Supplementary Table 2. Detailed overview of the studies included in the analysis.

Author, year of publication and reference	**Characteristics of tumor samples**	**Tumor content**	**Characteristics of control samples**	**Study phase**	**qRT-PCR Platform**	**Microarray platform**	**Relevant findings**	**GEO Database and MIAME accession numbers**
Guled M *et al.* 2009 [71]	Fresh tissue: MM (Total, 17: 10 epith, 1 sarc, 5 biph, 1 other)	30-90%	Fresh tissue: pericardium (Total, 1)	Screening	/	Agilent's miRNA microarray system (V.2) - Agilent Technologies	12 miRNAs exclusively expressed in MM samples, 9 miRNAs exclusively expressed in control samples. (Analysis of association with histopathological subtypes)	/
Busacca S *et al.*2010 [82]	Cell lines: MPP-89 (spindle-shaped), REN (epithelial-like)	/	Cell lines: HMC-TERT (immortalized human mesothelial cells-telomerase reverse transcriptase) (Total, 1)	Screening and validation	TaqMan MicroRNA assays - Applied Biosystem (Ref Gene: U6, calibrator sample)	miRCURY locked nucleic acid [LNA] microarray kit, V.8 - Exiqon	65 dysregulated miRNAs and 10 miRNAs validated by qRT-PCR	A-MEXP-1260, E-MEXP-1699
	FFPE tissue: MM (Total, 24: 8 epith, 8 sarc, 8 biph)	>80%	/	/	TaqMan MicroRNA assays - Applied Biosystem (Ref Gene: U6, calibrator sample)	/	10 miRNAs (analysis of association with histopathological subtypes)	
Pass HI *et al.* 2010 [74]	Fresh-frozen tissue: MPM (Total, 142: 81 epith, 48 other)	129/142 good RNA quality	/	Training set, test set	/	Nexterion® Slide	Analysis of association with histopathological subtypes and prognosis.	/
	16 MPM samples (8 good prognosis, 8 poor prognosis)	/	/	Validation	qRT-PCR (Ref Gene: miR-181a, miR-let-7c, miR-193a-5p, miR-27b, miR-339-5p)	/	Elevated miR-29c*is associated with longer survival	
	Cell lines: HP1, HP3, H2373, H2452, H2591, H2595, H2596, H2461	/	Cell lines: NYU-590.2 (primary mesothelial cell culture), LP9 (TERT-immortalized mesothelial cell line), SV40-transformed mesothelial cell line Met-5A	/	qRT-PCR (Ref Gene: n.a.)	n.a.	MiR-29c* is downregulated in MM cell lines	
Ivanov SV *et al.* 2010 [84]	Cell lines: HP1, HP3, H2373, H2452, H2591, H2595, H2596, H2461	/	Cell lines: NYU-590.2 (primary mesothelial cell culture), LP9 (TERT-immortalized mesothelial cell line), SV40-transformed mesothelial cell line Met-5A	Analysis of chromosome deletion	Loop RT-PCR technology (Ref Gene: n.a.)	Nexterion® Slide	Loss of miR-31 has a pro-tumorigenic effect in MM	/
Benjamin H *et al.* 2010 [73]	FFPE tissue: MPM (Total, 47: 29 epith, 6 sarc, 6 biph, 6 other)	Used 33/47	FFPE tissues: carcinomas (Total, 210/259)	Biomarker discovery, training phases	qRT-PCR (Ref Gene: U6)	Nexterion® Slide	Search for miRNAs capable of differentiating MM from carcinoma	/
	FFPE tissue: MPM (Used n=14/47)	≥ 50%	FFPE tissues: carcinomas (Total, 49/259)	Validation phase	qRT-PCR (Ref Gene: U6)	/	MiR-193-3p, miR-200c, and miR-192 are useful to differentiate MPM from other	

							pleural malignancies (sensitivity 100%, specificity 94%)	
