

## Supplementary Information for:

### Cooperation and antagonism among cancer genes: the renal cancer paradigm

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### Supplementary Methods

SNP arrays of clear cell renal cell carcinoma (ccRCC) primary tumors were acquired from GSE14994 (1) and GSE25540 (2). Raw intensity files were analyzed and segmented as previously described (2) and displayed as a heatmap using NCBI36.1 annotation (hg18).

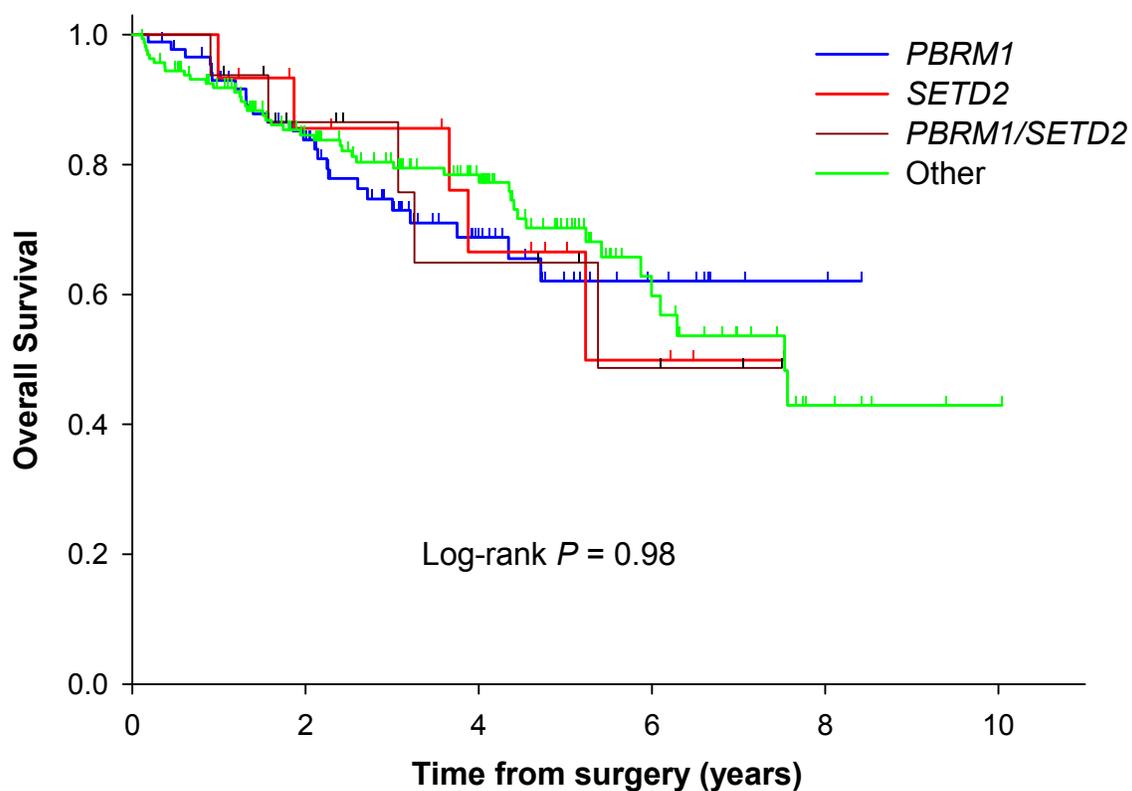
Clinical information and information about somatic mutations of ccRCC patients was obtained from The Cancer Genome Atlas (TCGA) portal (3) on January 26<sup>th</sup>, 2013. The range of expected double mutants was calculated based on a hypergeometric distribution. Odds ratios were calculated to assess the magnitude of the overlap of mutations between two genes. The odds ratios for the combination of studies were evaluated using the Mantel-Haenszel test. For all datasets, differences between actual and expected values were evaluated with a Fisher's exact test.

Overall survival was computed from the date of surgery to the date of death. Patients alive at the end of the study period were censored at the date of last follow-up or the last date the patient was known to be alive, whichever was longer. Kaplan-Meier was used to estimate the survival curves and comparisons were performed using the log-rank test. Statistical analyses were conducted using SPSS Statistics 17.0, except for the Mantel-Haenszel test, which used SAS 9.0.

### Supplementary References

1. Beroukhi R, Brunet JP, Di Napoli A, Mertz KD, Seeley A, Pires MM, et al. Patterns of gene expression and copy-number alterations in von-hippel lindau disease-associated and sporadic clear cell carcinoma of the kidney. *Cancer Research*. 2009;69:4674-81.
2. Peña-Llópez S, Vega-Rubín-de-Celis S, Liao A, Leng N, Pavía-Jiménez A, Wang S, et al. BAP1 loss defines a new class of renal cell carcinoma. *Nature Genetics*. 2012;44:751-9.

3. <https://tcga-data.nci.nih.gov/tcga>



Supplementary Figure 1. Kaplan-Meier curves of overall survival for tumors with mutations in *PBRM1* and *SETD2*.