mutant BRAF knockdown. Protein lysates from indicated cell lines were immunoblotted for anti-phospho-ERK, anti-total-ERK, anti-BRAF and anti-tubulin.

Supp. Figure 2: A. *CD200* expression in NIC60 cell lines. Source data are median-centered and described in Ross *et al*, Nature Genetics 2000 (38). Note the markedly increased expression of *CD200* in the melanoma cluster, with an expression pattern comparable to established melanoma transcripts (*CD200* clustered closely with ENDRB and DCT in this data set and the set of primary tumors shown below). **B.** Median centered *CD200* expression was analyzed in source data from Haqq *et al*. PNAS 2005 (39). In this independent data set of melanocytic lesions, relative levels of *CD200* mRNA expression correlates with tumor progression.

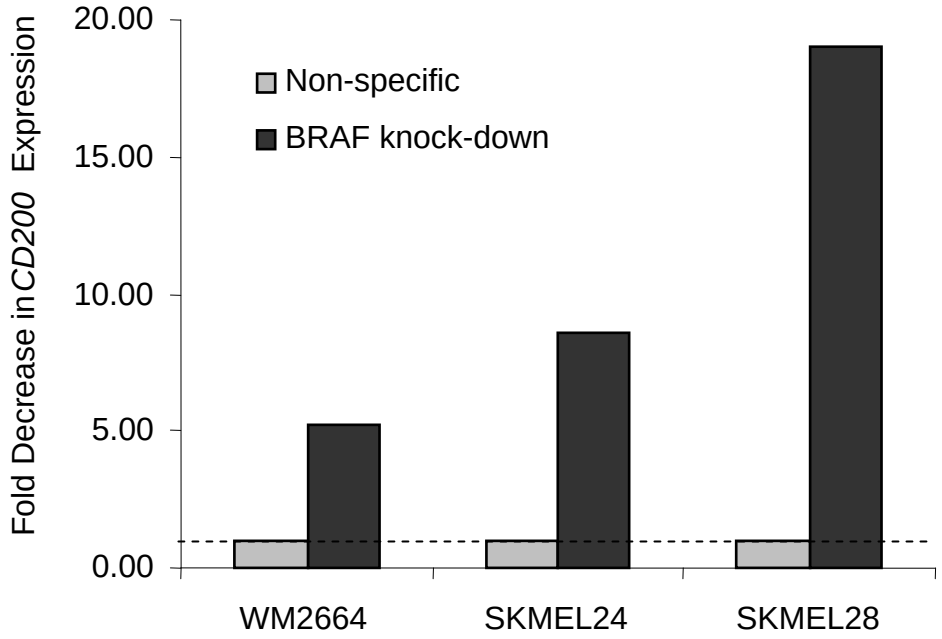
Supp. Figure 3: A. shRNA oligonucleotides targeting human CD200 were cloned into pLenti-lox 3.7 vector. EGFP is driven by the CMV promoter; therefore cells that are transduced with shRNA CD200 are green. **B.** Representative flow histogram of CD200 expression. Before FACS sorting, there is a mixed population of transduced and untransduced melanoma cells. After sorting, the population is homogenous, which is then used in the mixed lymphocytic reactions (MLRs).

Supp. Figure 4: A. IFN-γ production by T lymphocytes during MLRs with the addition of human melanoma cell lines with varying levels of CD200 expression. WM2664, SKMEL24, and SKMEL28 express high levels of CD200; PMWK, MEL505, and

SKMEL187 express low levels of CD200. IFN-γ production, a marker of T cell activation, was determined by ELISA after 72 hours of incubation. **B**. MLRs in the presence of WM2664, SKMEL24 and SKMEL28 transduced with non-specific hairpin (WMNS, SK24NS, SK28NS) and WM2664, SKMEL24 and SKMEL28 transduced with CD200 knockdown (WMKD, SK24KD, SK28KD). Dendritic cells and T cells were mixed with indicated human melanoma cell lines +/- CD200 shRNA knockdown. IFN-γ production was significantly higher in CD200 knockdown melanoma cell lines (WMKD, SK24KD, SK28KD) when compared to the isogenic lines transduced with a non-specific shRNA (WMNS, SK24NS and SK28NS). Error bars +/- standard error of the mean (SEM), results represent three independent experiments.

