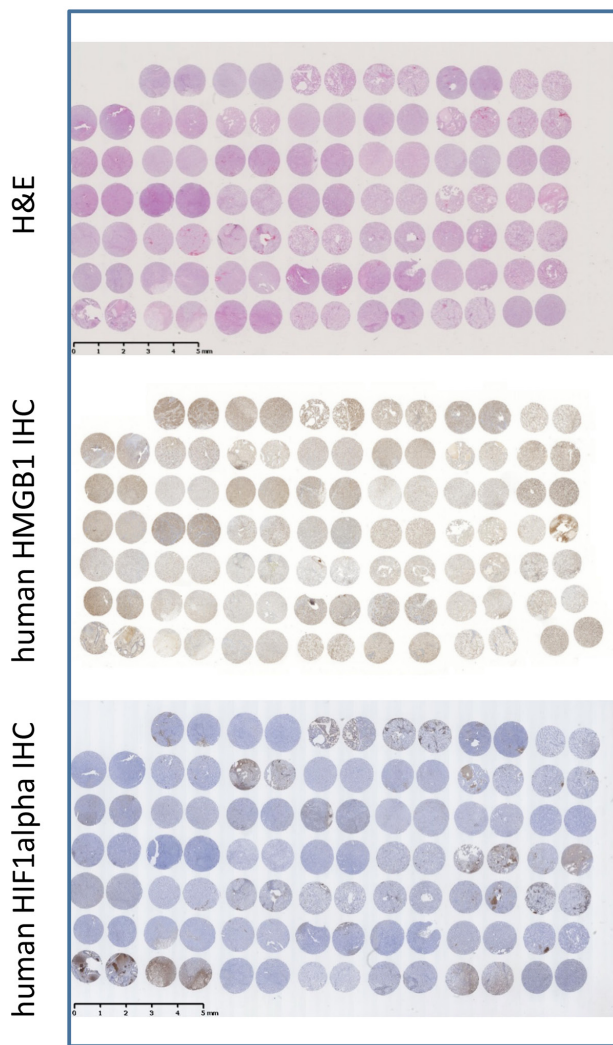


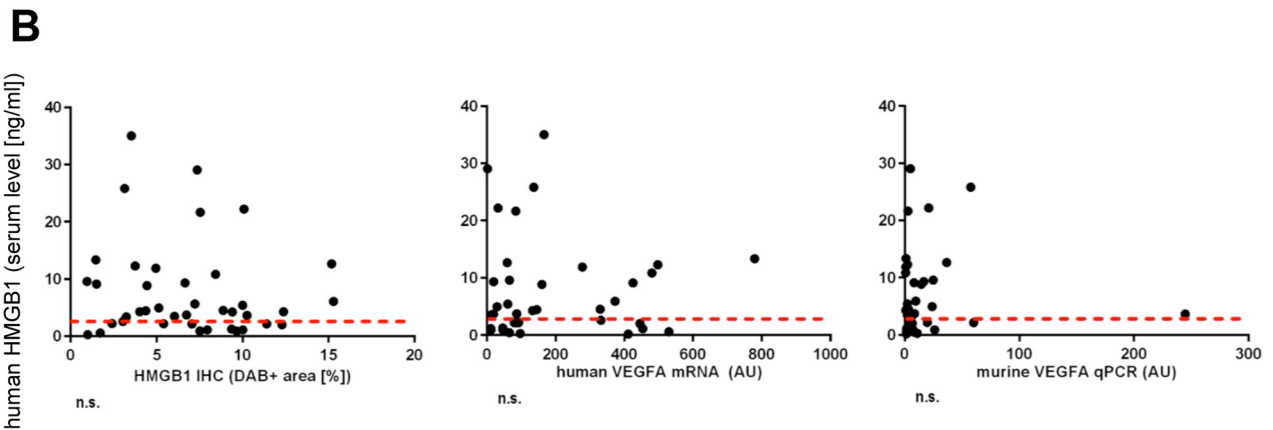
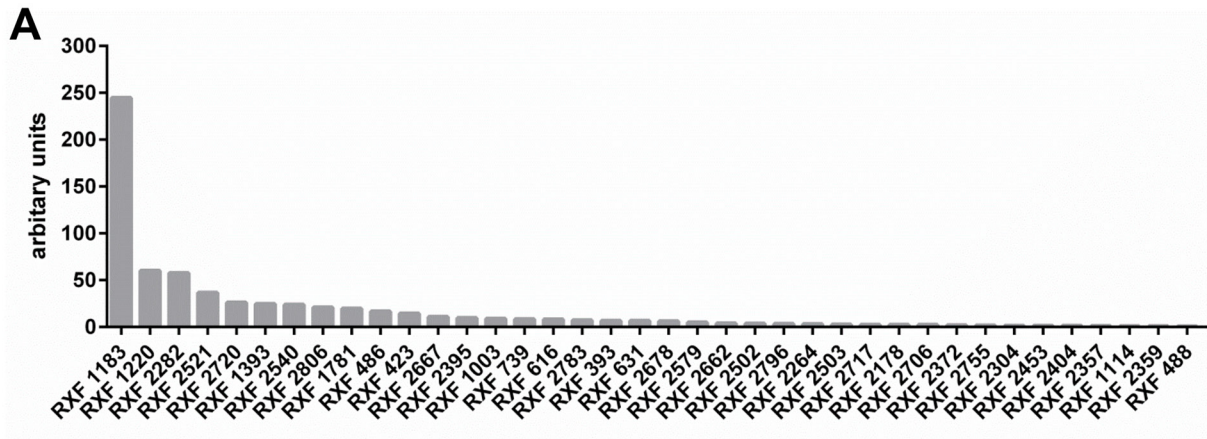
Patient derived renal cell carcinoma xenografts exhibit distinct sensitivity patterns in response to antiangiogenic therapy and constitute a suitable tool for biomarker development

