Supporting Information

Pichiorri *et al.* 10.1073/pnas.0806202105

SI Methods

Cell Collection and Total RNA Purification. Samples included PCs from 16 newly diagnosed cases of MM, 6 patients with MGUS, and 6 healthy donors (normal PCs). Written informed consent was obtained in keeping with institutional policies. PC isolation from mononuclear cell fraction was performed by immunomagnetic bead selection with monoclonal mouse anti-human CD138 antibodies using the AutoMACs automated separation system (Miltenyi-Biotec). PC purity is shown in Table 2, immunocytochemistry for cytoplasmic light-chain Ig (Ig), and morphology by Wright-Giemsa staining. Three of the six healthy PCs were obtained from ALLCELLS, and the purity of PCs was assessed by FACScan Analysis and was more than 80%. MM cell lines (listed in Table S3) [courtesy of Dr M. Kuehl (National Cancer Institute, MD), Dr. Joshua Epstein (Little Rock, AR), Dr. S. Rosen (Chicago, IL), Dr. M. Gramatzki (Kiel, Germany)] and an EBV-transformed B-lymphoblastoid cell line (ARH-77, ARK, UCLA-1) were grown as recommended (American Type Culture Collection). Total RNA was isolated with TRIzol extraction reagent (Invitrogen).

Luciferase Reporter Vectors. PCAF and SOCS1 3′UTR containing predicted microRNA binding site were amplified by PCR from genomic DNA (293T/17cells) and inserted into pGL3 control vector (Promega) by using an XbaI site immediately downstream from the stop codon of firefly luciferase. Deletion of the first six nucleotides of each complementary seed-region complementary site were inserted in mutant constructs using quick-change site-directed mutagenesis kit (Stratagene), according to the manufacturer's protocol. Primer sequences are available upon request.

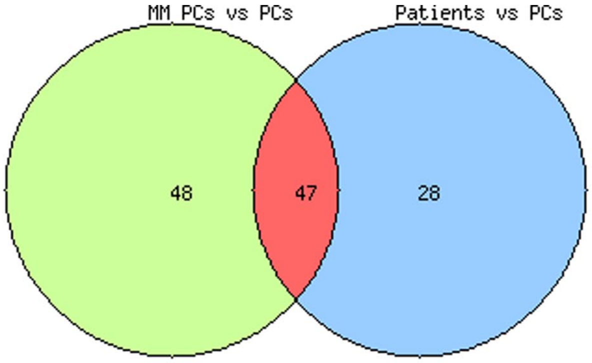
Luciferase Assays. QBI293 and Meg01 cells were cotransfected in six-well plates with 1 μg of pGL3 firefly luciferase reporter vector (see luciferase reporter vector method), 0.1 μg of the phRL-SV40 control vector (Promega), and 100-nM miRNA precursors (Ambion) using Lipofectamine 2000 (Invitrogen). Firefly and Renilla luciferase activities were measured consecutively by using the Dual Luciferase Assay (Promega) 24 h after transfection. Each reporter plasmid was transfected at least twice (on different days) and each sample was assayed in triplicate.

Xenograft Model. Studies were performed under an Institutional Animal Care and Use Committee (IACUC) approved protocol. Eight-week-old male athymic *nu*/*nu* mice (Charles River Laboratories) were maintained in accordance with IACUC procedures and guidelines. A mixture of 30 $\times$ 10^6 U266 cells or JJN3 transfected cells were suspended in 0.10 ml of extracellular matrix gel (BD Biosciences) and the mixture was injected s.c. into the right and left flanks. Serial measurements of xenograft growth were performed, and tumor volume was estimated using the formula 4/3
116 (L*W*H/8).

Western Blotting. Immunoblot analyses were performed as described (10), using: rabbit polyclonal antiSOCS-1 (Abcam); rabbit polyclonal antisera against GADPH, Bim, Stat-3, P-Stat-3 (Tyr-705) (Cell Signaling); rabbit polyclonal PCAF, and monoclonal p53 (Santa Cruz). Protein levels were normalized relative to β-ACTIN or GAPDH level, detected with appropriate antisera (Santa Cruz Biotechnology).