Supp. Figure 5: A. WM2664 and SKMEL24 (high CD200) show an increase in the formation of T cell rosettes when compared to PMWK and MEL505 (low CD200) in MLRs. A mix of T cells + DC was used as a positive control (first panel). **B.** Quantification of T cell rosettes, WM2664 and SKMEL24 show a significant increase in the formation of T cell rosettes when compared to PMWK and Mel505 (**=$p<0.005$; *=$p<0.05$). Error bars +/- standard error of the mean (SEM).

A



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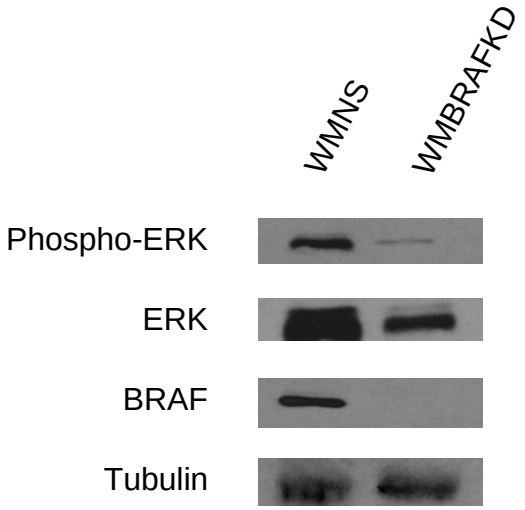
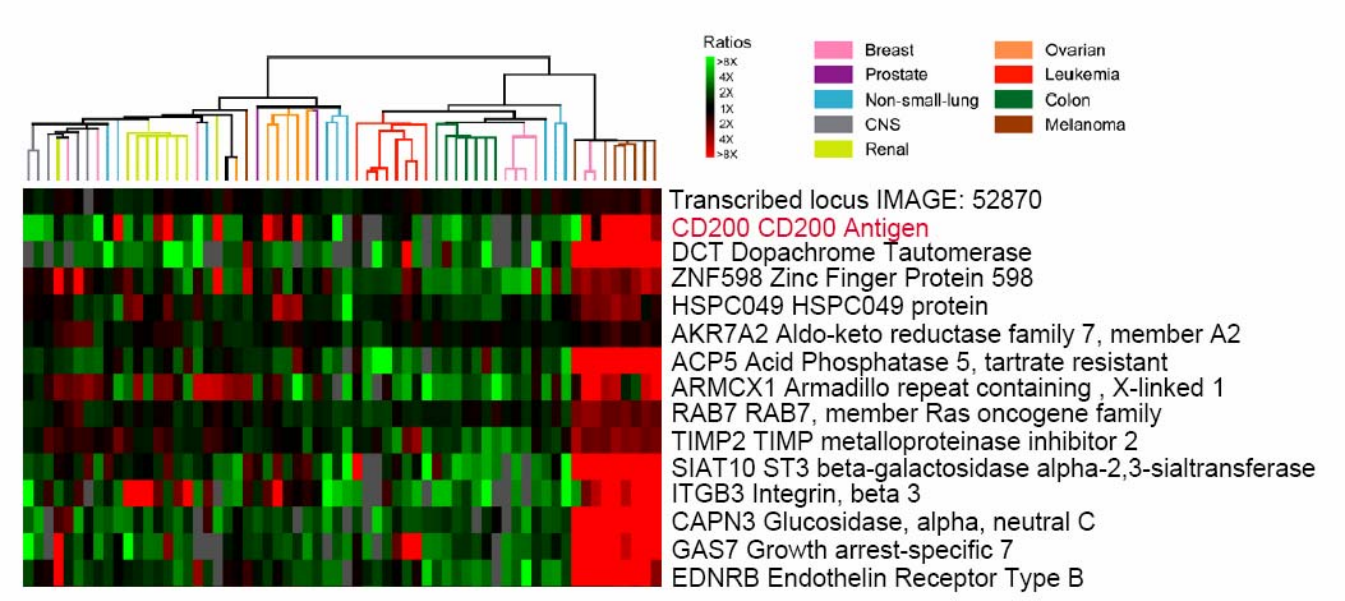


