Figure S1. Microarray data analysis. (A) PCA plot showing six distinct clusters: PM, WM266-4 and HAC15 cells. Notably, correlation coefficient analysis demonstrated differences in expression at the transcriptome level between primary and established melanoma cells (control and after treatment). (B) Two cells types revealed similar expression of key markers of melanoma: CSPG4, FN1, TYRP1, MCAM and SPP1, different from that of the HAC15 cell line. PCA, principal component analysis; PM, primary melanoma; Dim, dimension; CSPG4, chondroitin-sulfate proteoglycan 4; FN1, fibronectin 1; TYRP1, tyrosinase-related protein 1; MCAM, melanoma cell adhesion molecule; SPP1, secreted phosphoprotein 1.