SUPPLEMENTARY MATERIALS

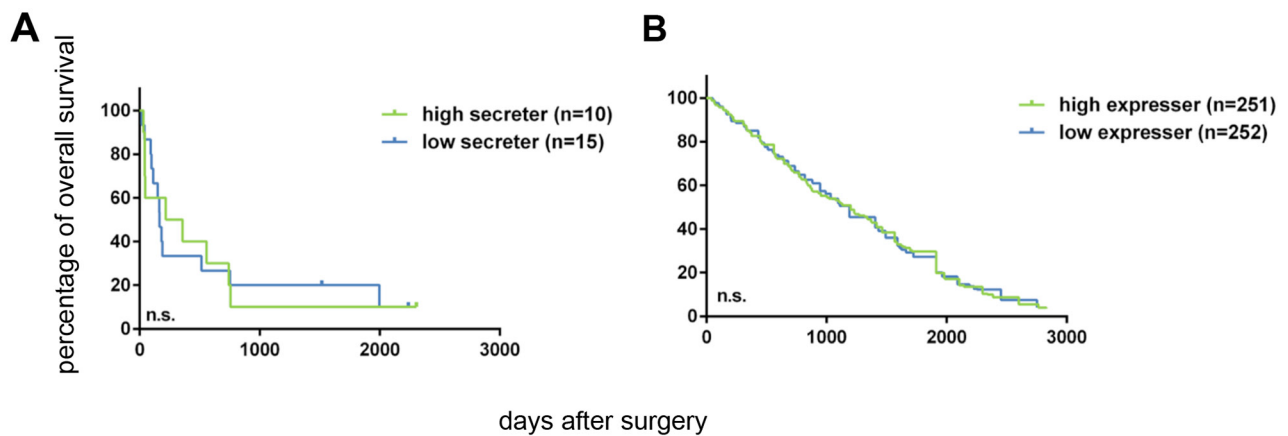


| | | | | | | | | | | | | | |
|----------|----------|-----------|-----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|
| | | MRI-H-166 | MRI-H-166 | CAKI | CAKI | RXF 2830 | RXF 2830 | RXF 2829 | RXF 2829 | RXF 2806 | RXF 2806 | RXF 2796 | RXF 2796 |
| RXF 2783 | RXF 2783 | RXF 2773 | RXF 2773 | RXF 2765 | RXF 2765 | RXF 2755 | RXF 2755 | RXF 2720 | RXF 2720 | RXF 2717 | RXF 2717 | RXF 2706 | RXF 2706 |
| RXF 2678 | RXF 2678 | RXF 2667 | RXF 2667 | RXF 2662 | RXF 2662 | RXF 2579 | RXF 2579 | RXF 2543 | RXF 2543 | RXF 2540 | RXF 2540 | RXF 2527 | RXF 2527 |
| RXF 2521 | RXF 2521 | RXF 2516 | RXF 2516 | RXF 2503 | RXF 2503 | RXF 2502 | RXF 2502 | RXF 2453 | RXF 2453 | RXF 2404 | RXF 2404 | RXF 2395 | RXF 2395 |