Gee GV *et al.* 2010 [72]	Fresh tissue: MPM (Total, 15 other)	/	Fresh tissues: lung adenocarcinoma (Total, 10)	Screening	/	Affimetrix gene chip miRNA microarrays (TGmirV1b520432f)	Mesothelial-specific downregulation of 7 miRNAs in MPM compared with lung adenocarcinoma	/
	Fresh tissue: MPM (Total, 100: 39 epith, 10 sarc, 19 biph, 32 other)	/	Fresh tissue: lung adenocarcinoma (Total, 32) and normal lung tissue (Total, 4)	Validation	TaqMan MicroRNA assays - Applied Biosystem (Ref Gene: RNU44, RNU48)	/	MPM can be distinguished from lung adenocarcinoma by downregulation of 7 miRs	
Balatti V *et al.* 2011 [81]	Cell lines: MSTO-211H, MPP-89, IST-MES2,NCI-H2052, NCI-H28 (Total, 5)	/	Cell lines: HMCs (primary mesothelial cell culture: 4N, 6N, 13N, 16N, 26N) (Total, 5)	Screening	/	Agilent Human microRNA microarray G4470A - Agilent Technologies	MiRNAs found to be dysregulated may be potential MPM targets	/
				Validation	TaqMan MicroRNA assays - Applied Biosystem (Ref Gene: U6)	/		
Santarelli L *et al.* 2011 [85]	Fresh tissue: MPM (Total, 10: 9 epith, 1 sarc)	/	Fresh tissue: adjacent non-cancerous tissues (Total, 5)	Screening	/	miRNA qRT-PCR array MAH-102A - SABiosciences (Ref Gene:	Several downregulated miRs in MPM specimens	/
	Fresh tissue: MPM (Total, 27: 23 epith, 1 sarc, 3 biph)	/	FFPE tissue: adjacent non-cancerous tissues (Total, 27)	Larger-scale analysis	TaqMan MicroRNA assays - Applied Biosystem (Ref Gene: U6)	/	MiR-126 allows to discriminate cancer from non-malignant tissue	
	Serum: MPM patients (Total, 44: 30 epith, 6 sarc, 8 biph) and healthy asbestos-exposed subjects (Total, 196)	/	Serum: healthy subjects (Total, 50)	Validation	TaqMan MicroRNA assays - Applied Biosystem (Ref Gene: U6)	/	MiR-126, in association with SMRPs, was proposed as a marker for early detection of MPM	
Kubo T *et al.* 2011 [101]	Cell lines: NCI-H28, NCI-H290, NCI-H2052, NCI-H2452, HP1, MSTO-211H (Total, 6)	/	Cell cultures: non-malignant mesothelial primary cultures (Total, 2)	Analysis of expression status and methylation	qRT-PCR (Ref Gene: Expression levels of 2 non-malignant mesothelial cells mixed)	/	MiR-34b/c expression was reduced in all methylated MPM cell lines and tumors	/
	Fresh tissue: MPM (Total, 47: 32 epith, 4 sarc, 10 biph, 1 lymph) only 10 samples used for miRNA expression analysis	/	Fresh frozen tissue: non-neoplastic pleura from lung cancer patients (Total, 10)		qRT-PCR (Ref Gene: Expression levels of two non-malignant mesothelial cells mixed)	/		
Fassina A *et al.* 2011 [92]	FFPE tissue: 74 MPM and 35 peritoneal MM. Total, 109: 58 epith (35 pleural, 23 peritoneal), 25 sarc (18 pl+7 p), 26 biph (21 pl+5 p)	/	/	Analysis of miR-205	*In Situ* Hybridization and NCodeTM miRNA qRT-PCR - Invitrogen (Ref Gene: RNU6B)	/	MiR-205 downregulation correlated with both the mesenchymal phenotype and a more aggressive behavior	/
	Cell lines: H2452, MSTO-211H (Total, 2)	/	Cell line: SV40-transformed mesothelial cell line Met-5A (Total, 1)		NCodeTM miRNA qRT-PCR - Invitrogen (Ref Gene: RNU6B)	/		

