



Supplemental Material to:

**Banumathy Gowrishankar, Ilsiya Ibragimova, Yan Zhou,
Michael J Slifker, Karthik Devarajan, Tahseen Al-Saleem,
Robert G Uzzo, and Paul Cairns**

**MicroRNA expression signatures of stage, grade,
and progression in clear cell RCC**

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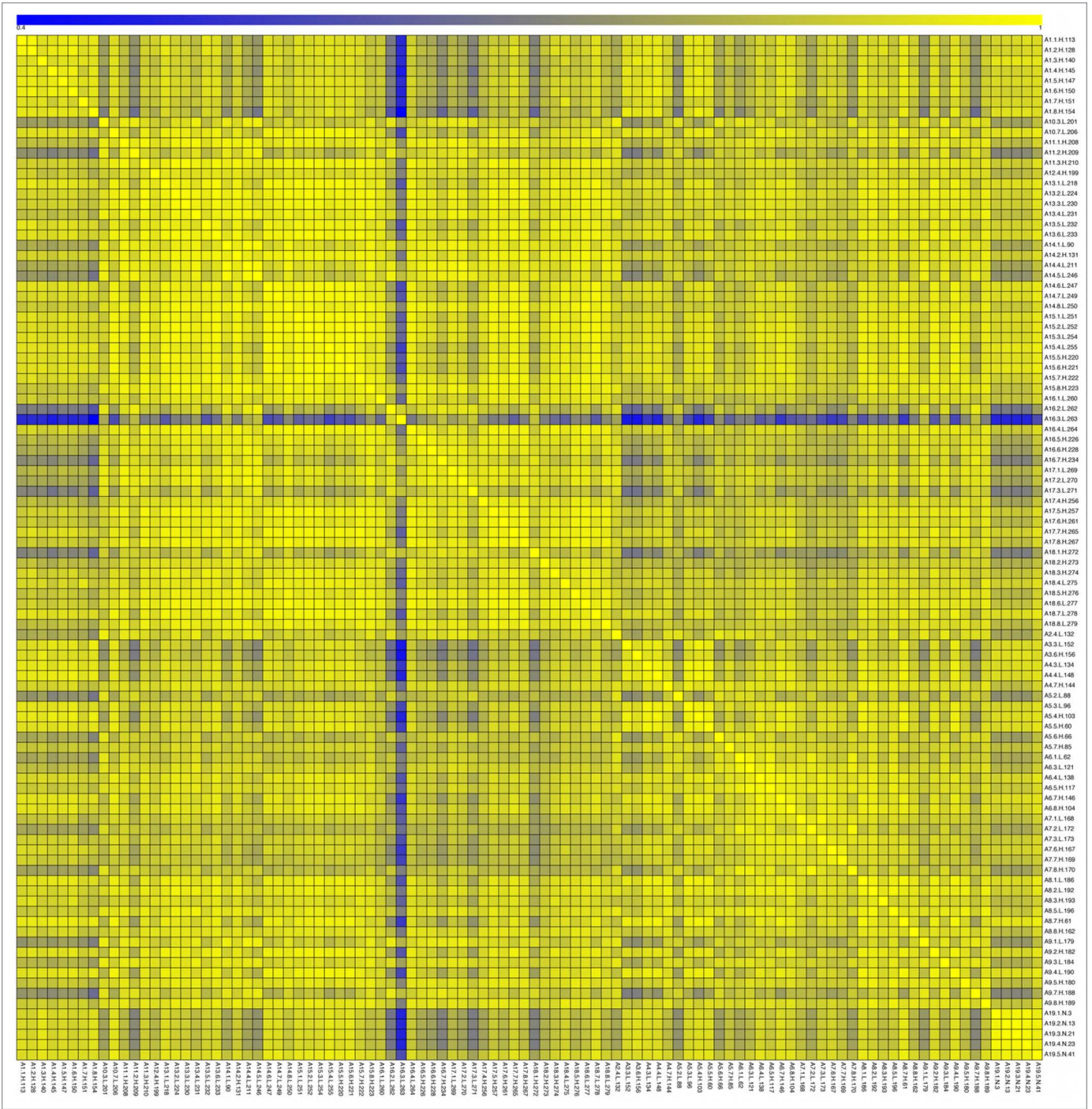


Figure S1. Correlation heat map showing the Pearson coefficient of each sample against itself or every other sample in the microarray. The Pearson coefficient ranges between 0.7 and 1.0.