| RXF 2372 | RXF 2372 | RXF 2359 | RXF 2359 | RXF 2357 | RXF 2357 | RXF 2304 | RXF 2304 | RXF 2282 | RXF 2282 | RXF 2264 | RXF 2264 | RXF 2258 | RXF 2258 |
| RXF 2178 | RXF 2178 | RXF 1781 | RXF 1781 | RXF 1393 | RXF 1393 | RXF 1220 | RXF 1220 | RXF 1183 | RXF 1183 | RXF 1114 | RXF 1114 | RXF 1003 | RXF 1003 |
| RXF 739 | RXF 739 | RXF 631 | RXF 631 | RXF 616 | RXF 616 | RXF 488 | RXF 488 | RXF 486 | RXF 486 | RXF 423 | RXF 423 | RXF 393 | RXF 393 |

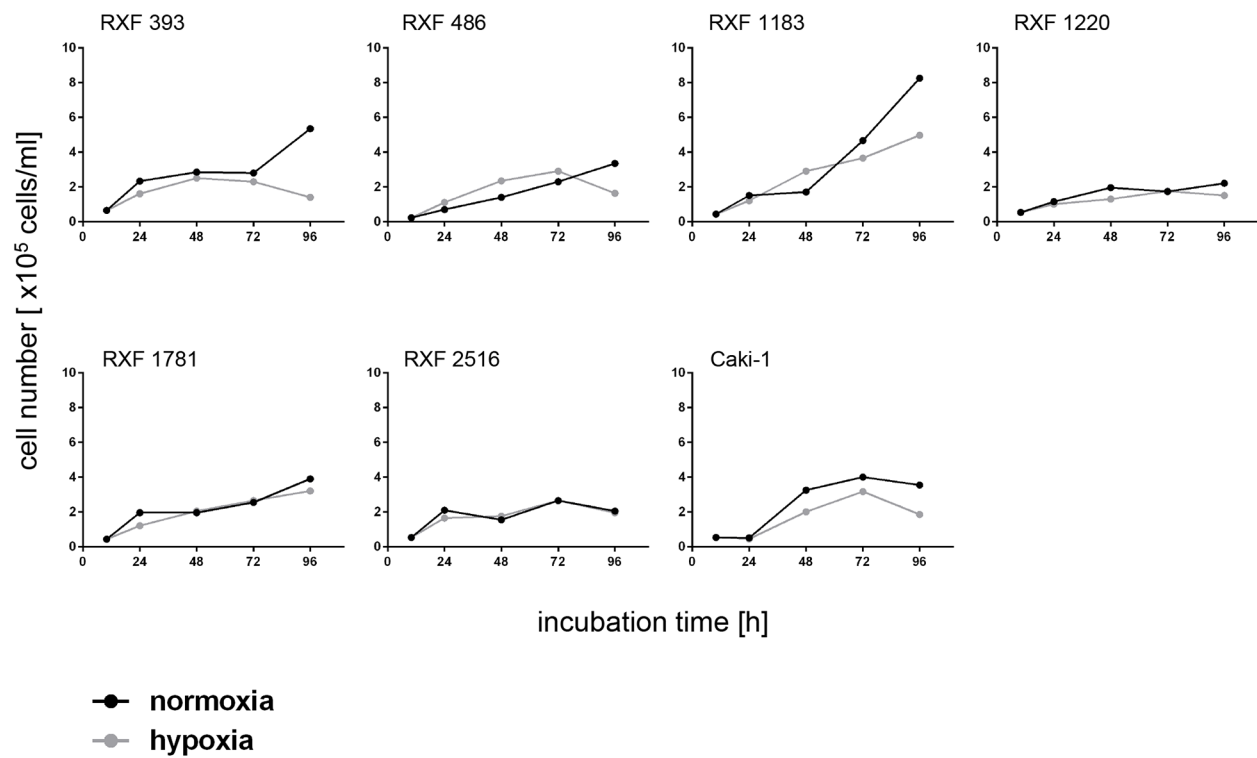
Supplementary Figure 1: A TMA was prepared representing 44 established renal cancer PDX models in duplicate and two additional renal cancer cell line derived xenografts (Caki1 and MRI-H-166). Representatives of all three histological subtypes - clear cell, papillary and chromophobe carcinoma - were included. H&E, HMGB1 and HIF-1 alpha IHC are shown, as well as the detailed layout.



