Supplemental Figures
A.

B.


Figure S1. Accompanies Figure 1 and 2. A, PCa cells lines do not respond to 25D. RT-qPCR for CYP24A1 following 16 hours of $50 \mathrm{nM} / \mathrm{L}$ 25D treatment in serum free conditions. B, PC3 and MDA-PCa-2B (MDA) cell lines do not express LRP2. Expression shown as mean relative quantitation to HPRT1. Error bars are SEM. *p<0.01


Figure S2. Accompanies Figure 2. No differences in bitransgenic mouse prostate histology, weights and fertility. A, representative H\&E of prostates from 16-week old TAM-treated $\operatorname{lrp} 2^{f f f}$ and lrp2 ${ }^{f / f} \mathrm{Cr}^{+/+}$mice from each lobe; ventral prostate (VP), dorsal prostate (DP), lateral prostate (LP) and anterior prostate (AP). B, prostate weights of 3 month old male mice from $\operatorname{Irp} 2^{f f f}$ and $\mathrm{Irp}^{2 f f} \mathrm{cre}^{+/+}$mice. C, number of pups per litter. Note that at prior to the 5 week litter, 2 of the bitransgenic mice cages passed away from a flooded cage, so no error bars at this time point. D, time between litters.
A.

5'CCTGTATCCTATCAGGGGAAACCAAGATATCCGAAGGAGCCTAGAGAGATCAGGCCAGGAATGAAGGT VDR1
CACAGATCTCCATCCAGCAGGCTCTTTACTCCTTCCCTTCCCTACCCCCGCCTCTTTCCCTTTCTTTCTCT TTCCTTCATTTTTACTTGTCTGGTTGTGCTTTCCTTTTCCATTTCTTATTTTTTCTTTCTCTTCTCTATTCTTG ACTTTCCTCCTCGTCCATTTCTTTCCATTGCTCATTTAGTAAAACTGCGTCCGTGCAGATTTCCCCGTGAG CCGCCTCGCCGGCTTCACTTAGGAGTGCATGCGCCTGTATGAGTGCGTGTGTCTGTGCGGGGCAAACCC TGCGGAGAGGCGAGGGCAGCGCGTGTGCACGTGTGAGTGTGCCTGTGAGAGTGTGCGCACAGGAGTGT GCTCTTGTATGCACGCGTAAAGGGGACTGTGTATGTCGGCGTTGAAGTGTGACTGTGGAATGTGCGCGC GTGTGTGACTGGCGTGTATGAGTGAATCTGTGTCAGTTGGTGTGAGAGTGTGCACACGCCTGTGTGAGT GTCCCTGTGTGAGCACGCGTGTGTTCGAGTGCCCACTCCTCCCCGCGCTGCAAAGTGCAGGGGGCGGG VDR4
CCGGGCGGCAGGGGGCCTGCCCGCTGGATTCCCGCATGCTTGTTCCGGGGCGGTCGGGTCTAAAGGG VDR2
CTTTATGCACTGTCTGGAGGGTGGGGACTGGCGCGGGTAGAAAACGGGATGCCTCGGGCGTGGGGGCA GGCTTTTGGCCACTAGGAGCTGGCGGAGGTGCAGACCTAAAGGAGCGTTCGCTAGCAGAGGCGCTGCC GGTGCGGTGTGCTACGCGCGCCCACCTCCCGGGGAAGGAACGGCGAGGCCGGGGACCGTCGCGGAG VDR3 ATGGATCGCGGGCCGGCAGCAGTGGCGTGCACGCTGCTCCTGGCTCTCGTCGCCTGCCTAGCGCCGGC

CAGTGGCCAAGGTAAGAGCCCAGCCAGAG-3'

## B.

| Motif ID | P-Value | Matched Sequence |
| :--- | :--- | :--- |
| RXRA::VDR 1 | 0.000307 | AGGTCACAGATCTCC |
| RXRA::VDR 2 | 0.002520 | GGGCGGTCGGGTCTA |
| RXRA::VDR 3 | 0.006550 | CGGTCCCCGGCCTCG |
| RXRA::VDR 4 | 0.006940 | GCGCTGCAAAGTGCA |

Figure S3. Relates to Figure 3. Vitamin D receptor and androgen receptor response elements in LRP2 promoter. A, -791 bp of LRP2 promoter showing mapped areas for VDR response elements. B, JASPAR prediction of the binding sites with P -value. Note that VDR binds VDREs as an obligate heterodimer with RXRa.


