Supplemental Data

Table S1: Patient demographic characteristics for sample microRNA expression analyses.

Institution	**RNA Source**	**Groups**	**Age (years)**	**Race (W/B/O)**[a]	**Gender (M/F)**	**FVC**[b] **(% predicted)**
The Ohio State University Medical Center	Lung	Control (n = 4)	52.7 ± 4.4	3/1/0	2/2	
		Sarcoid (n = 4)	51.8 ± 3.8	2/2/0	1/3	86.5 ± 3.6
	Lymph Node	Control (n = 4)	46.4 ± 5.9	2/2/0	2/2	
		Sarcoid (n = 4)	45.0 ± 5.5	2/2/0	2/2	85.7 ± 6.6
	PBMC	Control (n = 5)	45.8 ± 3.1	4/1/0	3/2	
		Sarcoid (n = 10)	50.6 ± 2.9	7/3/0	4/6	90.9 ± 4.2
Oregon Health and Science University	Lymph Node	Control (n = 7)	45.1 ± 3.2	5/1/1	4/3	
		Sarcoid (n = 7)	45.6 ± 5.3	6/0/1	4/3	83.6 ± 4.4

[a] White/Black/Other
[b] Forced Vital Capacity

MicroRNA	**Assay Number**
has-miR-92b	286
has-miR-22	398
has-miR-204	508
has-miR-302c#	534
has-miR-25	403
has-miR-199a-5p	498
has-miR-214	517
has-miR-216	519
has-miR-383	573
has-miR-486-5p	1278
has-miR-19b	396
has-miR-16	391

Table S2. MicroRNA Assay Index File (AIF) numbers corresponding to each miRNA sequence used for qRT-PCR validation. See the following website for detailed primer sequences: http://www6.appliedbiosystems.com/support/miRNA_aif.xls

Table S3: The most differentially expressed transcripts (Sarcoidosis vs. Control) identified by genome-wide miRNA expression profiling in human lung tissue.

Most Overexpressed miRs[a]		
miR	**Fold Difference**	**Chromosomal Location**
125a	13.4	19q13.41
92a-1	11.8	13q31.3
204	8.5	9q21.12
122a	7.3	18q21.31
206	7.1	6p12.2
1-1	6.5	20q13.33
627	6.3	15q15.1
196a-2	6.2	12q13.13
190	5.8	15q22.2
595	5.4	7q36.3

Most Underexpressed miRs[a]		
miR	**Fold Difference**	**Chromosomal Location**
181a	0.05	1q32.1
590	0.06	7q11.23
22	0.09	17p13.3
597	0.10	8p23.1
329-2	0.11	14q32.31
126-3p	0.13	9q34.3
148b	0.13	12q13.13
518b	0.13	19q13.42
154-5p	0.15	14q32.31
302c	0.16	4q25

[a] p-value < 0.05, false discovery rate < 0.1

Table S4: The most differentially expressed transcripts (Sarcoidosis vs. Control) identified by genome-wide miRNA expression profiling in human peripheral blood mononuclear cells (PBMC).

Most Overexpressed miRs[a]		
miR	**Fold Difference**	**Chromosomal Location**
204	22.5	9q21.12
619	16.5	12q24.11
580	13.0	5p13.2
566	10.5	?
596	9.7	8p23.3
214	8.5	1q24.3
589	8.5	7p22.1
579	8.3	5p13.3
598	8.3	8p23.1
616	8.0	12q13.3

Most Underexpressed miRs[a]		
miR	**Fold Difference**	**Chromosomal Location**
199a	0.06	19p13.2
148a	0.08	7p15.2
363-3p	0.08	Xq26.2
92-2	0.09	13q31.3
25	0.11	7q22.1
24-5p	0.13	9q22.32
583	0.13	5q15
123	0.14	?
486-5p	0.14	8p11.21
215	0.16	1q41

[a] p-value < 0.0001, false discovery rate < 0.01

Figure S1. PCR validation of tissue miRNA differential expression for selected transcripts. A subgroup of DE-miRNAs identified by array analysis were validated by PCR in frozen lung tissue [left column: controls (n = 4); sarcoid (n = 4)], frozen lymph node samples [center column: controls (n = 4); sarcoid (n = 4)], and formalin-fixed paraffin-embedded (FFPE) lymph node samples [right column: controls (n = 7); sarcoid (n = 7)].

Figure S2. PCR validation of PBMC miRNA differential expression for selected transcripts. Several of the DE-miRNAs identified by miRNA array of PBMC samples were selected for validation by PCR in all of the samples (10 sarcoidosis; 5 controls). The expression trends, significant for 3 of the 6 transcripts, were the same as predicted by the miRNA array analysis.

