

Supporting Information Fig. S10. (A) Analysis of the differential expression profiles of LNCaP cells transfected either using non-targeting mimic analog or using miR-204 targeting mimic analog. The spectral counts were used to calculate the differential expression ratio between the two conditions with p-value of probability. The DEGUST server was used to obtain an impression on the log-fold change (logFC) of differential expression between two conditions using a derivative of the MA-Plot FC (Robinson & Oshlack, 2010), FDR cut-off 1, abs log FC 0. (B) Same DEGUST analyzed differential expression data (fold change) are represented using clustering represented as color heatmap. Log fold change of -2 is represented as dark blue, while Log fold change of 2 is represented as red. Values in-between are represented as shades of blue or red, as values closing to 0 are represented as white. (C) Venn Diagrams of enriched PANTHER pathways shared between iPathway and EGAN detected. Venn Diagram of shared genes (proteins) between differentially expressed (iPathway), Genes regulated by Androgen (MSigDB, EGAN) miR-204 targeted (MSigDB, EGAN), DNA Methylation (GO, EGAN), 5-AzaC upregulated in PCa (MSigDB, EGAN).

