



Figure S1: Co-expression of down-regulated and validated genes.

Schematic representation of up-regulated and validated genes: a. *AR*, b. *CLU*, c. *DAB2*, d. *FOXL2*, e. *IGFR1*, f. *LYN*, g. *PGR* and h. *VIM*. Edges are colour-coded to highlight the range of Pearson's correlation coefficient in co-expression network: black (>0.7), grey (0.65-0.7), dark blue (0.60 - 0.65), blue (0.55-0.60), dark green (0.50-0.55), green (0.45-0.05), yellow (0.40-0.45), red (0.35-0.40) and brown (0.30-0.35). Co-expressed neighbours and their associated co-expression Pearson's correlation values are available from Additional File 1