

Supplementary Information

Multi Omics analysis of fibrotic kidneys in two mouse models

Mira Pavkovic^{1,2*}, Lorena Pantano^{3,*}, Cory V. Gerlach^{1,2,4}, Sergine Brutus^{1,4,5}, Sarah A. Boswell¹, Robert A. Everley¹, Jagesh Shah^{1,2}, Shannan H Sui³, Vishal S. Vaidya^{1,2,4}

1. Laboratory of Systems Pharmacology, Harvard Medical School, Boston, MA
2. Department of Medicine – Renal Division, Brigham and Women’s Hospital, Boston, MA
3. Bioinformatics Core, Harvard T.H. Chan School of Public Health, Boston, MA
4. Department of Environmental Health, Harvard T. H. Chan School of Public Health, Boston, MA
5. Department of Systems Biology, Harvard Medical School, Boston, MA

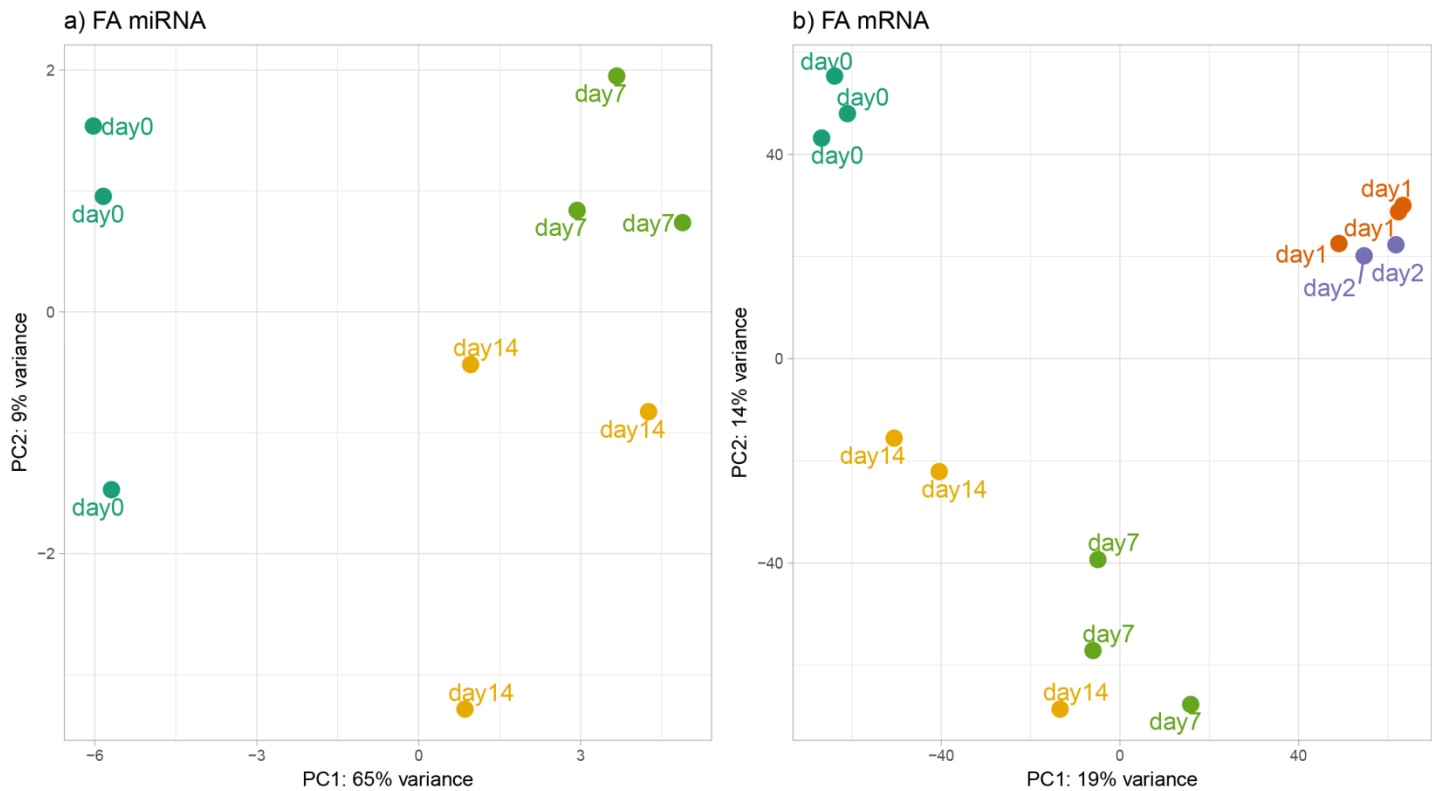
* co-first

corresponding author: Vishal S. Vaidya (vvaidya@partners.org)

