Unsupervised Hierarchical Clustering of 20 samples (HaCaT n=4, patient skin derived keratinocytes n=5, A431 n=3, SiHa n=4 and CaSki n=4) analyzed for gene expression. The genes with low variance across the arrays were filtered out imposing that the variance of the log-ratios for each gene compared to the median of all the variances yielded $p<0.01$. After filtering, 4914 genes were included in the unsupervised hierarchical analysis using centered correlation metric and average linkage.

Supplementary Figure 1