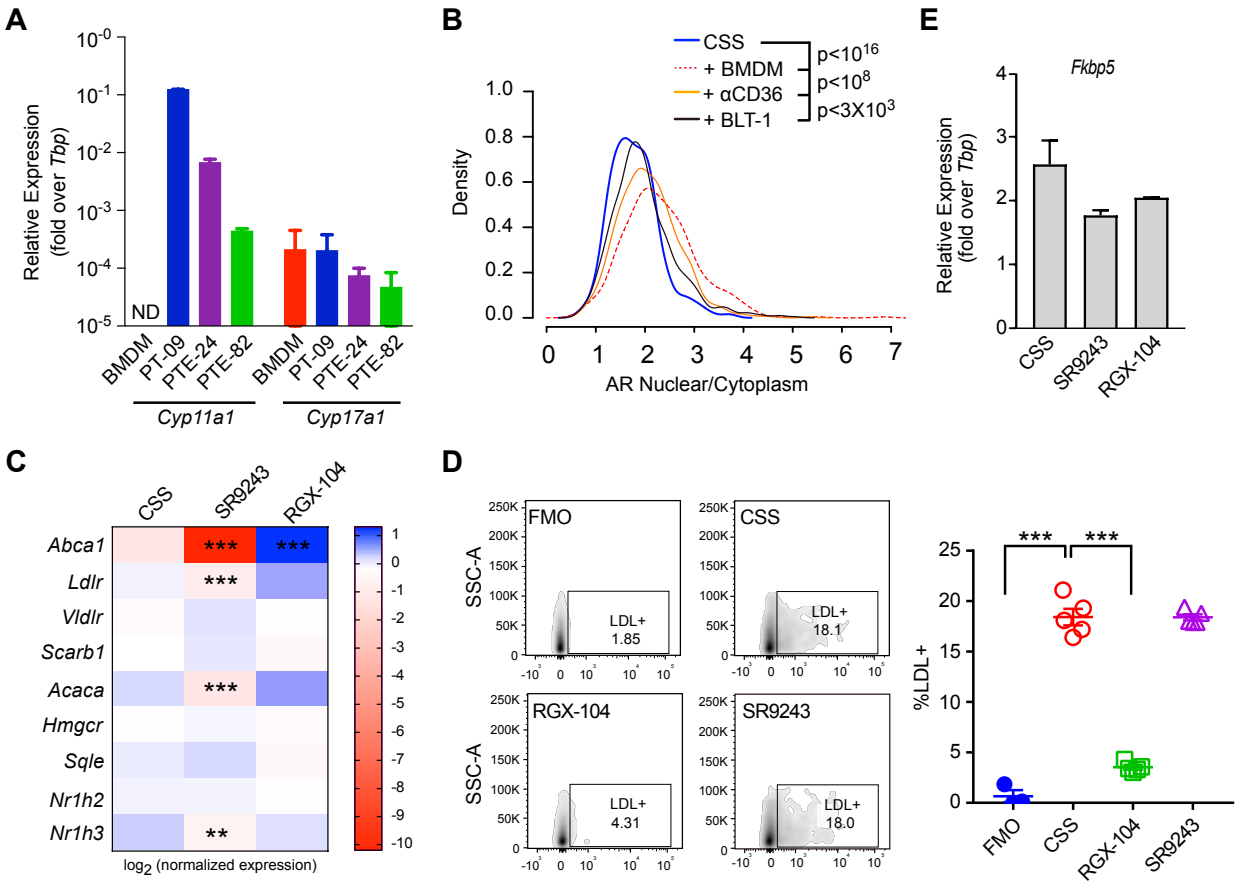
Figure S5


A
Relative Expression (fold over Tbp)
ND
BMDM
PT-09
PTE-24
PTE-82
Cyp11a1
Cyp17a1
B
CSS
+ BMDM
+ αCD36
+ BLT-1
p<10^16
p<10^8
p<3X10^3
Density
AR Nuclear/Cytoplasm
E
Fkbp5
Relative Expression (fold over Tbp)
CSS
SR9243
RGX-104
C
CSS
SR9243
RGX-104
Abca1
Ldlr
Vldlr
Scarb1
Acaca
Hmgcr
Sqle
Nr1h2
Nr1h3
log2 (normalized expression)
D
FMO
CSS
RGX-104
SR9243
SSC-A
LDL+ 1.85
LDL+ 18.1
LDL+ 4.31
LDL+ 18.0
%LDL+

Supplemental Figure 5, Related to Figure 5. A) Expression of *Cyp11a1* and *Cyp17a1* in prostate cancer cell lines and BMDMs, as determined by real time PCR. n=3-5, data shown as the mean ± SEM from one experiment. B) Nuclear to cytoplasmic AR ratio of GFP^+ PTE-82 cells cultured in CSS or co-cultured with BMDMs. 1 μM BLT-1 (SCARB1 inhibitor) and 5 μg/ml αCD36 were added to co-cultures as indicated. 6-8 randomly selected images from two wells of the chamber slide were pooled for analysis. Data reflects one of two independent experiments. Significance determined by Mann-Whitney. C) PTE-82 cells were treated with the LXR modulators RGX-104 (5 μM) and SR9243 (5 μM) for 48 hrs and effects on gene expression related to cholesterol influx/efflux (*Abca1*, *Ldlr, Vldlr, Scarb1*), cholesterol *de novo* synthesis (*Acaca, Hmgcr, Sqle*), and the LXR family (*Nr1h2, Nr1H3*) were determined by real time PCR. Expression was normalized across groups and is shown as a heat map. Data represents the mean of 3 technical replicates, with significance determined by two-way ANOVA. One of two representative experiments is shown. D) PTE-82 cells were treated with 5 μM RGX-104 and 5 μM SR9243 for 48 h and uptake of pHrodo Red labeled LDL (1 μg/ml) was measured by flow cytometry after a 3 hr incubation. Data shown as the mean ± SEM of 3-5 technical replicates, with significance determined by one-way ANOVA. One of three representative experiments is shown. E) PTE-82 cells were treated with 5 μM RGX-104 and 5 μM SR9243 for 48 hrs and expression of the androgen responsive gene, Fkbp5 was determined by real time PCR. n=3, data shown as the mean ± SEM with one of two representative experiments shown.