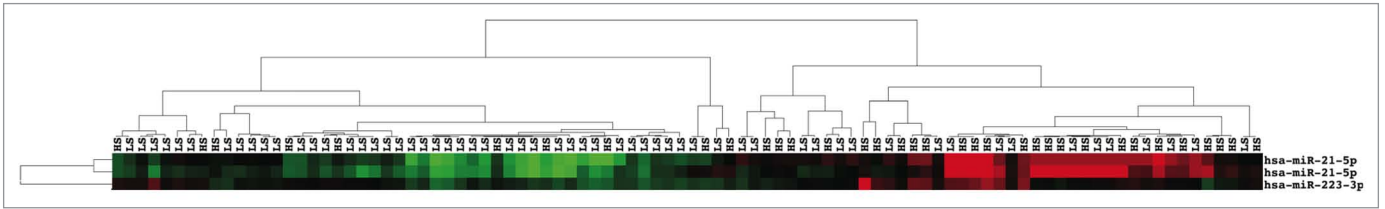


Figure S2. Clustering analysis by clinical stage. Unsupervised two-dimensional hierarchical clustering with a data matrix of 3 probes in 94 ccRCC (59 LS and 35 HS).

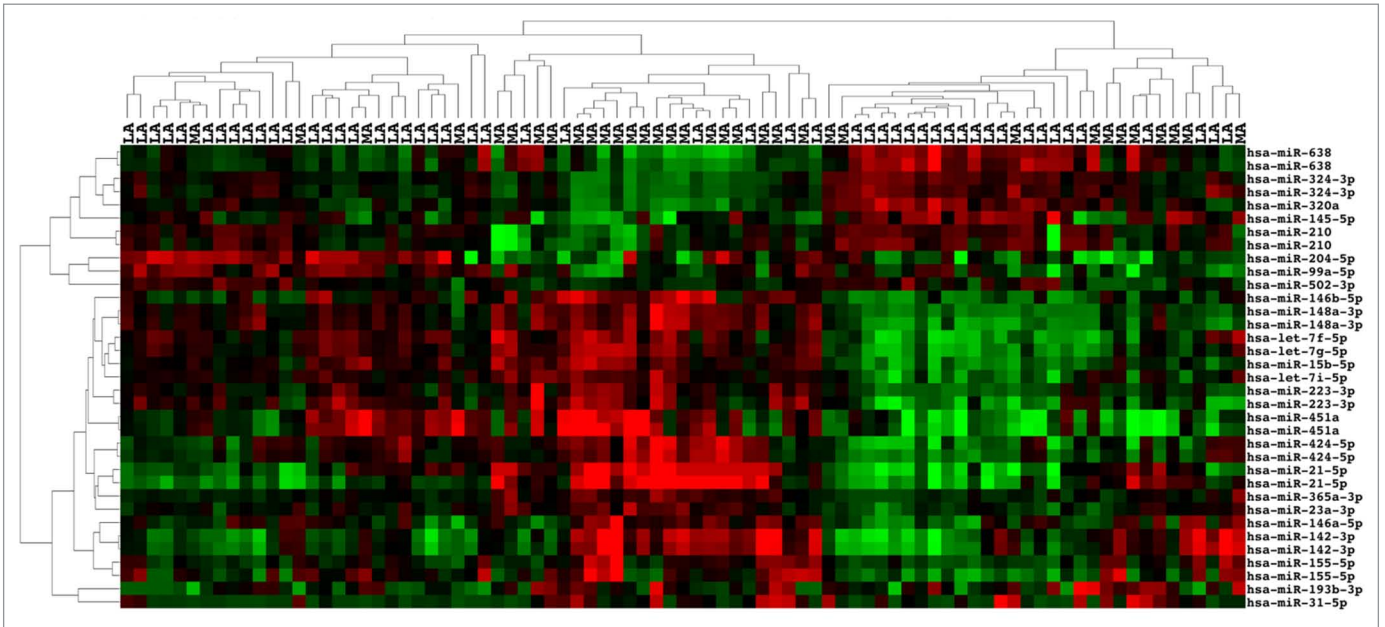


Figure S3. Clustering analysis by aggressiveness. Unsupervised two-dimensional hierarchical clustering with a data matrix of 35 probes in 85 ccRCC (51 LA and 34 MA).

