

Supplementary Figure 4. Graphics show the methylation levels of CDH1 in Normal, PIA and PC tissues. A. Greyscale heatmap showing a minimum (0 - white) and maximum (100 – black) methylation levels per sample. B. Boxplot representation of the methylation level in Normal, PIA and PC tissues (t-test: ****P < 0.001). Methylation levels are represented by the average of 5 CpGs evaluated in the promoter region of the CDH1 gene. Heatmaps were constructed using Morpheus (https://software.broadinstitute.org/morpheus).