**Legends of Supplementary Figures**

**Fig S1**. **PDXs derived from mixed adeno- and neuroendocrine human prostate carcinoma recapitulating only one morphologic component**. MDA PCa 112 adenocarcinoma was derived from a mixed adeno- and neuroendocrine human prostate carcinoma. MDA PCa 181 neuroendocrine carcinoma was derived from a mixed adeno- and neuroendocrine human prostate carcinoma. Representative photomicrograph images of sections stained with HE and immunostained for AR and markers of neuroendocrine differentiation CGN, SNP, and CD56 are shown. HE, hematoxylin and eosin; AR, androgen receptor; CGA, chromogranin; SNP, synaptophysin.

**Fig S2. ETV1 rearrangement by RNA *in situ* hybridization in MDA PCa 177-B**. Whole section view of MDA PCA 177. (**A)** RNA *in situ* hybridization staining for ETV1 on MDA PCa 177 positive for ETV1 rearrangement. ETV1 expression is shown as red punctate dots only in the human PDX tissue and not in the surrounding mouse tissue. (**B)** Enlarged view shows the red punctate dots in the cytoplasm corresponding to ETV1 RNA transcripts.

**Fig S3**. **Comparison of copy number changes in MDA PCa 144 PDXs**. High resolution aCGH analysis identified loss of CDKN2C (1p32.3) and PTEN (10q23.31), and a partial loss of RB in both MDA PCa 144-13 and MDA PCa 144-4.

**Fig S4**. **Whole-genome analysis of copy number changes in MDA PCa 144 PDXs.** Array comparative genomic hybridization analysis shows that MDA PCa 144-13 and MDA PCa 144-4 have significant differences in copy number changes (**upper panel**), which can be better resolved at higher resolution (**middle and lower panels**). In upper panel, areas marked in boxes show the difference in copy number changes between MDA PCa 144-13 (blue) and MDA PCa 144-4 (red). A ratio profile shift to the right indicates copy number gain, and a shift to the left indicates copy number loss.

**Fig S5. Whole-genome analysis of copy number changes in MDA PCa 146 PDXs.** MDA PCa 146-10 (purple), MDA PCa 146-12 (blue), and MDA PCa 146-20 (green) share most of the changes per aCGH analysis, but there are notable differences in copy number changes (**upper panel**, boxed area) that can be appreciated at higher resolution (**middle panels**). In particular, ADAM3A loss is not seen in MDA PCa 146-20, but it is deleted in the other two PDXs (**lower panels**).

**Fig S6. Comparison of copy number changes in MDA PCa 150 PDXs**. Array comparative genomic hybridization analysis shows that MDA PCa 150-1 (blue) and MDA PCa 150-3 (red) have many common losses and gains (**upper panels**), which can be appreciated at higher resolution (**middle and lower panels**). There are no notable differences in copy number between the two PDXs.

**Fig S7. Whole-genome copy number analysis of 3 MDA PCa PDXs.** MDA PCa 155-12 (blue) and -16 (red); MDA PCa 175-10 (blue), -2 (red), and -6 (green); and MDA PCa 180-11 (blue) and -30 (red) share most gains and losses, except for a few regions highlighted in the boxed area.

**Fig S8**. Whole-genome copy number analysis of 37 MDA PCa PDXs derived from 28 human donor PCas.