

Figure S1. (A) Western blots of lysates from UMC026 tet-Cas9 and UMC026 CRISPR BAP1-KO cells reveal increase of PROS1 protein following BAP1 KO by densitometric quantitation of multiple blots (n=3). (B) Western blots of lysates from Mel202 tet-shBAP1 uninduced and Mel202 tet-shBAP1 uninduced reveal increase of PROS1 protein following BAP1 knockdown by densitometric quantitation of multiple blots (n=3). Error bars=SEM.

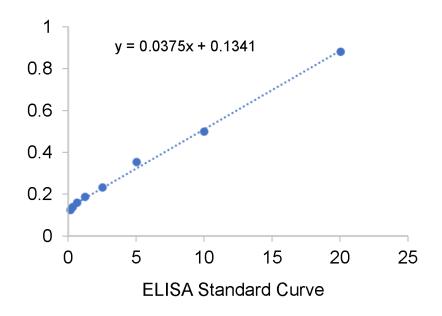


Figure S2. ELISA standard curve documenting linearity of analyte concentration.

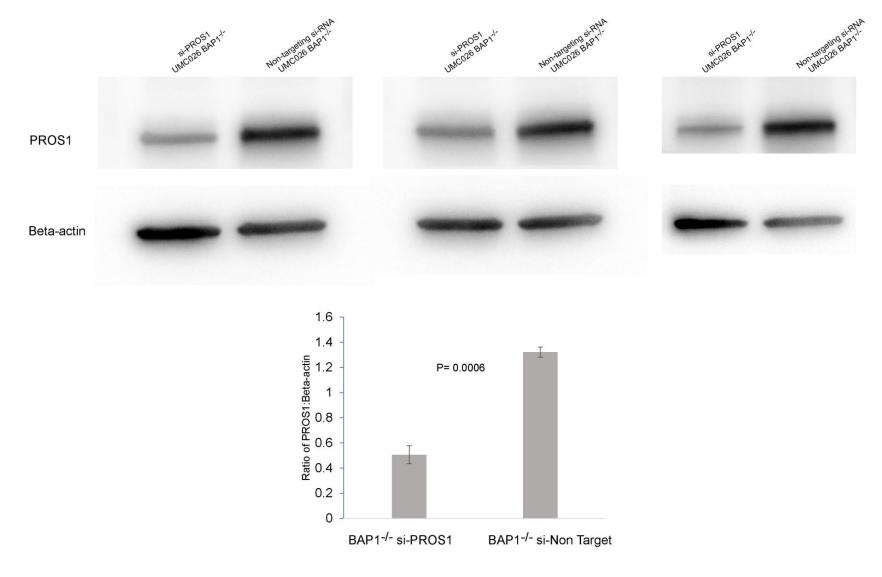


Figure S3. Confirmation of PROS1 knockdown in UMC026 BAP1-negative cells used in RAW 264.7 cell co-culture functional assays. Western blots of lysates from the UMC026 BAP1-KO cells used in co-culture experiments (**Figure 3E, F**) indicate siRNA knockdown of PROS1 in a range of 52-75% by densitometric quantitation of multiple blots (n=3). Error bars=SEM.

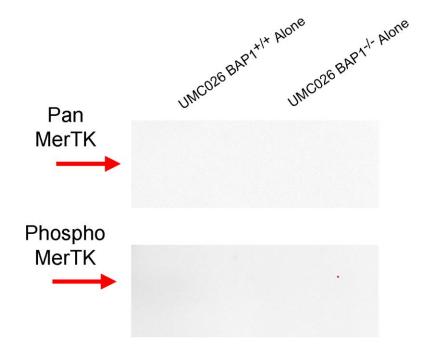


Figure S4. Immunoprecipitated MERTK expression is undetected when the melanocyte cell lines are cultured independently of RAW 264.7 cells.

