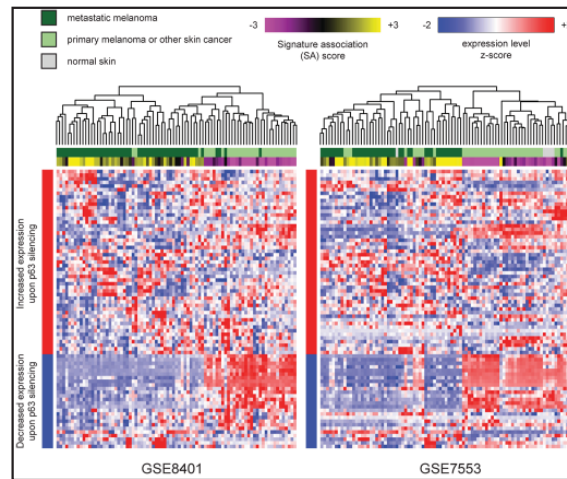


openSESAME



openSESAME (Search of Expression Signatures Across Many Experiments) identifies that loss of p63 is associated with metastatic melanoma.

Over 2000 GEO series (corresponding to Affymetrix HG-U133-generation microarrays) were retrieved and processed, and expression measurements for each gene were z-score normalized within each series to produce relative expression levels (red and blue indicate high or low expression relative to the mean, respectively). A previously reported signature of genes whose expression was up- or down-regulated upon silencing of p63 expression in several squamous cell lines was obtained (Barbieri et al., *Cancer Res* 2006 66(15):7589-97), and for each sample in each series, a Wilcoxon test was performed between the relative expression values of the “up” and “down” gene sets. This yielded a signature association (SA) score that varies from negative (purple) to positive (yellow). Fisher’s exact test was used to determine that the distribution of SA scores in two independent experiments, GEO series GSE8401 and GSE7553, is significantly different from the distribution of SA scores across all samples in all series retrieved from GEO ($p = 5.66E-19$ and $3.77E-08$ for GSE7553 and GSE8401, respectively). In both experiments, openSESAME identified that primary (light green) and metastatic (dark green) melanomas were negatively and positively associated with the p63-silencing signature, respectively, which mirrors the loss of p63 expression that is frequently observed in metastatic melanomas.