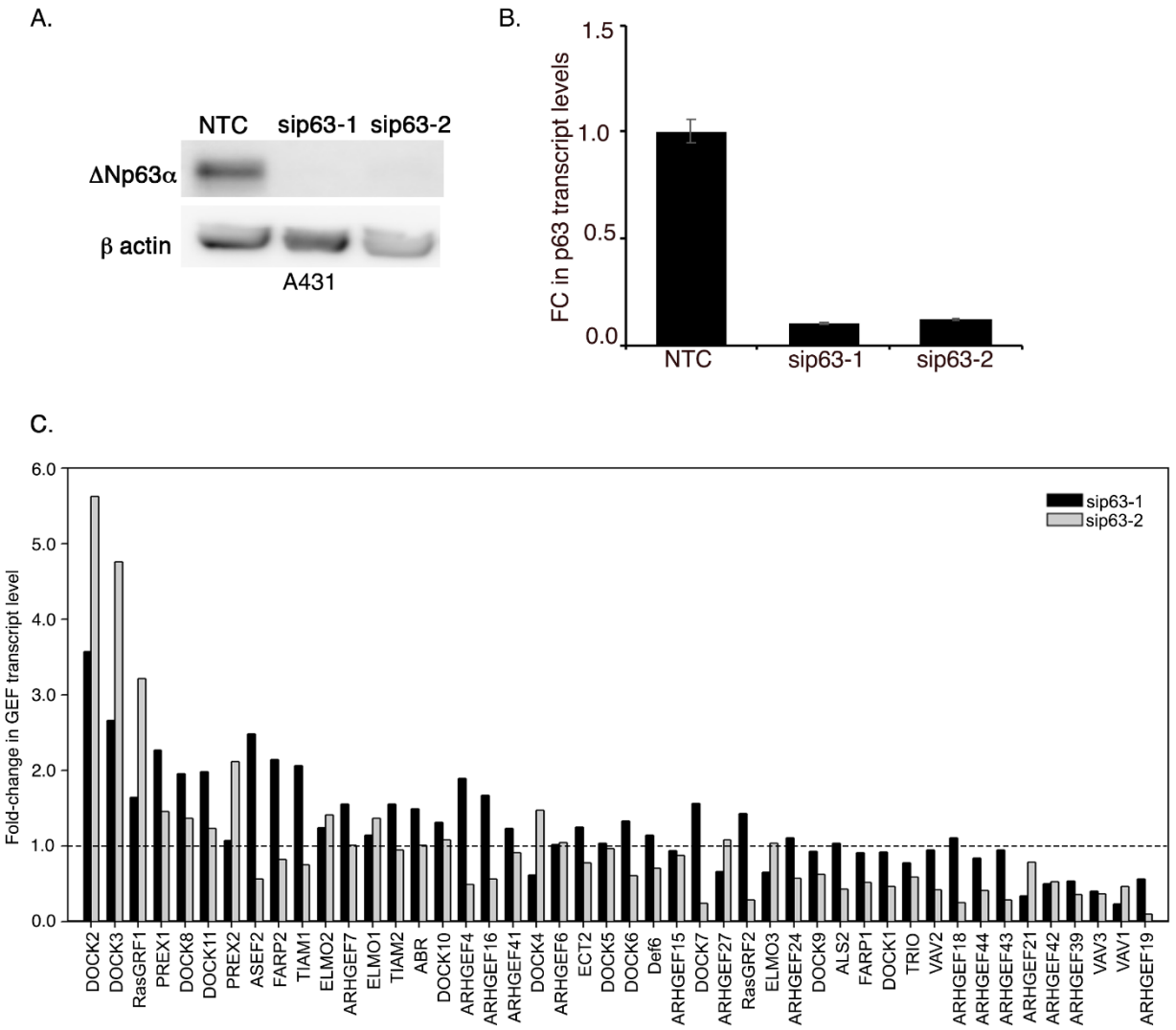
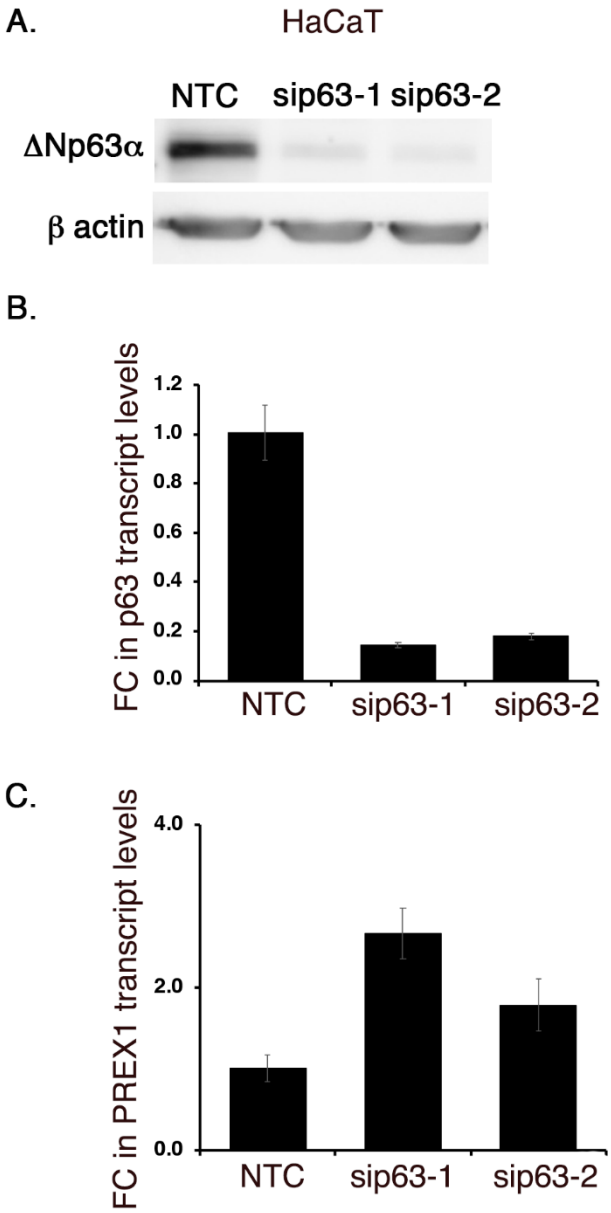
Supplemental Figures