UV and Nutlin3a Treatment. MM1s and U266 MM cell lines were transfected with *miR-181s*, *miR-106b-25, miR-32,* and *miR-19s* ASOs as described above, and at 24 h after transfection U266 cells were treated with 10μM Nutlin3a (Cayman Chemical Company) and MM1S were treated with 6 J/m^2 UV (Ultra LUM. Inc.) and harvested at the time described in *Results* .

Data Analysis. Microarray images were analyzed by using GenePix Pro 6.0. Average values of the replicate spots of each miRNA were background-subtracted and subject to further analysis. MiRNAs were retained when present in at least 50% of samples and when at least 50% of the miRNA had a fold-change of more than 1.5 from the gene median. Absent calls were thresholded to 4.5 in log2 scale before normalization and statistical analysis. This level is the average minimum intensity level detected above background in miRNA chip experiments. Quantile normalization was implemented using the Bioconductor package/function. Differentially expressed microRNAs were identified by using the univariate *t* test within the BRB tools version 3.5.0 set with a significant univariately at alpha level equal to 0.01. This tool is designed to analyze data using the parametric test t/F tests, and random variance t/F tests. The criteria for inclusion of a gene in the gene list is either a P value less than a specified threshold value, or specified limits on the number of false discoveries or proportion of false discoveries. The latter are controlled by use of multivariate permutation test.



A MM PCs vs PCs

hsa-let-7e
hsa-let-7e*
hsa-let-7f-1*
hsa-let-7i
hsa-miR-101
hsa-miR-106b*
hsa-miR-122*
hsa-miR-125b-2*
hsa-miR-130b
hsa-miR-133a
hsa-miR-133b
hsa-miR-135a*
hsa-miR-135b*
hsa-miR-137
hsa-miR-139-3p
hsa-miR-140-5p
hsa-miR-142-5p
hsa-miR-147
hsa-miR-16
hsa-miR-17
hsa-miR-181a*
hsa-miR-181a-2*
hsa-miR-183
hsa-miR-193a-3p
hsa-miR-194*
hsa-miR-195
hsa-miR-19a
hsa-miR-21*
hsa-miR-217
hsa-miR-219-2-3p
hsa-miR-27b
hsa-miR-296-3p
hsa-miR-299-3p
hsa-miR-29a
hsa-miR-29c
hsa-miR-301a
hsa-miR-302a
hsa-miR-302c
hsa-miR-30c
hsa-miR-30e
hsa-miR-320
hsa-miR-323-3p
hsa-miR-324-3p
hsa-miR-33a
hsa-miR-342-3p
hsa-miR-34b
hsa-miR-367*
hsa-miR-374a*

C Common miRNAs

hsa-miR-100
hsa-miR-103
hsa-miR-106a
hsa-miR-106b
hsa-miR-107
hsa-miR-125a-3p
hsa-miR-125b
hsa-miR-130a
hsa-miR-138-1*
hsa-miR-146a
hsa-miR-15b
hsa-miR-16-2*
hsa-miR-181a
hsa-miR-181b
hsa-miR-188-5p
hsa-miR-191
hsa-miR-192*
hsa-miR-193a-5p
hsa-miR-196b
hsa-miR-198
hsa-miR-19b
hsa-miR-208
hsa-miR-20a
hsa-miR-21
hsa-miR-214
hsa-miR-221
hsa-miR-223
hsa-miR-23a
hsa-miR-23a*
hsa-miR-23b
hsa-miR-25
hsa-miR-26a
hsa-miR-26a-1*
hsa-miR-26b
hsa-miR-27a
hsa-miR-30a
hsa-miR-30b*
hsa-miR-30d
hsa-miR-32
hsa-miR-323-5p
hsa-miR-328
hsa-miR-335
hsa-miR-335*
hsa-miR-376c
hsa-miR-92a
hsa-miR-93
hsa-miR-95

B Patients vs PCs

hsa-miR-101*
hsa-miR-105*
hsa-miR-129-3p
hsa-miR-148a*
hsa-miR-149
hsa-miR-15a
hsa-miR-181c*
hsa-miR-186
hsa-miR-187
hsa-miR-190
hsa-miR-19b-1*
hsa-miR-200b
hsa-miR-200c*
hsa-miR-202
hsa-miR-218
hsa-miR-25*
hsa-miR-302b
hsa-miR-302d*
hsa-miR-30a*
hsa-miR-30c-1*
hsa-miR-338-3p
hsa-miR-339-5p
hsa-miR-33b
hsa-miR-346
hsa-miR-373*
hsa-miR-7
hsa-miR-92a-1*

Fig. S1. Common miRNAs expression. A Venn Diagram showing the common miRNAs (*C*) between the two class of comparisons, MM PCs versus healthy PCs (*A*) and PCs from MM patients versus healthy PCs (*B*).

