Figure S3. Proliferation, MITF correlation with BRN2, CD200, and MLANA, and MITF genomic copy number. (A) Proliferation rates of selected Motif 1 and Motif 2 cell lines. Invasive Motif 1 cell line NZM40 proliferated significantly faster than invasive NZM09 cells, or weakly invasive NZM06 and NZM42 cells (mean +/- SEM, n = 3, *** p < 0.001, two-way ANOVA). (B) Expression of CD200, a marker of ERK activation, correlated poorly with MITF expression ($r^2 = 0.00002$, p = 0.99). (C) Expression of MLANA, a transcriptional target of MITF, correlated strongly with MITF expression ($r^2 = 0.85$, p < 0.0001). The values reported are normalised log2 ratios from the two colour array data. (D) MITF and BRN2 expression did not show an inverse relationship in NZM cells. Samples sorted from highest to lowest MITF expression as determined by qPCR, with relative quantities expressed as mean-centred log-transformed delta-Cq values. (E) MITF and BRN2 showed a weak positive correlation in NZM cells ($r^2 = 0.2$, p = 0.04). (F) MITF genomic copy number was not significantly different between DNA from normal human peripheral blood and NZM cell lines with a 16-fold difference in MITF transcript abundance. qPCR was normalised to LINE element copy number and is expressed relative to normal DNA.