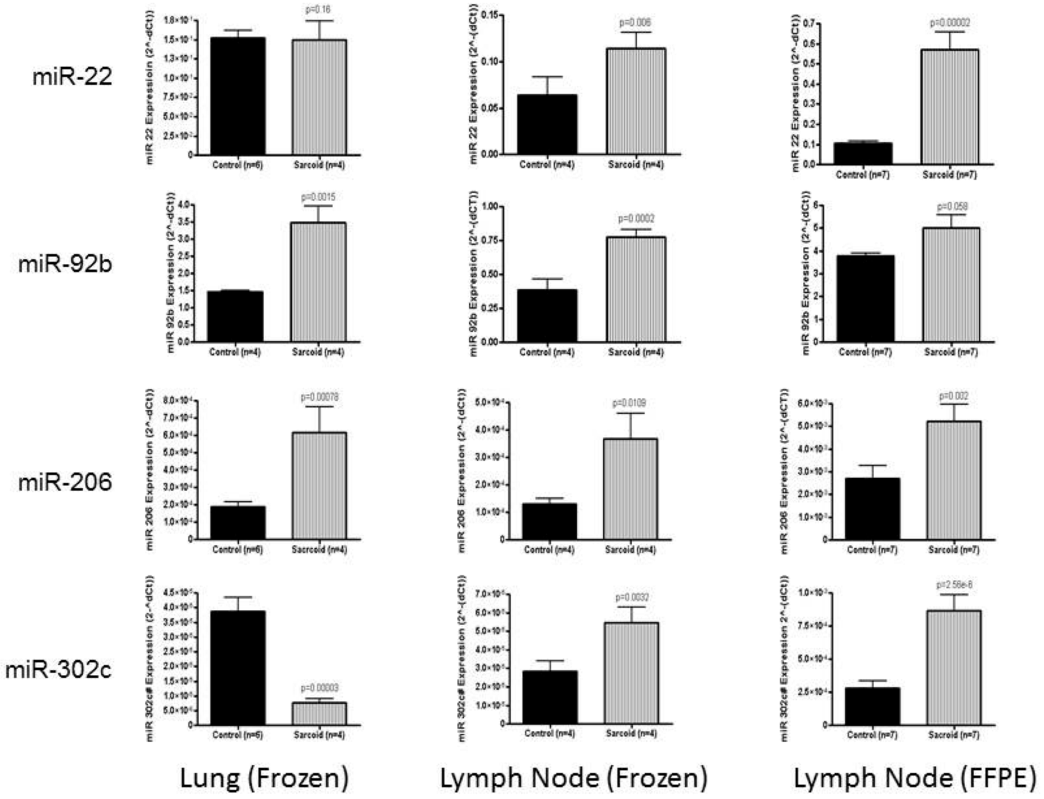

Figure S1

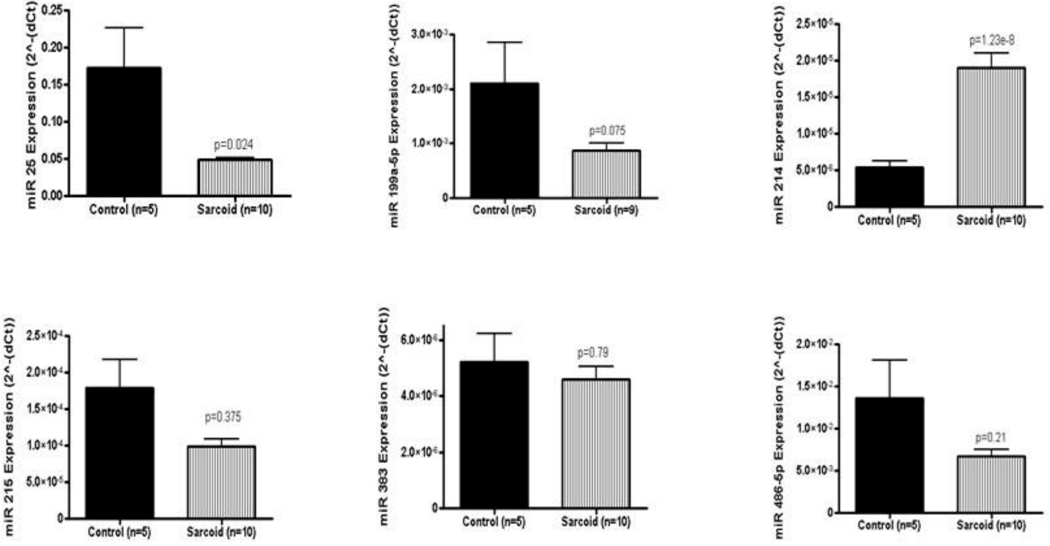
miR 25 Expression (2^-(dCt))
0.25
0.20
0.15
0.10
0.05
0.00
p=0.024
Control (n=5)
Sarcoid (n=10)
miR 199a-5p Expression (2^-(dCt))
3.0×10-3
2.0×10-3
1.0×10-3
0
p=0.075
Control (n=5)
Sarcoid (n=9)
miR 214 Expression (2^-(dCt))
2.5×10-5
2.0×10-5
1.5×10-5
1.0×10-5
5.0×10-6
0
p=1.23e-8
Control (n=5)
Sarcoid (n=10)
miR 215 Expression (2^-(dCt))
2.5×10-4
2.0×10-4
1.5×10-4
1.0×10-4
5.0×10-5
0
p=0.375
Control (n=5)
Sarcoid (n=10)
miR 383 Expression (2^-(dCt))
6.0×10-6
4.0×10-6
2.0×10-6
0
p=0.79
Control (n=5)
Sarcoid (n=10)
miR 486-5p Expression (2^-(dCt))
2.0×10-2
1.5×10-2
1.0×10-2
5.0×10-3
0
p=0.21
Control (n=5)
Sarcoid (n=10)

Figure S2