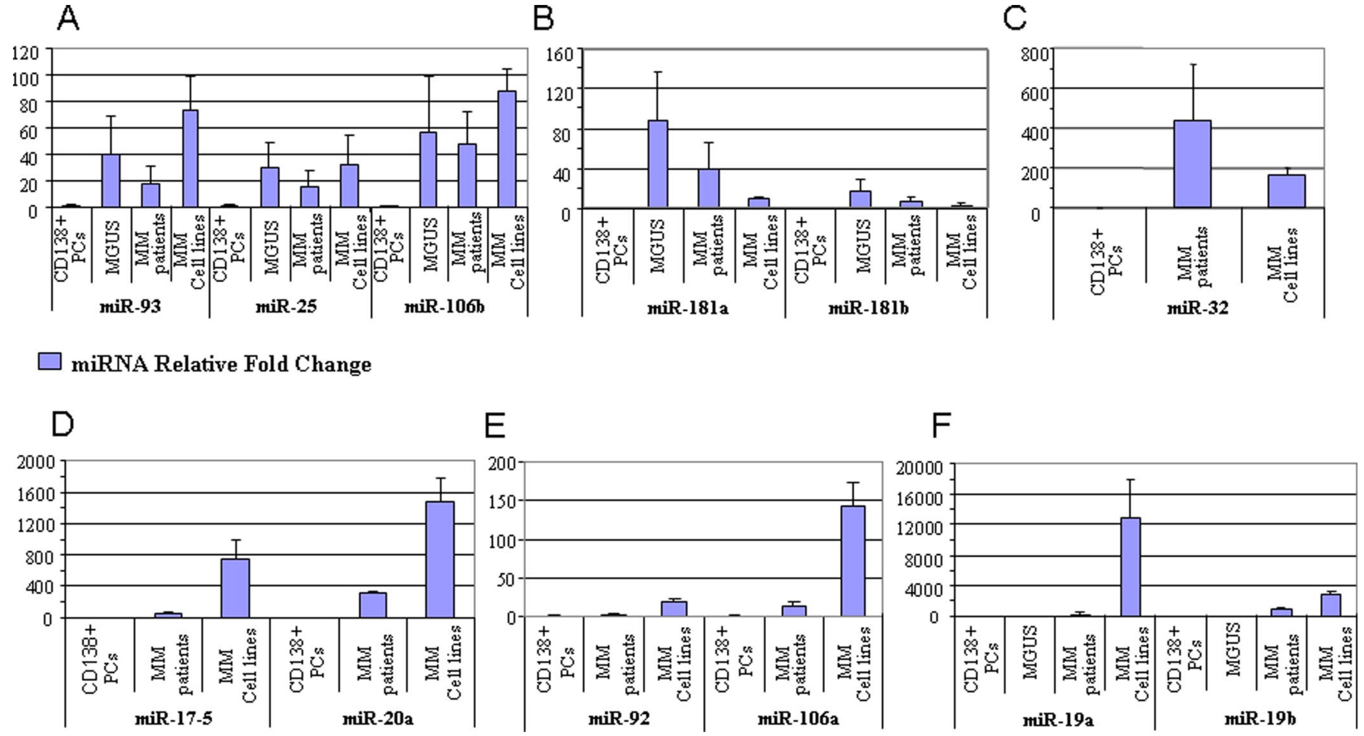


Fig. S2. Validation of microarray data in MM patients, MGUS and MM cell lines versus CD138+PCs healthy by q-RT-PCR. Average *miR-93, miR-25* and *miR-106b* (*A*), *miR-181a* and *miR-181b* (*B*), *miR-32* (*C*), *miR-17–5* and *miR-20a* (*D*), *miR-92 and miR-106a* (*E*), and *miR-19a* and *miR-19b* (*F*) expression in CD138+PCs from healthy donors ($n = 3$), from MGUS ($n = 3$), from MM patients ($n = 6$), and MM cell lines ($n = 15$) measured by q-RT-PCR. Bars represent relative fold-changes between MM PCs, MGUS, and healthy PCs ± SE. The miRNA expression between the different groups was compared after normalization with RN*U6*B.

