Supplementary figure 2. Correlation between the expression of OGT and candidate transcription factors in localized prostate cancer. Correlation analysis was performed with a web-based tool (http://www.betastasis.com/) that makes use of a published prostate cancer expression array data.

A) Correlation plot of the expression of OGT and c-Myc. (B) Co-expression has previously been used to successfully identify regulatory interplays between transcription factors and other genes, such as ERG and PLA1A in prostate cancer (Pearson correlation: 0.516) (Tomlins, S. A. et al. Role of the TMPRSS2-ERG gene fusion in prostate cancer. Neoplasia 10, 177-188 (2008)).

C) In order to understand the gene signature affected by OGT inhibitor, we took the 20 most down-regulated genes common to both time points after treatment with OGT inhibitor and used an analysis based on first neighbour associations with other factors as reported in the REACTOME database (http://www.reactome.org) accessible through Cytoscape (cytoscape.org). The 20 most downregulated genes are tightly associated with cell cycle regulation and c-Myc is the sole transcription factor linked to this process through its role as a regulator of CDC25A.