Supplemental Figure 1, Petermann *et al*

A



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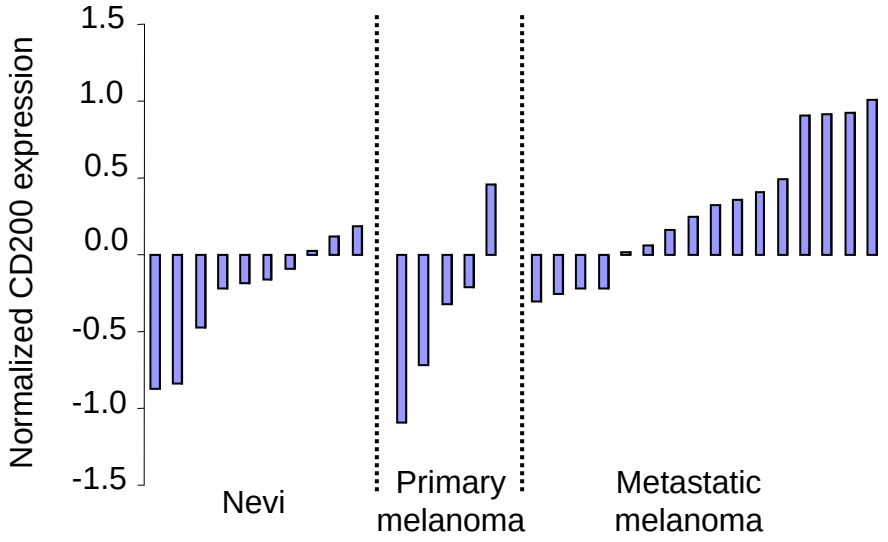
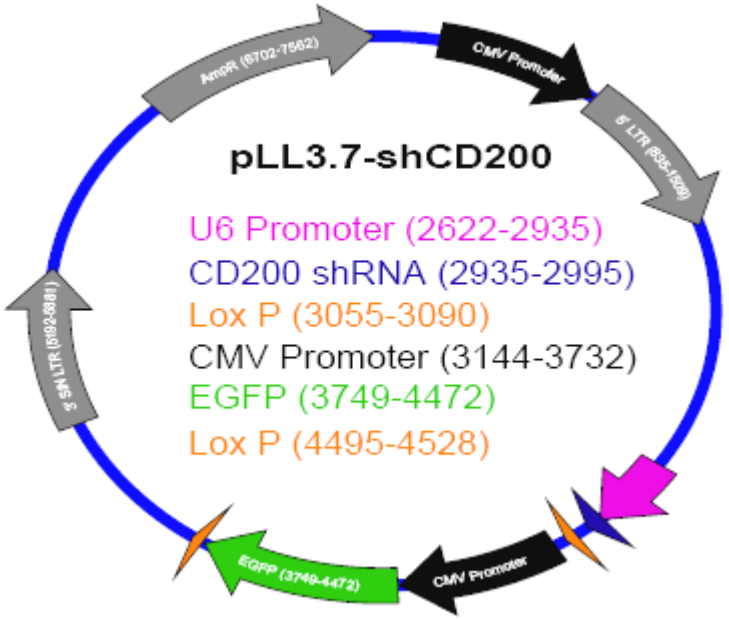