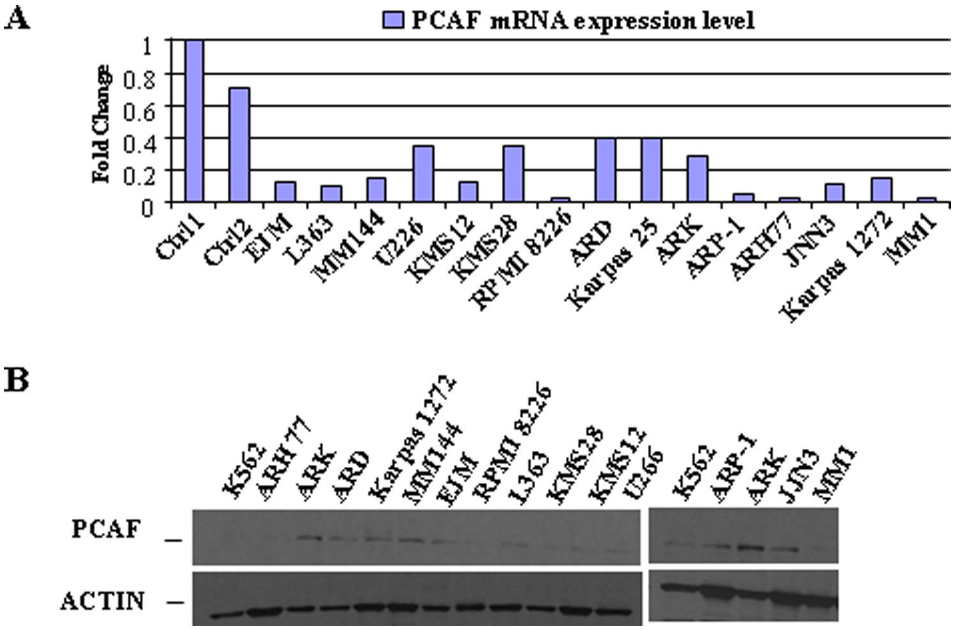


Fig. S3. PCAF expression in MM cell lines. (*A*) Real-time RT-PCR analyses for PCAF expression in 15 MM cell lines and 1 healthy CD138+PC sample. The PCR product was normalized to GADPH and ACTIN expression and each point was repeated in quadruplicate; differences were significant ($P < 0.001$). (*B*) Immunoblot analysis of 15 MM cell lines showing expression of PCAF normalized for ACTIN expression.