Figure S4. Relates to Figure 3. Prostate slices express hormone response components and respond to 25D and T. A, mean Ct of hormone response genes in TS1. B, Expression of CYP24A1, a vitamin D response gene, in slices treated for 24 h with $50 \mathrm{nM} / \mathrm{L} 25 \mathrm{D}$ with and without DBP. C, Expression of $K L K 3$, an androgen response gene, in slices treated for 24 h with $50 \mathrm{nM} / \mathrm{L}$ T with and without SHBG. Data shown as mean and SEM of biological replicates from 3 patients. D, areas of cancer on the prostate explants had very low expression of megalin, which is consistent with Figure 5 quantitation in patient samples.
A. B.


Figure S5. Relates to Figure 4. Androgen levels by Gleason and Age. A, Serum levels of T in all patients shown by Gleason sum. Benign transurethral resection of prostate (TURP) shown as control. B, Plot of serum T to age shows no significant correlation. C, Prostate DHT levels in all patients shown by Gleason sum. DHT was measured in benign areas of prostates and the Gleason score is from the tumor within the same prostate. TURP shown as control. D, Plot of prostate DHT to age shows no significant correlation.
A.

DFKZ Cancer Cell 2018 age
TCGA age


B.

TCGA
DFKZ, CancerCell 2018



Figure S6. Relates to Figure 6. Expression of $L R P 2$ by age and BCR in DFKZ and TCGA cohorts. A, $L R P 2$ expression does not correlate with age. $\mathbf{B}$, mixed results for $\angle R P 2$ expression and BCR in TCGA and DFKZ cohorts. Analyses on Cbioportal.

Table S1. Cell and tissue characteristics

| MODEL | TISSUE | MORPHOLOGY | DISEASE | ETHINICITY |
| :---: | :--- | :---: | :---: | :---: |
| PrE-AA1 | Prostate | Epithelial | Benign | African American |
| PrE-AA2 | Prostate | Epithelial | Benign | African American |
| 957E-hTERT | Prostate | Epithelial | Cancer (local) | White European <br> descent |
| HEK293 | Kidney | Epithelial | Benign | Unknown |
| 22Rv1 | Prostate | Epithelial | Malignant origin <br> Behaves benign | White European <br> descent |
| LNCaP | Prostate | Epithelial | Cancer (lymph node) | White European <br> descent |
| PC3 | Prostate | Epithelial | Cancer | White European <br> descent |
| MDA-Pca-2B | Prostate | Epithelial | Cancer | African American |
| TS-AA1 | Prostate | Epithelial | Benign | African American |
| TS-H1 | Benign | Hispanic |  |  |

Table S2. Primer sequences

| SPECIES | GENE | FORWARD (5' -> 3') | REVERSE ( $\mathbf{\prime}^{\prime}$-> $\mathbf{3}^{\prime}$ ) |
| :---: | :---: | :---: | :---: |
| HUMAN | LRP2 | CTCCTGGGTGTGTGACCAA | CATCGGGGCAGTCTCTGAC |
|  | KLK3 | tCCAATGACGTGTGTGCGCA | CCTTGATCCACTTCCGGTAA |
|  | CYP24A1 | GGCAACAGTTCTGGGTGAAT | ATtTGAGGACAATCCAACA |
|  | CYP27B1 | TTTGCATCTCTTCCCTTTGG | CTCAGGCTGCACCTCAAAAT |
|  | VDR | GACCTGTGGCAACCAAGACT | GAACTTGATGAGGGGCTCAA |
|  | SRD5A2 | ATATATTGCGCCAGCTCAGG | GGAAATTGGCTCCAGAAACA |
|  | $A R$ | TTGTGTCAAAAGCGAAATGG | CAATGGGCAAAACATGGTC |
|  | RPL13A | GGATAAGAAACCCTGCGACA | CTCGACCATCAAGCACCAG |
|  | HPRT1 | TGCTGACCTGCTGGATTACA | CTGCATTGTTTTGCCAGTGT |
| MOUSE | Pb-MerCreMer-mutant (genotyping) | ACGACCAAGTGACAGCAATG | TAAGCAATCCCCAGAAATGC |
|  | Pb-MerCreMer-wild type (genotyping) | CTAGGCCACAGAATTGAAAGATCT | GTAGGTGGAAATTCTAGCATCATC |
|  | Lrp2-Flox (genotyping, $w t=206 \mathrm{bp}$, flox=320bp) | CACCATGTCCCTCAGTTGTG | CACCATGTCCCTCAGTTGTG |
|  | Lrp2 exons 71-75 (recombination) | CACCGTTGAGTGTGATGCAG | CACCGATGTCCATGTTCACA |
|  | Lrp2 exons 76-77 (control) | CTGGTTTTCCACATTTTCTGG | CTGGTTTTCCACATTTTCTGG |