Nymark P *et al.* 2011 [70]	13 lung tumors from asbestos-exposed patients (large cell lung cancer, adeno-squamous cell carcinoma, small cell lung cancer, adenocarcinoma)	/	8 control patients (hamartoma, lymph node, lymphoid hyperplasia, tuberculoma, inflammatory pseudotumor, lung abscess) and 13 lung tumors from non-exposed patients (large cell lung cancer, adeno-squamous cell carcinoma, small cell lung cancer, adenocarcinoma)	/	/	Agilent Human miRNA v2 G2565CA - Agilent Technologies	13 novel asbestos-related miRNAs were identified	Accession number: GSE25508
Kemp CD *et al.* 2012 [93]	Cell lines: H28, H2052, H2452, NCI-SB-MES1-4 (MPM primary culture) (Total, 4)	/	Cell lines: LP3, LP9, NCI-SB-NMES1-2 (isolated from normal pleura) (Total, 3)	Association of EZH2 with miRNA expression	qRT-PCR - Applied Biosystems (Ref Gene: RNU44)	/	EZH2 overexpression coincided with decreased miR-101 and miR-26a levels	/
	MPM tissue (n.a.)	/	Normal pleura tissue (n.a.)		(n.a.)	/		
Weber DG *et al.* 2012 [88]	Cellular fraction of peripheral blood: MM patients (Total, 23: 12 epith, 1 sarc, 7 biph, 3 other)	/	Cellular fraction of periferal blood: asbestos-exposed subjects (Total, 17) and healthy subjects (Total, 25)	Screening and validation	TaqMan MicroRNA assays - Applied Biosystem (Ref Gene: miR-125a)	MirVana miRNA Probe Set v2.0 - Ambion	34 down-regulated and 15 up-regulated miRNAs. A cut-off for miR-103 was determined to discriminate MM patients from asbestos-exposed and healthy subjects	Accession number: GSE29707 http://www.ncbi.nlm.nih.gov/geo/
Tomasetti M *et al.* 2012 [86]	Serum: MM patients (Total, 45 other)	/	Serum: NSCLC patients (Total, 20) and healthy subjects (Total, 56)	Clinical validation	qRT-PCR - Applied Biosystems (Ref Gene: U6 RNA, cel-miR-39)	/	MiR-126 differentiated MM patients from healthy controls and NSCLC from MM, but not NSCLC from control subjects	/
Kirschner MB *et al.* 2012 [90]	Plasma: MM patients (Total, 5: 3 epith, 2 sarc)	/	Plasma: healthy subjects (Total, 3)	Screening	/	Human 8x15K miRNA Microarray Kit V3 - Agilent Technologies	15 miRNAs showed significantly higher plasma levels in patients *vs.* controls; only 3 miRNAs had previously been reported	/
	Plasma: MM patients (Total, 15: 9 epith, 2 sarc, 3 biph, 1 other)	Free hemoglobin level < 0.25	Plasma: healthy subjects (Total, 14)	Test	microRNA-specific TaqMan Assays - Applied Biosistems (Ref Gene: miR-16)	/	MiR-625-3p, miR-29c*, and miR-92a levels were higher in MM patients *vs.* controls	
	Serum: MM patients (Total, 30: 29 epith, 1 other)	Free hemoglobin level < 0.25	Serum: asbestosis (Total, 10)	Validation	microRNA-specific TaqMan Assays - Applied Biosistems (Ref Gene: miR-16)	OpenArray platform - Applied Biosystens	MiR-625-3p levels discriminated MM patients from asbestosis patients (accuracy 79.3%, sensitivity 70%, specificity 90%)	
	FFPE tissue-LCM: MM (Total, 18: 15 epith, 3 biph)	LCM	FFPE tissue: pericardium (Total, 7)	Tissues analysis	microRNA-specific TaqMan Assays - Applied Biosistems (Ref Gene: RNU6B)	/	Only high miR-625-3p level was confirmed	
