

Supporting Information Fig. S8. (A) Box-plot of normalized peptide spectral counts from LTQ Orbitrap data. Samples – VCaP cells transfected with miR-204 mimic or non-targeting control. (B) MA-Plot FC of Quantile normalized peptide spectral counts. MA-Plot FC (fold change): The data are represented as point with coordinates $\{Mg', Ag\}$, where g is the specific gene id, and Mg' represents actually $\log FC$. The $\log FC$ is the log of the ratio of the predicted expression levels in both biological groups, whereas Ag indicates the average expression level. Thus the data are plotted normalized to the control group average expression (i.e. over $Ag = 0$, x-axis) vs $\log FC$ ($\log FC$, y-axis), colored by FDR significance cutoff ($FDR < 0.05$ in red, others in blue). $M = \log_2 (D1/D2)$, $A = 0.5 * \log_2 (D1 * D2)$. Colors: green (data), LOESS line (red).