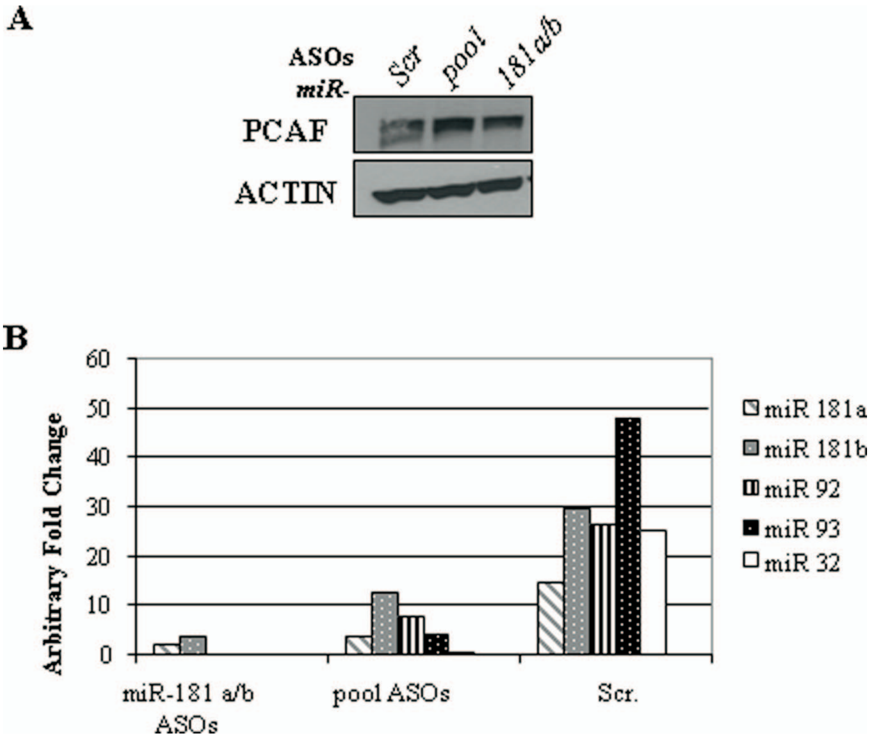


Fig. S4. Validation of ASOs transfection. (*A*) Immunoblot analysis showing PCAF protein expression in MM1s cells at 48 h after *miR-181a/b, miR-106b-25 cluster*, *miR-32* (pool) or *miR-181a/b* or scrambled ASOs transfection in MM1 cells; GADPH was internal loading control. (*B*) Stem-loop q-RT-PCR to validate the expression of endogenous *miR-181a/b, miR-106b-25 cluster*, *miR-32* at 48 h after transfection of MM1s cells with antagonizing oligonucleotides, after normalization with *U6.*

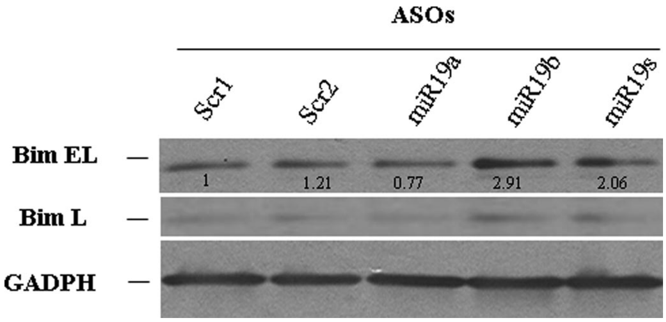


Fig. S5. *miR-17–92 cluster* targets Bim. Immunoblot analyses showing BIM-EL, BIM-L, and GADPH expression at 48 h after transfection with *miR-19a* or *miR-19b* or together ASOs in U266 cells. Densitometry based on GADPH levels shows increased level of BIM-EL and BIM-L in the presence of *miR-19b* and *miR-19a* and *b* together ASOs in U266 cells.

Table S1. Patient samples clinical data

Sample BM	Sex	Age	CD138 + PCs %	Purification
MM patients				
Pt1	F	52	75%	Miltenyi (CD138) / Trizol (RNA)
Pt2	M	69	65%	Miltenyi (CD138) / Trizol (RNA)
Pt3	F	48	85%	Miltenyi (CD138) / Trizol (RNA)
Pt4	M	59	75%	Miltenyi (CD138) / Trizol (RNA)
Pt5	M	54	90%	Miltenyi (CD138) / Trizol (RNA)
Pt6	F	53	80%	Miltenyi (CD138) / Trizol (RNA)
Pt7	M	62	80%	Miltenyi (CD138) / Trizol (RNA)
Pt8	F	71	90%	Miltenyi (CD138) / Trizol (RNA)
Pt9	F	61	70%	Miltenyi (CD138) / Trizol (RNA)
Pt10	F	49	65%	Miltenyi (CD138) / Trizol (RNA)
Pt11	M	72	83%	Miltenyi (CD138) / Trizol (RNA)
Pt12	M	80	85%	Miltenyi (CD138) / Trizol (RNA)
Pt13	F	71	97%	Miltenyi (CD138) / Trizol (RNA)
Pt14	F	47	82%	Miltenyi (CD138) / Trizol (RNA)
Pt15	M	81	96%	Miltenyi (CD138) / Trizol (RNA)
Pt16	M	37	94%	Miltenyi (CD138) / Trizol (RNA)
MGUS				
MGUS 1	M	55	70%	Miltenyi (CD138) / Trizol (RNA)
MGUS 2	M	71	75%	Miltenyi (CD138) / Trizol (RNA)
MGUS 3	F	65	70%	Miltenyi (CD138) / Trizol (RNA)
MGUS 4	M	62	92%	Miltenyi (CD138) / Trizol (RNA)
MGUS 5	M	58	50%	Miltenyi (CD138) / Trizol (RNA)
MGUS 6	F	78	73%	Miltenyi (CD138) / Trizol (RNA)
Healthy				
Healthy1	M	81	71%	Miltenyi (CD138) / Trizol (RNA)
Healthy2	M	68	75%	Miltenyi (CD138) / Trizol (RNA)
Healthy3	F	64	80%	Miltenyi (CD138) / Trizol (RNA)
Healthy4	F	45	84%	FACScan (CD138)/Trizol (RNA)
Healthy5	F	43	91%	FACScan (CD138)/Trizol (RNA)
Healthy6	F	44	81%	FACScan (CD138)/Trizol (RNA)