ΔNp63a inhibits Rac1 activation through suppression of *PREX1* leading to inhibition in cancer cell invasion

Amjad A. Aljagthmi[1], Akshay Hira[1], Jin Zhang[1], Mariana Cooke[2], Marcelo G. Kazanietz[2], Madhavi P. Kadakia[1]



Supplemental Figure 1. Effect of ΔNp63α knockdown on expression of 43 Rac-GEFs. A431 cells were transfected with non-targeting control (NTC) or two different p63-targeted siRNAs, sip63-1 or sip63-2. **(A)** Immunoblots of ΔNp63α in A431 samples used in the Rac-GEF array. **(B)** Total RNA was extracted and ΔNp63α transcript levels were measured by TaqMan based qRT-PCR. Data are presented as mean ±1 SD. **(C)** Transcription of Rac-GEFs in A431 cells transfected with NTC, sip63-1 or sip63-2 as determined by GEF Array. Transcripts for 43 Rac-GEFs were quantified by qRT-PCR in 96-well plates and normalized to beta-2-microglobulin and ubiquitin C (UBC). The fold-change in each transcript relative to NTC-transfected cells was calculated for sip63-1 (black bars) or sip63-2 (gray bars).



Supplemental Figure 2. ΔNp63α knockdown upregulates *PREX1* transcript in HaCaT cells. HaCaT cells were transfected with non-targeting control (NTC) or two different p63-targeted siRNAs, sip63-1 or sip63-2. **(A)** Immunoblot of p63 in HaCaT cells transfected. Total RNA was extracted and **(B)** ΔNp63α or **(C)** *PREX1* mRNA was quantified using Taqman qRT-PCR. The fold-change (FC) in ΔNp63α and *PREX1* mRNA was calculated in sip63-1 and sip63-2 transfected cells relative to NTC-transfected cells. Error bars indicate +1 SD.