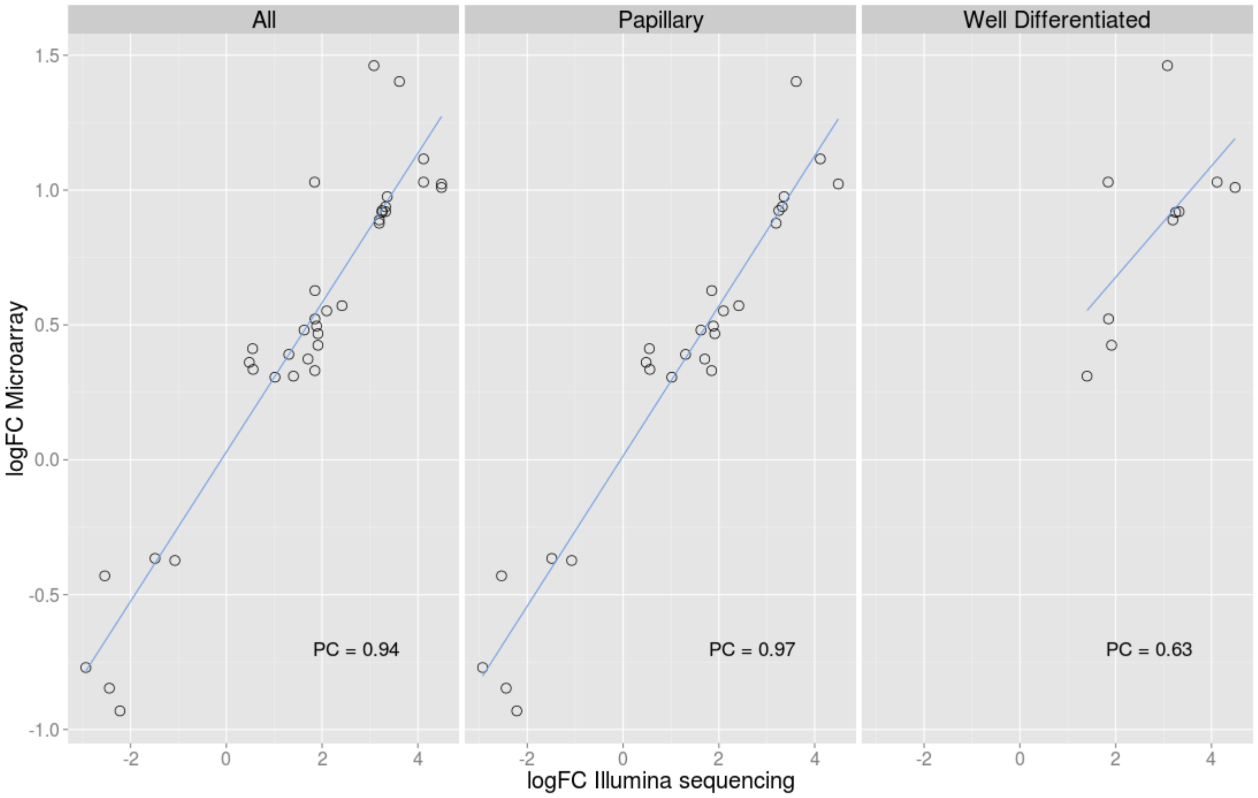

Supplementary Figure 1: Regression analysis comparing fold change (FC) values from miRNAs identified as significantly dysregulated in microarray analysis to FC values from RNA-Seq analysis of the same tissue. When all samples where compared to their matched D-NT tissue FC values were strongly correlated (Pearson's correlation of 0.94; PC on graph). Similarly, when analyses were broken into comparisons between samples of the same histological grade, strong correlation was observed in the FC values obtained using both methods.