Table S2. miRNAs differentially expressed between MGUS versus healthy PCs

miRNA	Parametric *P* value	FDR*	Fold change
Up-regulated in MGUS			
hsa-miR-95	0.022746	0.1681209	25.91
hsa-miR-30a	0.0019756	0.127183	18.103
hsa-miR-30b	0.0082978	0.1681209	16.184
hsa-miR-26b	0.0250236	0.1690601	16.018
hsa-miR-21	0.0153221	0.1681209	15.616
hsa-miR-126	0.0335521	0.1822612	14.62
hsa-miR-142–5p	0.0100072	0.1681209	14.545
hsa-miR-26a	0.0226355	0.1681209	14.104
hsa-miR-181a	0.0266934	0.1714849	13.98
hsa-miR-330–5p	0.0029962	0.127183	13.694
hsa-miR-93	0.0164683	0.1681209	13.416
hsa-miR-17	0.0051508	0.1681209	13.365
hsa-miR-16	0.0216348	0.1681209	12.977
has-miR-1	0.0029996	0.127183	12.417
hsa-miR-200c	0.0174383	0.1681209	12.16
hsa-miR-30c	0.0147266	0.1681209	11.397
hsa-miR-195	0.0163475	0.1681209	11.022
hsa-miR-181c	0.0377125	0.1950012	10.677
hsa-miR-106b	0.0018947	0.127183	10.453
hsa-miR-23a	0.0318172	0.1822612	10.068
hsa-let-7f	0.013552	0.1681209	10.002
hsa-miR-130b	0.0024791	0.127183	9.488
hsa-miR-29b	0.0135475	0.1681209	8.606
hsa-miR-126*	0.0126018	0.1681209	8.112
hsa-miR-103	0.0153529	0.1681209	7.781
hsa-miR-133b	0.0304084	0.1822612	7.38
hsa-miR-9*	0.0498178	0.2155382	7.27
hsa-miR-29a	0.0145431	0.1681209	7.216
hsa-miR-107	0.0220383	0.1681209	7.117
hsa-miR-25	0.0206808	0.1681209	7.041
hsa-miR-376c	0.0222829	0.1681209	6.9
hsa-miR-29c	0.0096085	0.1681209	6.709
hsa-miR-106a	0.0473103	0.2155382	5.843
hsa-miR-15a	0.0155799	0.1681209	5.302
hsa-miR-148a	0.0343889	0.1822612	4.217
hsa-miR-210	0.0341297	0.1822612	4.178
hsa-miR-27a	0.0222155	0.1681209	4.106
hsa-miR-222	0.0179643	0.1681209	3.781
hsa-miR-30d	0.0389809	0.1967607	3.599
hsa-let-7c	0.0314064	0.1822612	3.313
hsa-let-7 g	0.0455525	0.2155382	2.915
Down-regulated in MGUS			
hsa-miR-187	0.0439327	0.2155382	0.4
hsa-miR-124*	0.027717	0.1728236	0.388
hsa-miR-96	0.0474581	0.2155382	0.298
hsa-miR-326	0.0255185	0.1690601	0.185
hsa-miR-328	0.0487384	0.2155382	0.152
hsa-miR-339–5p	0.0237907	0.1681209	0.099
hsa-miR-34c-3p	0.0236422	0.1681209	0.066

MiRNAs are sorted by *P* value of the univariate test (BRB tools). The first 48 genes are significant at the nominal 0.05 level of the univariate test.