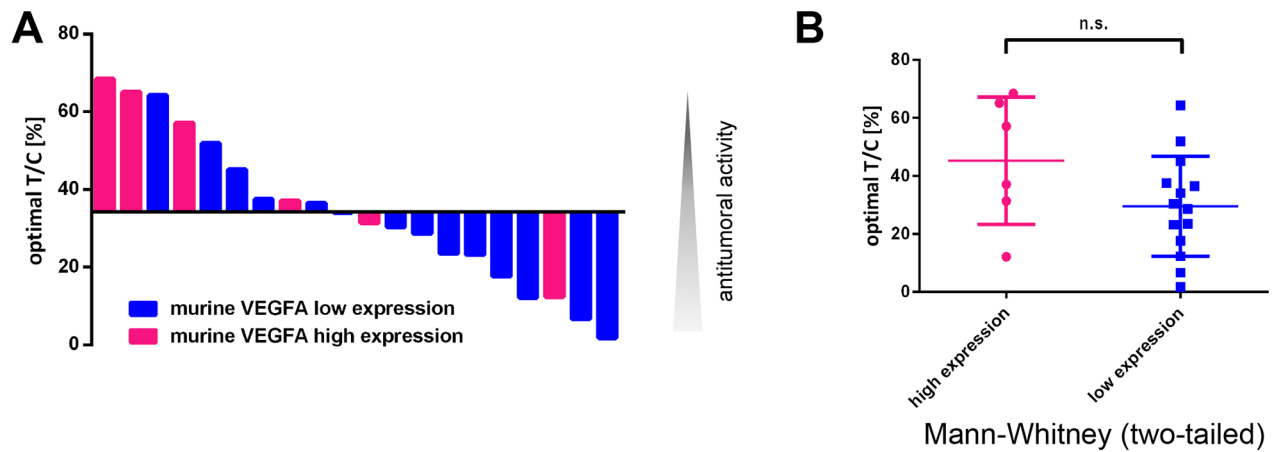
Supplementary Figure 2: (A) mRNA expression of mouse VEGFA determined by qPCR on lysates of renal cancer PDX tissue. The expression level in arbitrary units is calculated as the ratio of mouse VEGF to mouse TBP. **(B)** Serum levels of HMGB1 and levels of HMGB1 determined by IHC, or human VEGFA as well as murine VEGFA expression determined by qRT-PCR did not correlate. The high secretors (above the red dotted line) exhibited all different levels of IHC staining intensity and qRT-PCR expression, respectively.