Supplemental Figure 2, Petermann *et al*

A



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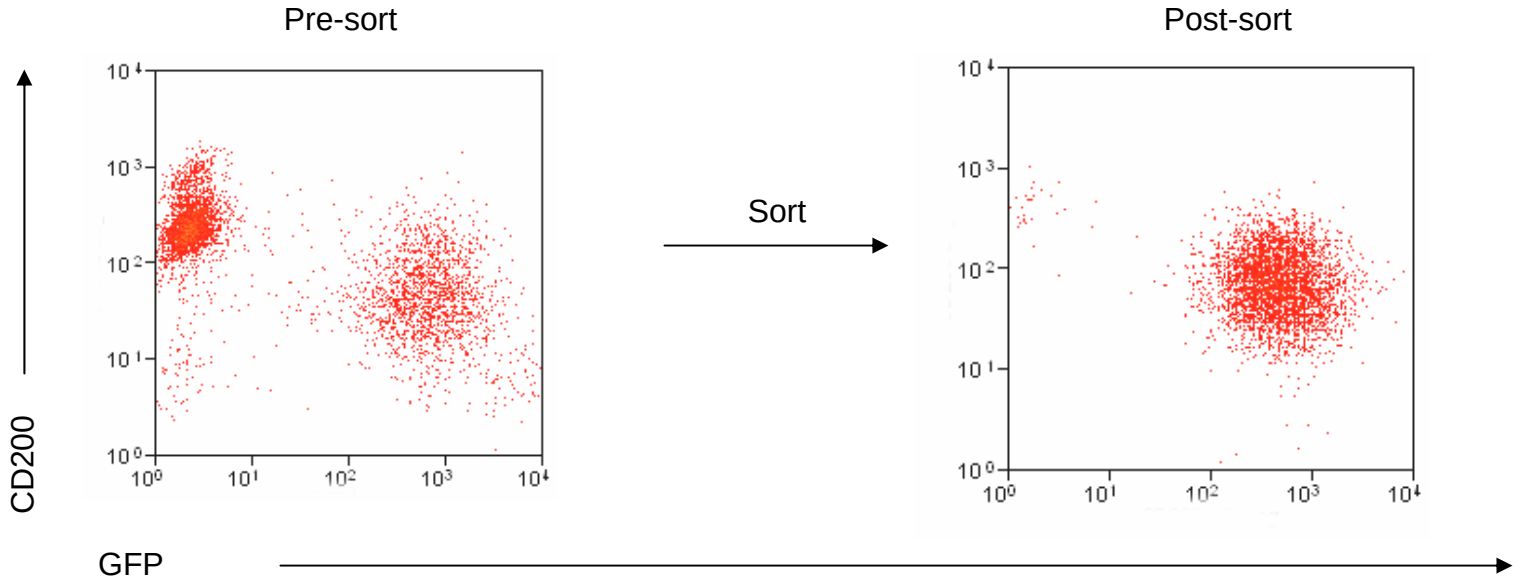
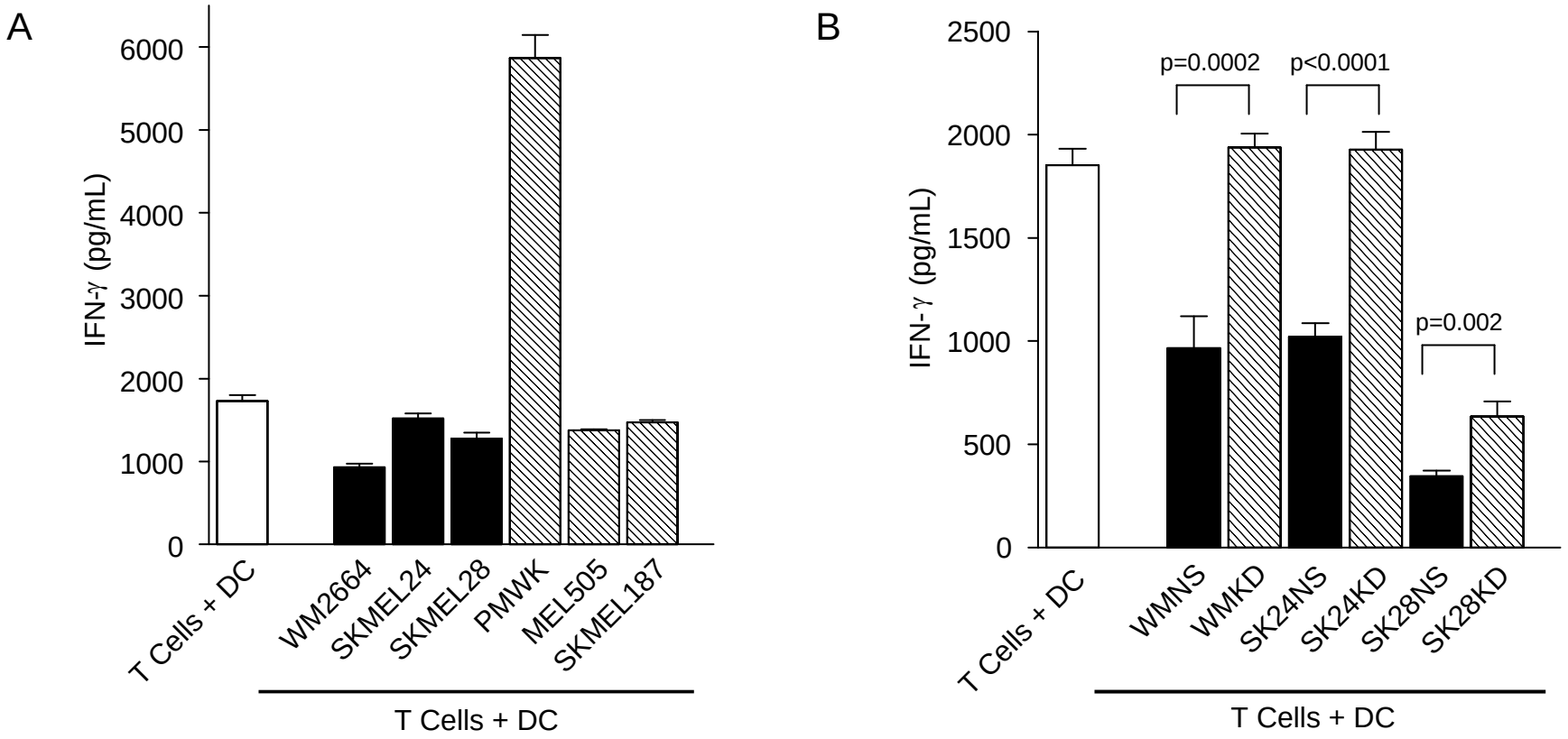