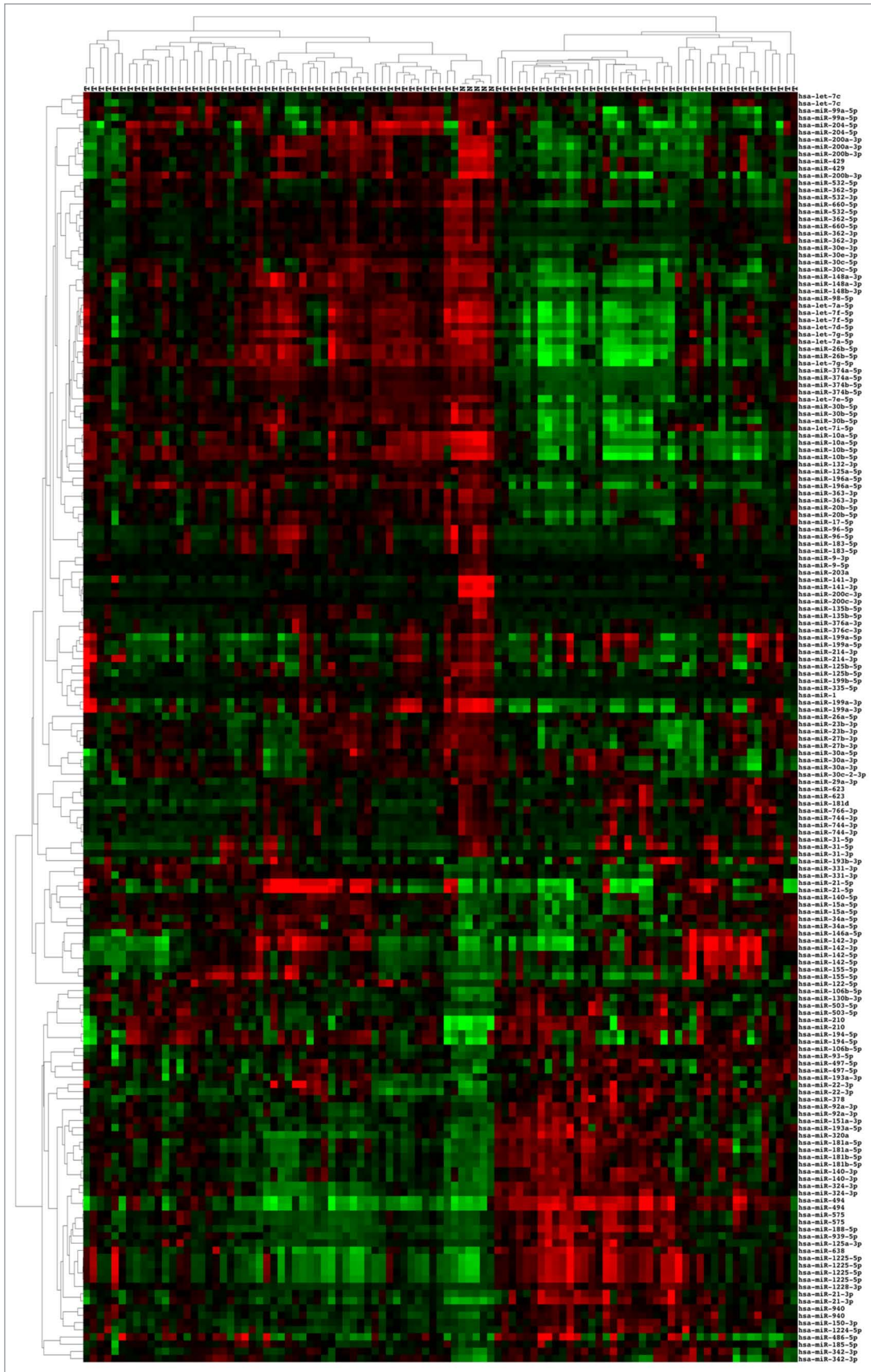


Figure S4. Differences in miRNA expression between ccRCC and normal renal parenchyma. Unsupervised two-dimensional hierarchical clustering with a data matrix of 176 probes in 99 renal samples (94 ccRCC and 5 NRP).

For **Tables S1–S11**, please visit www.landesbioscience.com/journals/cbt/article/27314 and download the file named Tables S1–S11.

Table S1. miRNA expression data and statistical analysis: Typical high grade high stage (29) vs. low grade low stage (29)

Table S2. miRNA expression data and statistical analysis: High stage annotated (35) vs. low stage annotated (46)

Table S3. miRNA expression data and statistical analysis: High stage (35) vs. low stage (59)

Table S4. miRNA expression data and statistical analysis: High grade (50) vs. low grade (44)

Table S5. miRNA expression data and statistical analysis: Grade IV (16) vs. grade I (7)

Table S6. miRNA expression data and statistical analysis: Low stage high grade (21) vs. low stage low grade (38)

Table S7. miRNA expression data and statistical analysis: Progression (19) vs. no progression (51)

Table S8. miRNA expression data and statistical analysis: More aggressive (43) vs. less aggressive (51)

Table S9. miRNA expression data and statistical analysis: Metastatic (34) vs. non-metastatic (51)

Table S10. miRNA expression data and statistical analysis: Tumor (94) vs. normal (5)

Table S11. DIANA mirpath analysis. List of KEGG pathways significantly ($P < 0.05$) overrepresented as targets of the set of dysregulated miRNAs (**A**) in subsets of ccRCC and (**B**) in ccRCC compared to NRP.