



Supplemental Figure 1: Schematic representation of the method for selecting the differentially expressed genes specific to oral cancer. A) To obtain the list of differentially expressed genes only between cancer and control that were not also differentially expressed in dysplastic lesions, the dysplastic lesions and controls were grouped together and the gene expression was compared to that of the invasive tumors. Using this list of genes, we then excluded those that were differentially expressed between control and dysplasia (i.e. Δ and \blacksquare) using NFD=1 criterion. The remaining genes were those whose expression levels remained the same between control and dysplasia (i.e. \bullet), but were up- or down-regulated in cancer. B) Conversely, we sought to determine those genes whose differential expression between cancer and controls appears to occur early in the process of carcinogenesis. For this analysis, we grouped the dysplastic lesions with the cancer samples and the gene expression was compared to that of the controls. Using this list of genes, we then excluded those that were differentially expressed between dysplasia and cancer (i.e. Δ and \blacksquare) using NFD=1 criterion. The remaining genes were those whose expression levels remained the same between dysplasia and cancer (i.e. \bullet), but were up- or down-regulated compared to controls.