Supplementary Figure 3: (A) Survival data from donor patients were accessible for 25 PDX models. The cohort was divided into high and low HMGB1 secretors, as determined from their corresponding PDX models. No significant difference between the two cohorts could be detected. **(B)** TCGA data from 505 renal cancer patients were analyzed. The cohort of renal cancer patients was divided by the median of HMGB1 gene expression and the data adjusted for stage. The two groups showed no significant difference in overall survival. Taken together, HMGB1 does not appear to be a prognostic marker for overall survival.



Supplementary Figure 4: A panel of six PDX derived and one commercially available RCC cell line were cultured under normoxic and hypoxic conditions. 10h, 24h, 48h, 72h and 96h after seeding cell numbers per ml were determined. The reduction of O₂ markedly reduced tumor cell proliferation in four out of seven investigated lines.



Supplementary Figure 5: (A) The optimal T/C values were plotted as waterfall plot for 20 renal cancer PDX models treated with bevacizumab. The dark blue bars represent mouse VEGFA-low expressing models (n = 14); the red bars represent mouse VEGFA-high expressing models (n = 6). **(B)** The difference between the T/C values of the groups was not statistically significant (Mann-Whitney test).

Supplementary Table 1: Selected mutations determined by whole exome sequencing in 39 human renal cancer PDX models.

See Supplementary File 1

Supplementary Table 2: Treatment of RCC PDX-derived cell lines with Bevacizumab under Normoxia and Hypoxia

| -96 h | -72 h | 0h | 24h- 120h | 120h |
|----------------------|----------------------|---------------------------|--|-----------------|
| Induction of hypoxia | Induction of hypoxia | Seeding in 96-well plates | Treatment with Bevacizumab, DMSO or Staurosporin | Cell titer blue |
| RXF 486 | RXF 1781 | | | |
| RXF 1183 | RXF 2282 | | | |
| RXF 1220 | RXF 2516 | | | |
| | RXF 393 | | | |
| | RXF | | | |
| | Caki1 | | | |

Supplementary Table 3: Treatment regimen of PDX-bearing immune compromised mice

| Treatment | Daily dose [mg/kg] | Schedule | Application route |
|--------------|--------------------|-------------------------------------|-------------------|
| axitinib | 25 | Twice daily until end of experiment | po |
| bevacizumab | 40/20 | Once weekly | iv |
| pazopanib | 60 | Daily until end of experiment | po |
| sorafenib | 200 | Daily until end of experiment | po |
| sunitinib | 40 | Daily until end of experiment | po |
| temsirolimus | 100 | Five consecutive days | iv |

po: per oral

iv: intravenous injection

Supplementary Table 4: Primers for qRT-PCR analyses

| Species | Official Gene Symbol | Gene Title | Primer F sequence (5'-3') | Primer R sequence (5'-3') | Amplicon Size (bp) |
|---------------|----------------------|--------------------------------------|---------------------------|---------------------------|--------------------|
| human | HMGB1 | High-mobility group box 1 | TGATCGTCCCATCACAGTGT | TCCTACAATGTCTGAGCAATGG | 213 |
| human | VEGFA | vascular endothelial growth factor A | GGGCAGAATCATCACGAAGTG | GGTCTCGATTGGATGGCAGTA | 72 |
| mouse | VEGFA | vascular endothelial growth factor A | CGGGATTGCACGGAAACTT | GCGCAGACCACGGCTACTAC | 69 |
| human | TBP | TATA box binding protein | GGCCGCCGGCTGTT | GCTGGGTCACTGCAAAGATCA | 60 |
| mouse | TBP | TATA box binding protein | GGCGGTTTGGCTAGGTTT | GGGTTATCTTCACACACCATGA | 83 |
| human & mouse | RNA18S | Ribosomal RNA 18S | CTACCACATCCAAGGAAGGCA | TTTTTCGTCACTACCTCCCCG | 71 |