Andersen M *et al.* 2012 [83]	FFPE tissue: MPM (Total, 13 epith)	/	FFPE tissue: diagnostic biopsies (Total, 12) and NNP treat (Total, 13)	Analysis of 4 previously reported miRNAs	TaqMan MicroRNA Assays - Applied Biosystems (Ref Gene: RNU6B)	/	Significant downregulation of miR-17-5p and upregulation of miR-221 (opposite of expression pattern previously reported in cell lines)	/

Xu Y *et al.* 2013 [75]	Fresh frozen tissue: (Total, 25: 18 epith, 3 sarc, 4 biph)	> 80%	Fresh tissue: normal pleura (Total, 6)	Screening and validation	ViiA™ 7 RT-PCR System - Applied Biosystems (Ref Gene: RNU44)	Human miRNA BeadChip v2 - Illumina	MiR-1 is downregulated in MM and its forced expression induces growth arrest and apoptosis	Accession number: GSE40345 http://www.ncbi.nlm.nih.gov/geo/
Reid G *et al.* 2013 [94]	FFPE tissue: MPM (Total, 60: 46 epith, 16 biph)	/	FFPE tissue: normal pleura (Total, 23)	Analysis and validation of 4 miRNAs	microRNA-specific TaqMan assays - Applied Biosistems (Ref Gene: RNU6B)	/	MiR-15/16 family is downregulated and has tumor suppressor function in MPM	/
	Cell lines: H2052, H2452, H28, H226, MSTO-211H (Total, 5) and cell cultures: MM05 (primary mesothelioma cell line)	/	Cell line: MeT-5A (immortalized mesothelial cell line) (Total, 1)					
Cioce M *et al.* 2013 [76]	FFPE tissue: MPM (Total, 29: 25 epith, 3 biph, 1 desm)	/	FFPE tissue: mesothelial cysts (Total, 12)	Screening	/	Human miRNA microarray V2 Rel.16 - Agilent Technologies	MiR-145 downregulation is a characteristic trait of malignant *vs.* benign mesothelial tissue	/
	Fresh tissue: MPM (Total, 6), fresh frozen tissue: MPM (Total, 36)	/	Fresh-frozen tissue: normal pleura (Total, 14) and matched peritonea (Total, 36)	Double step validation	TaqMan MiRNA Assays - Applied Biosystems (Ref Gene: RNU6B, RNU49)	/		
	Cell lines: H2052, H2452, H28, H226, MSTO-211H (Total, 5) and cell cultures: MM05 (primary mesothelioma cell line)		Cell line (mesothelial cell line, Total, 1)					
Cheng YY *et al.* 2013 [95]	Cell lines: H2052, H2452, H28, H226, MSTO, REN (Total, 6) and cell cultures: MM05 (primary mesothelioma cell line)	/	Cell cultures: HMCs (normal human mesothelial cells) (Total, 1) and cell line MeT-5A (immortalized mesothelial cell line) (Total, 1)	Screening and validation	miRNA-specific TaqMan assays - Life Technologies (Ref Gene:	Ncode Human miRNA Microarray V3 system - Life Technologies	4 miRNAs were higher in MPM cells with reduced *ZIC1* expression	/
	FFPE tissue-LCM: MPM (Total, 27/31: 27 epith, 4 biph)	LCM	/	Analysis of expression status and survival	miRNA-specific TaqMan assays - Life Technologies (Ref Gene: RNU6B)	/	Higher expression in tumors correlates with shorter survival	
Andersen M *et al.* 2014 [77]	FFPE tissue: preoperative MPM diagnostic biopsy and post-treatment samples (Total, 5+5 epith)	40-85%	FFPE tissues: NNP post treatment (Total, 5)	Screening	miRCURY LNA Universal RT miRNA Ready-to-Use PCR, Human panels I + II version 2.M - Exiqon A/S (Ref Gene: SNORD49A)	/	23 miRNAs are differentially expressed between groups; chemotherapy reduces the differential expression	Accession number: GSE54394 http://www.ncbi.nlm.nih.gov/geo/
