

Supplemental Figure 2 (see separate attachment “CHEN Supplemental Figure 2”)

Legend for Supplemental Figure 2:

Supplemental Figure 2. Hierarchical clustering of the gene expression data using the top 131 probe sets differentially expressed in OSCC when compared to normal controls. The dendrogram at the top lists all of the samples tested and measures their degree of relatedness in gene expression. Each column represents the expression levels for all the probe sets in a particular sample, whereas each row represents the relative expression of a particular probe set across all samples. The expression level of any probe set in any given sample (relative to the mean expression level of that probe set across all samples) is reported along a color scale in which red represents transcription up-regulation, green represents down-regulation, and the color intensity indicates the magnitude of deviation from the mean. The color bar underneath the heat map color codes the tissue type of each sample in the heat map as normal control (aqua), OSCC (red), or dysplasia (yellow). These colors are also used in the dendrogram at the top of the heat map.