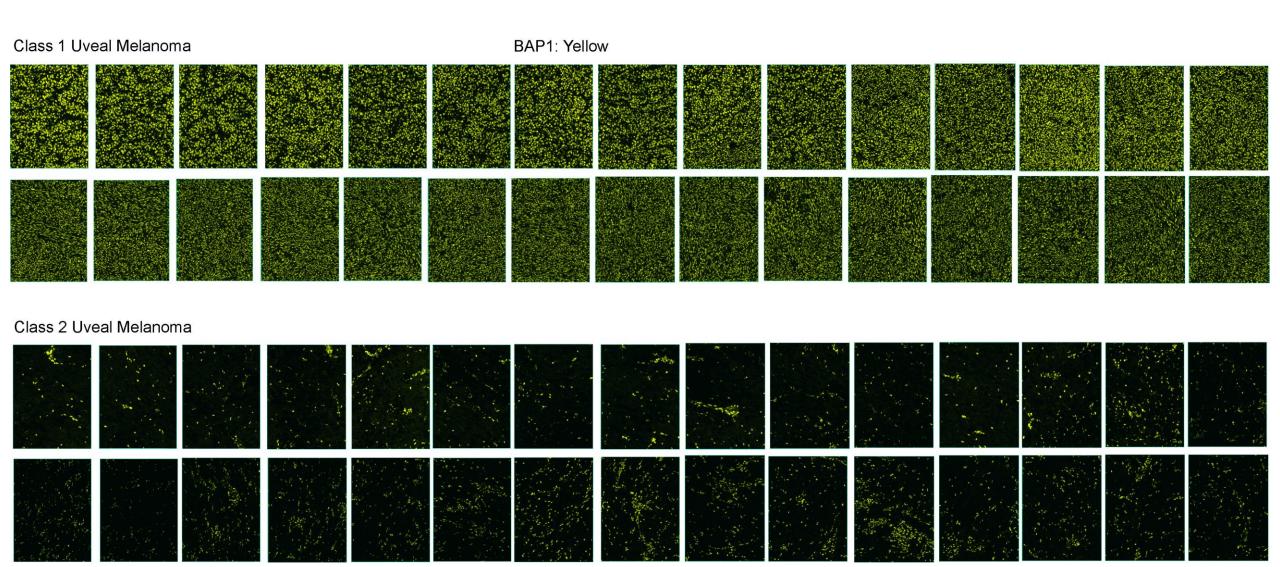


Figure S5. Immunohistochemistry for BAP1 from 60 regions from class 1 (UMM65, UMM79) and class 2 (UMM63, UMM69) uveal melanomas.

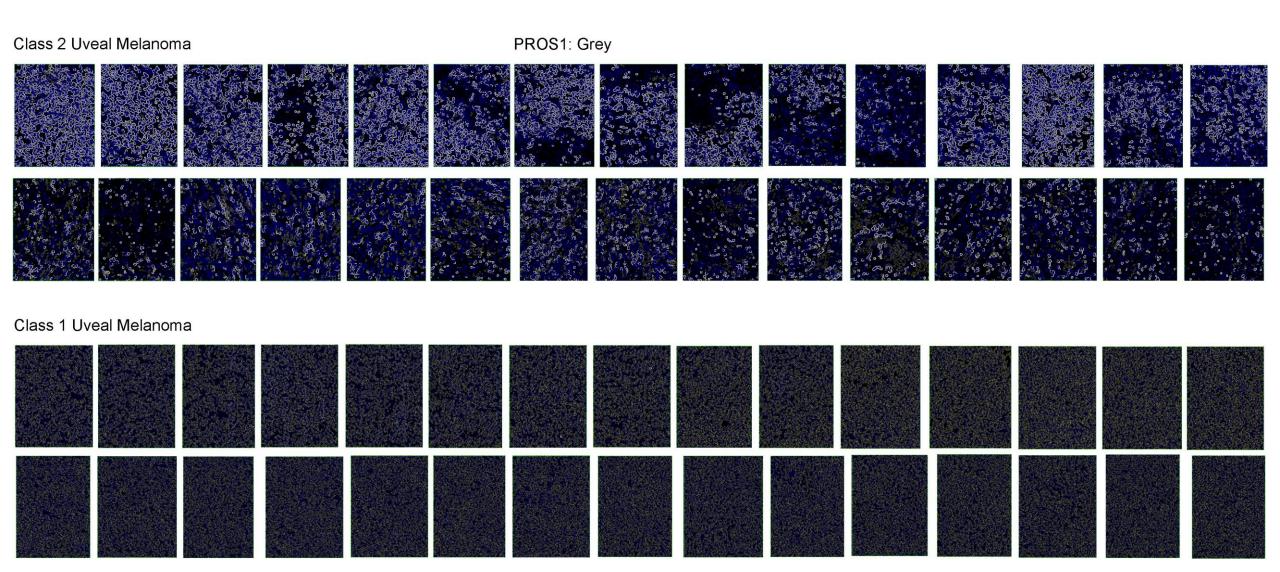


Figure S6. Immunohistochemistry for PROS1 from 60 regions from class 1 (UMM65, UMM79) and class 2 (UMM63, UMM69) uveal melanomas.