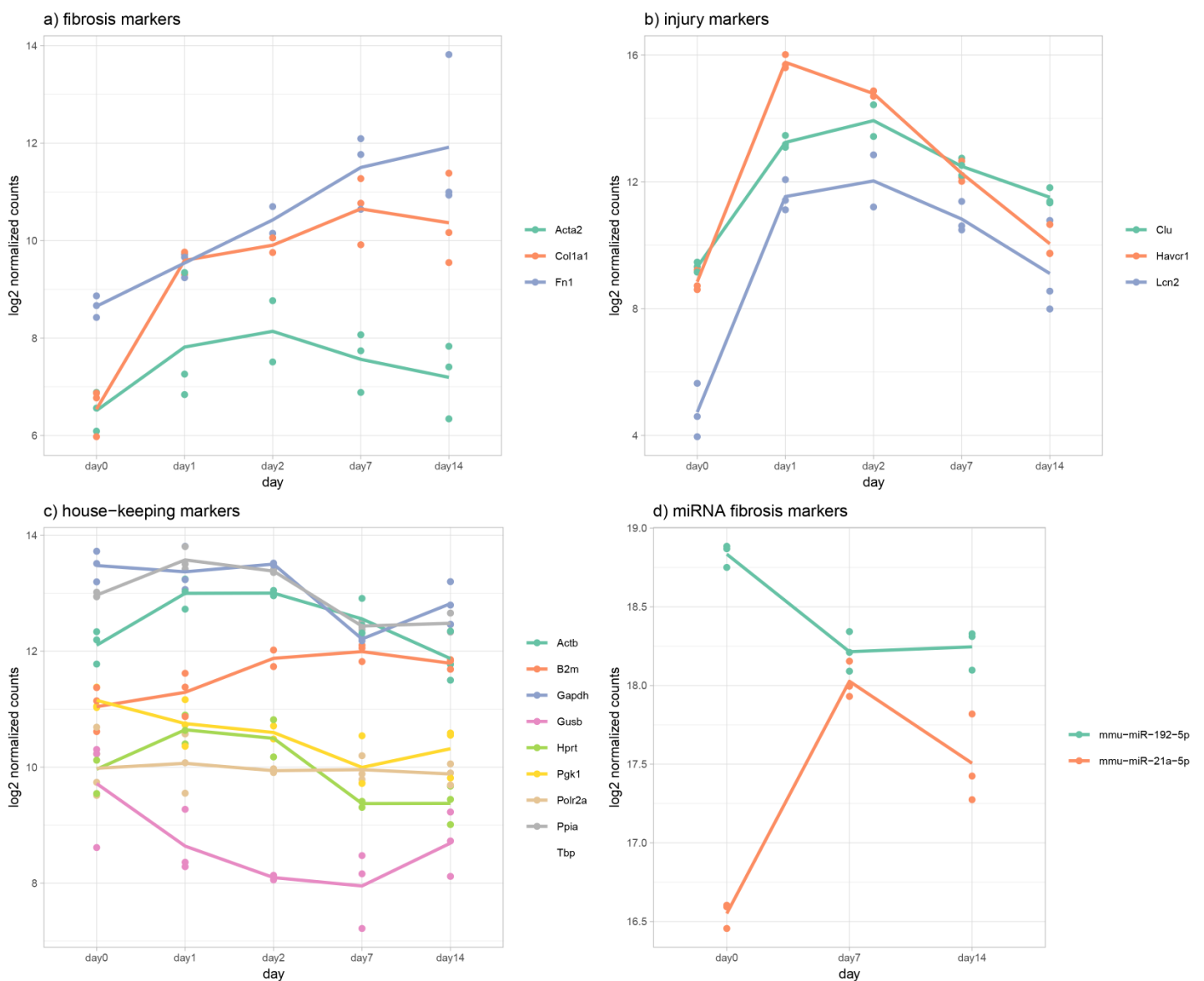
Contents

Supplementary Figure 1 Principal component analysis (PCA) of previously published data for FA mRNA and miRNA..	 2
Supplementary Figure 2 Expression profiles of fibrosis and injury markers and housekeeping genes from previously published FA mRNA and miRNA data.	3
Supplementary Table 1. Quality metrics of FA mRNA Seq data	4
Supplementary Table 2. Quality metrics of FA small RNA Seq data	5

Supplementary Figure 1 Principal component analysis (PCA) of previously published data for FA mRNA and miRNA. Raw data was re-analyzed and the normalized expression abundance of mRNAs and miRNAs was used. Each color represents a time point in the dataset. a) miRNA and b) mRNA expression in the FA model clusters for each time point, with PC1 separating normal from post injury groups, and PC2 separating the samples according to time points.



Supplementary Figure 2 Expression profiles of fibrosis and injury markers and housekeeping genes from previously published FA mRNA and miRNA data. Raw data was re-analyzed and mRNA expression was plotted for a) fibrosis and b) injury markers, and c) housekeeping genes, as well as miRNA expression for d) miR-192 and -21.



Supplementary Table 1. Quality metrics of FA mRNA Seq data

Sample Name	Reads	rRNA	5'-3' bias	M Aligned	Exon %
normal_1	97	0.6101	0.91	59	73.06
normal_2	178	0.5805	0.79	123	71.4
normal_3	76	0.6432	0.94	53	78.35
day1_1	88	0.5913	0.68	67	73.44
day1_2	152	0.5996	0.63	126	72.9
day1_3	165	0.5923	0.55	141	71.71
day2_1	179	0.5505	0.6	122	66.76
day2_2	63	0.5663	0.9	21	75.18
day2_3	85	0.5601	0.72	68	63.63
day3_1	97	0.5297	0.73	74	60.22
day3_2	78	0.5077	0.68	58	63.1
day3_3	121	0.5685	0.73	94	65.26
day7_1	81	0.5552	0.56	67	65
day7_2	74	0.5554	0.76	59	64.09
day7_3	112	0.5837	0.66	68	65.24
day14_1	87	0.6	0.66	57	70.97
day14_2	104	0.6463	0.74	72	74.43
day14_3	80	0.5952	0.86	62	63.33

Supplementary Table 2. Quality metrics of FA small RNA Seq data

Sample Name	M Seqs	% with Adapter	miRNAs	isomiRs
A196_normal	6.9	99	525	11305
A200_normal	8.4	99	557	13686
A201_normal	6.8	99	504	10677
A178_day3	7.9	98	594	12870
A74_day3	7.8	97	586	13474
A75_day3	6.6	97	549	11057
A180_day7	10.1	99	623	15538
A181_day7	7.0	99	553	11689
A80_day7	7.8	97	562	13506
A84_day14	8.1	99	568	14134
A85_day14	6.9	98	513	10462
A189_day14	6.7	94	562	12164