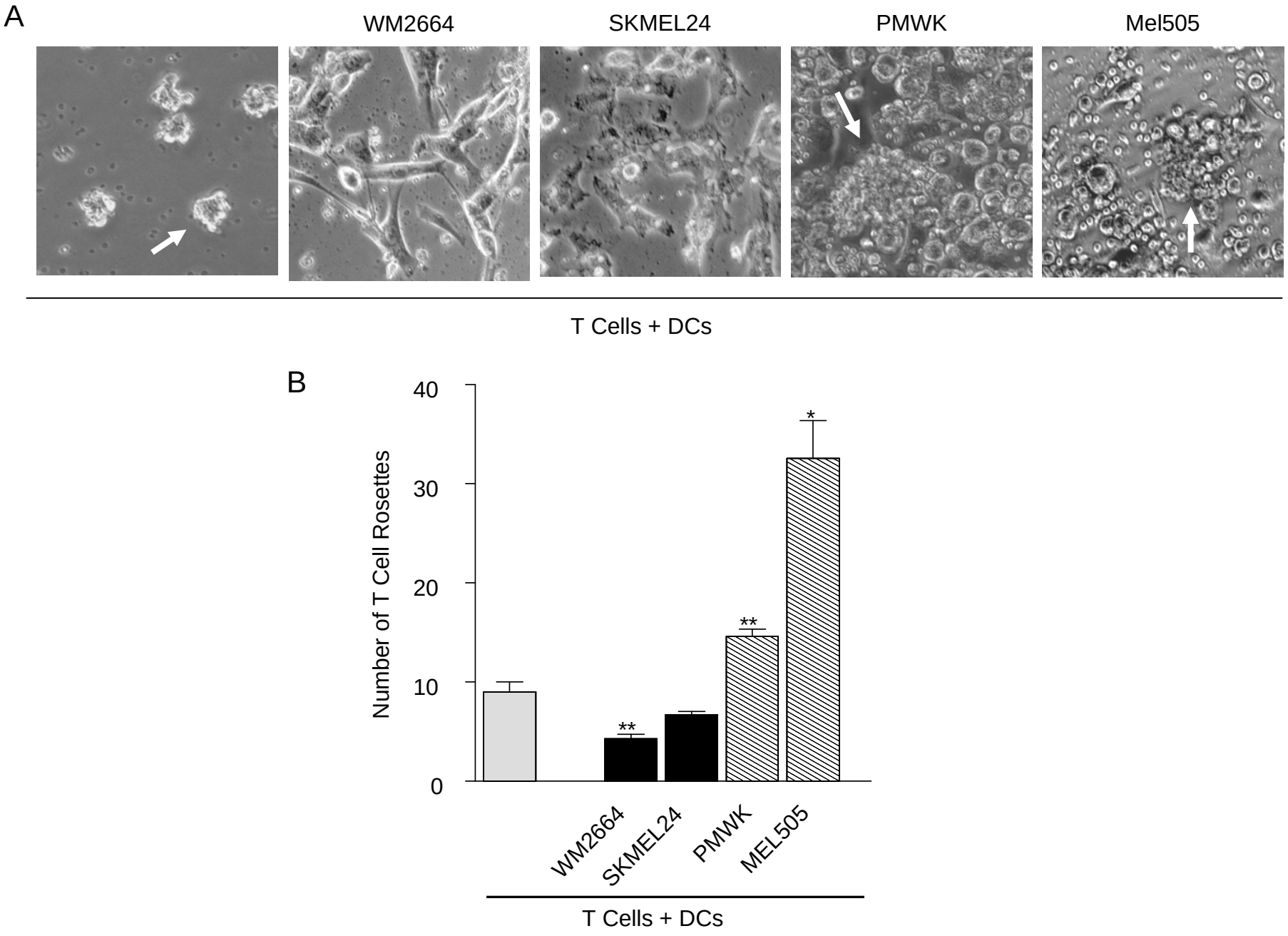


Supplemental Figure 3, Petermann *et al*



Supplemental Figure 4, Petermann *et al*



Supplemental Figure 5, Petermann *et al*