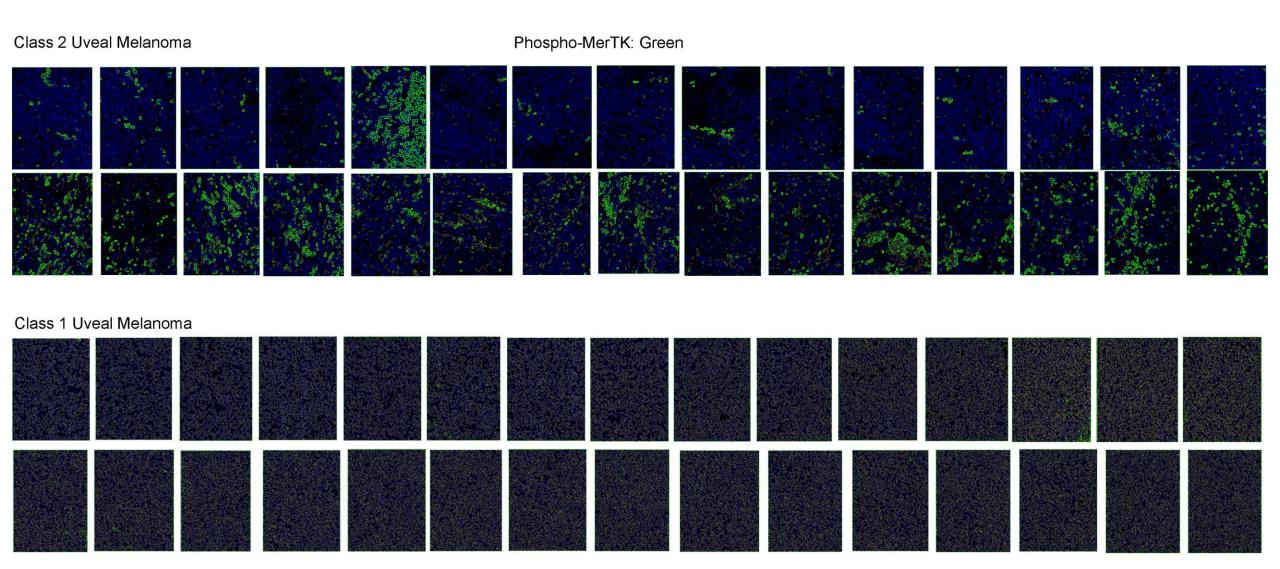


Figure S7. Immunohistochemistry for phospho-MERTK regions from class 1 (UMM65, UMM79) and class 2 (UMM63, UMM69) uveal melanomas.

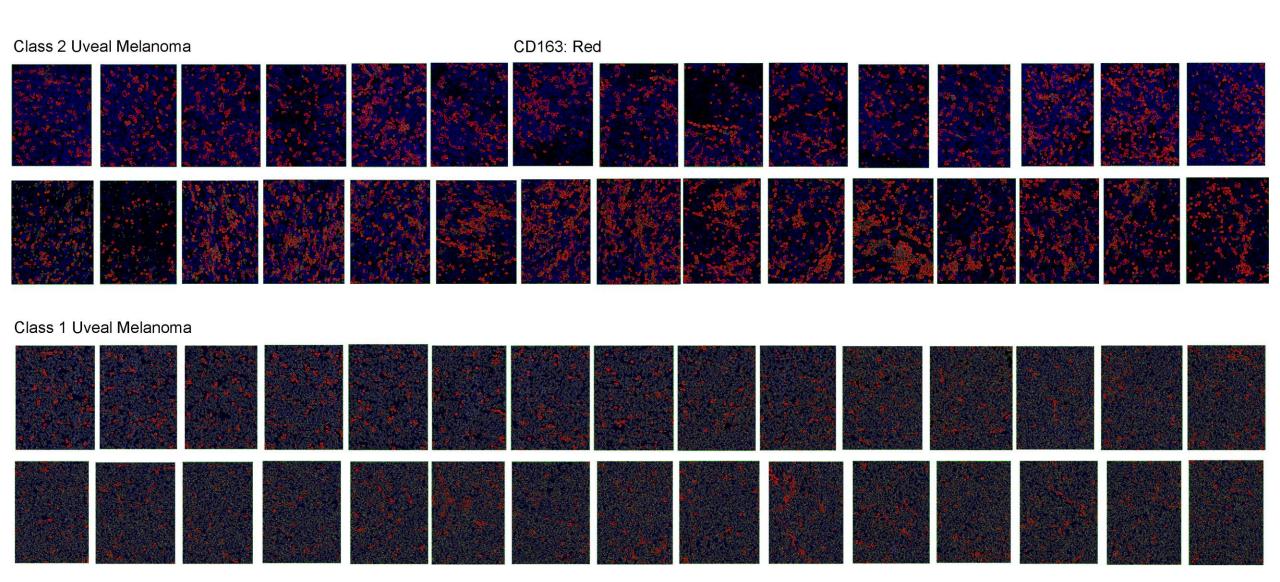


Figure S8. Immunohistochemistry for CD163 from 60 regions from class 1 (UMM65, UMM79) and class 2 (UMM63, UMM69) uveal melanomas.