	FFPE tissues: post-treatment MPM samples (Total, 40: 18 epith, 22 biph)	>50%	FFPE tissues: NNP treat (Total, 14) and PTHX (Total, 5)	Double step validation	TaqMan miRNA Assays - Life Technologies (Ref Gene: SNORD49A)	/	A 4-miRNA (miR-126, miR-143, miR-145, miR-652, downregulated) diagnostic classifier distinguishes MPM from NNP with high overall	
	FFPE tissues: MPM preoperative diagnostic	>40%						

	biopsies (Total, 12: 9 epith, 3 biph)						accuracy	
Riqueleme E *et al.* 2014 [96]	Cell lines: H28, H2452, HP10, HP7, HCT4012, H2052, MSTO-211H (Total, 7)	/	/	MiRNA analysis of in 8q24 region	TaqMan MicroRNA Assays - Applied Biosystems (Ref Gene: U6)	/	Different expression level of miRNAs spanning the *PVT1* region in MPM cell lines	/
Ramírez-Salazar EG *et al.* 2014 [78]	FFPE macro-dissected MPM tissues: (Total, 5 epith)	> 80%	FFPE tissues: PP (Total, 4), HP (Total, 5), Ctrl group (adjacent non-cancerous - non-inflammatory tissue, Total, 5).	Profiling	/	TaqMan Array Human MicroRNA Panel v2.0 (A+B) - Applied Biosystems	Bioinformatic and network analysis of deregulated miRNAs (19 in MM *vs.* Ctrl group)	/
Matsumoto S *et al.*2014 [97]	FFPE macro-dissected MPM tissues: (Total, 25: 16 epith, 5 sarc, 4 biph)	> 90%	FFPE tissue: RMPs (Total, 20)	Analysis of miR-31	TaqMan Universal PCR Master Mix, No AmpErase UNG and TacMa miRNA-specific Primers - Applied Biosystems (Ref Gene: RNU6B)	/	MiR-31 is down-regulated in MM *vs.* RMP, but miR-31 upregulation in MM patients with sarcomatoid component is significantly associated with a worse prognosis	/
Weber DG *et al.* 2014 [89]	Cellular fraction of peripheral blood: MM patients (Total, 43: 28 epith, 5 sarc, 6 biph, 4 other)	/	Cellular fraction of periferal blood: asbestos-exposed subjects (Total, 52)	Analysis of miR-103a-3p	TaqMan miRNA Assays - Life Technologies (Ref Gene: miR-125a)	/	Combination of miR-103a-3p and mesothelin showed 95% sensitivity and 81% specificity in discriminating epith and biph MM from controls	/
Kirschner MB *et al.* 2015 [79]	FFPE tissues: 8 long-term and 8 short-term MPM survivors (Total, 16 epith)	LCM	8 epith short-term *vs.* 8 epith long-term survivors	Discovery set	/	Agilent Technologies Human 8x15 k microRNA Array Kit V3 - Agilent Technologies	A 6-miRNA signature (miR-score) is associated with longer survival in MM patients undergoing EPP and palliative surgery	Accession number: GSE59180 http://www.ncbi.nlm.nih.gov/geo/
	FFPE tissues: MPM EPP including patients who received chemotherapy (13/48) and those who died <8 weeks after surgery (2/48) (Total, 48: 31 epith, 17 biph)	LCM	Median expression of miRNAs observed across all samples	Training set	Stem-loop primers and hydrolysis probes - Life Technologies (Ref Gene: RNU6B)	/		
	FFPE tisue: MPM patients undergoing (Total, 43: 25 epith, 5 sarc, 13 biph)	LCM		Validation set				
Ak G *et al.* 2015 [80]	Fresh-frozen tissue: MPM patients (Total, 18: 10 epith, 4 sarc, 4 biph)	> 50%	Fresh-frozen tissue: from BAPE patients (Total, 6)	Profiling	/	TaqMan Human MicroRNA Array Card A - Applied Biosystems	11 significantly up-regulated miRNAs in MPM compared with BAPE	/
