

Supplementary Table S1. The predicted sequence alignment between mouse miRNAs and NOX4 3'UTR.

ID		Alignment	Position	site
miR-9	Target (5'-3')	5'AACAGCUGUGCUAUG CCAAAGA	3' UTR	90-96
	miRNA(3'-5')	3' GUAUGUCGAUCUAU..... GGUUUCU		
miR-196b	Target (5'-3')	5' AGCUUAUCCUUA ACCAAAGA	3' UTR	761-768
	miRNA(3'-5')	3' AGUAUGUCGAUCUAU UGGUUUCU		
miR-148a	Target (5'-3')	5' UCAGAAGGAAAAUUU ACUACCUU	3' UTR	1048-1054
	miRNA(3'-5')	3' GGGUUGUUGUCCUU UGAUGGAU		
miR-215	Target (5'-3')	5' CACUAAUAUUAUUUU UGCACUGU	3' UTR	941-947
	miRNA(3'-5')	3' UGUUUCAAGACAUC ACGUGACU		
miR-203	Target (5'-3')	5' ACAUU UCAAAA AUUC AGGUCAAA	3' UTR	1565-1571
	miRNA(3'-5')	3' CAGAC AGUUU AGUA - UCCAGUA		
miR-203	Target (5'-3')		CDS	-
	miRNA(3'-5')			

Supplementary Table S2. The baseline characteristics of patients with transudate and tuberculous pleural effusion

Group	Subject	Age	Sex	Sputum AFB culture	PE AFB culture	PE ADA	PE/Serum protein	PE/Serum albumin
TB-PE	TB-PE 1	75	M	Negative	Positive	6.2	1	0.74
	TB-PE 2	21	M	Negative	Positive	6.7	0.61	0.67
	TB-PE 3	92	F	Positive	Negative	30	0.78	0.75
Transudate	T1	84	M	Negative	Negative	36.9	0.41	0.36
	T2	80	F	Negative	Negative	<4.0	0.26	0.21
	T3	92	F	Negative	Negative	7	0.39	0.44

PE, pleural effusion; AFB, acid-fast bacilli; ADA, adenosine deaminase; TB-PE, tuberculous pleural effusion; LDH, lactate dehydrogenase; CRP, C-reactive protein