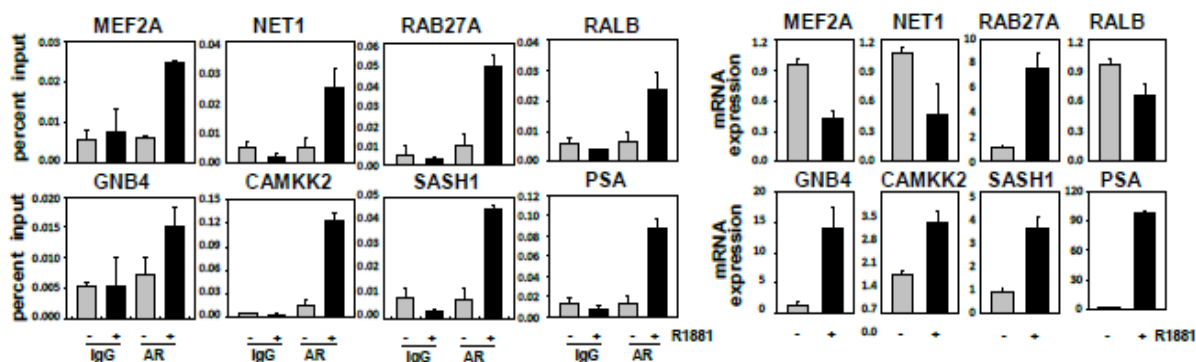
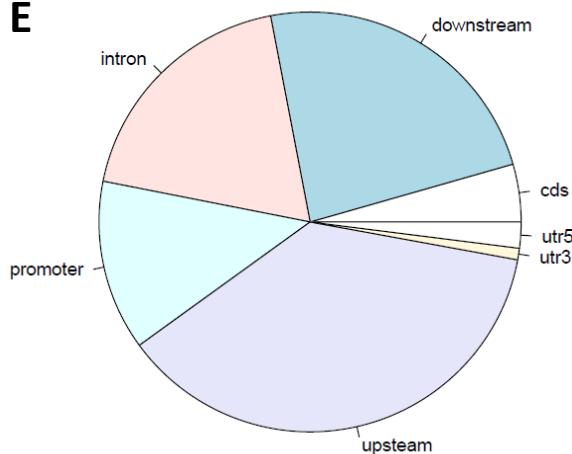


**A****C**

chromosome	# genes	# up	# down
1	36	21	15
2	37	19	18
3	33	16	17
4	17	11	6
5	32	20	12
6	30	17	13
7	28	17	11
8	24	11	13
9	13	6	7
10	14	7	7
11	22	10	12
12	32	18	14
13	9	5	4
14	14	8	6
15	16	12	4
16	9	4	5
17	26	10	16
18	10	6	4
19	17	6	11
20	7	1	6
21	10	9	1
22	7	4	3
X	9	3	6
total # genes	452	241	211

**B**

GENE	Log 2 fold change
PSA	2.32
TMPRSS2	2.76
FN1	-2.98
SERPINB5	-1.72
RALB	-1.05
MPRIIP	-1.26
GNL1	-1.24
GNB4	2.04
GUCY1A3	1.00
ARHGAP11A	-1.56
WASF3	-1.13
RAB27A	2.20

**D****E****F**

TF	z-score	p value
GR	-10.6382	9.895E-27
AR	-9.8945	2.1982E-23
FOXA2	-9.1851	2.0555E-20
DMRTA1	-7.6599	9.3018E-15
GR	-7.6108	1.3624E-14
FOXA1	-7.3416	1.0554E-13
PR	-7.3107	1.3289E-13
ZNF131	-7.0675	7.8866E-13
GTF2A1	-7.0588	8.396E-13
STAT1	-7.0374	9.7898E-13

Figure 1 - Supplementary Figure 1

### **Supplementary Figure 1 Isolation and validation of a 452 AR target gene signature**

(A) 1,590 of 12,629 genome-wide ARBS sites in LNCaP cells are present within 300Kb of the TSSs of 900 androgen-responsive genes. Of these 900 genes, 452 had at least a 2-fold change in expression upon exposure of LNCaP cells to 5nM of the synthetic androgen R1881 for 48 hours, as determined using a custom Agilent gene expression oligoarray. (B) Representative sample of 452 AR target genes. Log fold change indicates the level of androgen regulation. Fold change represent mean value obtained from biological triplicates. Green, androgen-induced gene; red, androgen-repressed gene. (C) Overview of chromosomal distribution of 452 AR target genes. Green, number of androgen-induced genes; red, number of androgen-repressed genes. (D) ChIP validation of androgen-dependent recruitment of AR to the predicted AREs within AR target genes (left panel). Real-time RT-PCR validation of androgen dependent changes in corresponding gene expression (right panel). Results reflect the effect of 16-hour treatment with 5nM R1881. (E) Genomic location of ARBSs within the 452 AR target genes. (F) Cistrome identification of 10 most significantly enriched TF binding sites in ARBSs of the 452 AR target genes, with corresponding z-scores and p values. The 2 GR entries reflect different consensus binding motifs.