Birnie KA *et al.* 2015 [98]	Cell lines: NO36, JU77, LO68 (MPM cell lines) (Total, 3)	/	Primary human mesothelial cells and Met-5A	Profiling and Validation of miR-223	TaqMan Universal PCR Master Mix, No AmpErase UNG - Life Technologies (Ref Gene: RNU48, RNU44, SNOR202)	Taqman Open Array - Life Technologies	MiR-223 showed reduced levels in MPM specimens. MiR-223 targets STMN1, a microtubule regulator associated with MPM.	/

	Cell lines: NO36, JU77, LO68, CRL2081, CRL5820 (MPM cell lines) (Total, 5) and mouse MPM cel lines (Total, 3)	/	Human and mouse mesothelial cells	Validation of miR-223	TaqMan Universal PCR Master Mix, No AmpErase UNG - Life Technologies (Ref Gene: RNU48, RNU44, SNOR203)	/		
	FFPE tissues: MPM (Total, 17: histology n.a.)	/	FFPE tissues: pericardial mesothelium samples (Total, 6)	Validatioin of miR-223	TaqMan Universal PCR Master Mix, No AmpErase UNG - Life Technologies (Ref Gene: RNU6B)	/		
	Cells from pleural effusion of MPM patients (histology n.a.)	/	Cells from pleural effusion of benign diseases	Profiling and Validation of miR-223	TaqMan Universal PCR Master Mix, No AmpErase UNG - Life Technologies (Ref Gene: RNU6B)	Taqman Open Array - Life Technologies		
Williams *M et al.* 2015 [99]	FFPE tissues: 59 EEP and 61 P/D (Total, 120: 72 epith, 9 sarc, 39 biph)	/	FFPE tissue: normal mesothelium (Total, 23)		See Reid G et al. 2013 and Kirschner MB et al. 2014	/	Levels of mature miR-193a-3p and miR-192 are reduced in MPM	/
	Cell lines H28, H2052, H2452, H226, MSTO-211H, MM05, VMC23, P31 , SPC111 and SPC212 (Total, 10)	/	MeT-5A, non-small cell lung cancer line A549 and LP9 (Total, 3)		TaqMan low-density array cards - LifeTechnologies (Ref Gene: RNU48)	/		
Lamberti M *et al.* 2015 [91]	Serum: MM patients (Total, 14: 7 epith, 3 sarc, 4 biph)	/	Serum: non-cancer-related pleural effusion patients (Total, 10)	Profiling and Validation	TaqMan microRNA Assays - Applied biosistems (Ref Gene: miR-16)	Megaplex Microfluidic Card Pool A - Applied Biosystems	Two distinctive miRNA signatures predicting histotype and survival in patients	

Note: characteristics of samples, miRNA detection methods, relevant findings, submission of array data to a public repository (GEO or ArrayExpress) are reported. Studies are listed by year of publication. The following abbreviations describe sample characteristics as reported in relevant papers. **BAPE:** benign asbestos-related pleural effusion, **biph:** epithelioid-sarcomatoid, **Ctrl group:** adjacent non-cancerous – non-inflammatory tissue, **DB:** preoperative diagnostic biopsies, **EPP:** extrapleural pneumonectomy, **epith:** epithelioid, **HP:** atypical mesothelial hyperplasia, **lym:** lymphohistiocytic, non-epithelioid or sarcomatoid and mixed, **n.a.:** not available, **NNP:** patient-matched non-neoplastic pleura, **PB:** peripheral blood, **P/D:** pleurectomy ± decortication, **PP:** pachypleuritis/chronic inflammation, **PTHX:** non-neoplastic reactive mesothelial proliferation due to pneumothorax, **RMPs:** reactive mesothelial proliferations, **sarc:** sarcomatoid, **treat:** three series of cisplatin and vinorelbine treatments, **WT:** non-transfected MM cell line.