*FDR, False discovery rate or *q* value is the expected percentage of genes identified by chance.[A]

Table S3. MM cell lines used for microarray analysis and stem-loop q-RT-PC

MM cell line	Microarray analysis	Stem-loop q-RT-PCR
ARH77	X	X
KMS11	X	
U266	X	X
ARK	X	X
ARP-1	X	X
Delta 47	X	
Dp6p43	X	
EJM	X	X
FLAM 76	X	
FR4	X	
H1112	X	
H929	X	
INA6	X	
JIM3	X	
JJN3	X	X
JK-6L	X	
KARPAS 620	X	
Kas6-p11p23	X	
KHM 1B	X	
KMS-12BM	X	
KMS-12PE	X	X
KMS18	X	
KMS26	X	
KMS-28BM	X	
KMS-28PE	X	X
KMS34	X	
LP1	X	
MM-M1	X	
OCI MY1	X	
OCI MY5	X	
OCI MY7	X	
OPM1	X	
PE1	X	
PE2	X	
Sachi	X	
SKMM2	X	
UCLA1	X	
XG1	X	
XG2	X	
XG6	X	
XG7	X	
RPMI8226		X
KARPAS25		X
KARPAS1272		X
L363		X
MM144		X
MM.1 s		X
ARD		X
U266		X

Table S4. miRNAs differentially expressed between MM patients and cell lines (MM PCs) versus healthy PCs

miRNA	Parametric *P* value	FDR	Fold change
Up-regulated in MM PCs			
hsa-miR-32	< 1e-07	< 1e-07	288.986
hsa-miR-25	< 1e-07	< 1e-07	224.305
hsa-miR-95	< 1e-07	< 1e-07	201.692
hsa-miR-20a	< 1e-07	< 1e-07	72.323
hsa-miR-106a	< 1e-07	< 1e-07	67.069
hsa-miR-27a	< 1e-07	< 1e-07	54.76
hsa-miR-93	< 1e-07	< 1e-07	48.178
hsa-miR-106b	< 1e-07	< 1e-07	38.494
hsa-miR-17	2.00E-07	2.60E-06	37.595
hsa-miR-19a	6.27E-05	0.000442	33.745
hsa-miR-125b	1.41E-05	0.00013	27.954
hsa-miR-181a	0.005455	0.017466	25.479
hsa-miR-100	1.00E-07	1.40E-06	25.214
hsa-miR-21	0.000197	0.001229	24.14
hsa-miR-107	< 1e-07	< 1e-07	20.1
hsa-miR-21	0.000914	0.004538	19.402
hsa-miR-33a	6.23E-05	0.000442	19.179
hsa-miR-183	0.000111	0.000722	18.952
hsa-miR-34b	5.00E-07	6.10E-06	18.494*
hsa-miR-26b	< 1e-07	< 1e-07	18.386
hsa-miR-130b	1.50E-05	0.000131	16.214
hsa-miR-191	2.00E-07	2.60E-06	15.675
hsa-miR-103	< 1e-07	< 1e-07	15.332
hsa-miR-193a-3p	0.000522	0.002918	13.738
hsa-miR-181b	0.001059	0.005161	13.735
hsa-miR-16–2*	1.30E-06	1.39E-05	13.46
hsa-miR-214	< 1e-07	< 1e-07	13.389
hsa-miR-15b	0.001777	0.007442	12.941
hsa-miR-130a	0.001496	0.006911	12.729
hsa-miR-30c	2.77E-05	0.000225	11.992
hsa-miR-142–5p	1.68E-05	0.000141	11.824
hsa-miR-92a	< 1e-07	< 1e-07	11.603
hsa-miR-376c	0.001601	0.007033	11.296
hsa-miR-27b	0.000464	0.002705	10.378
hsa-miR-26a	1.00E-07	1.40E-06	10.089
hsa-miR-30e	0.00258	0.010097	9.6
hsa-miR-195	1.00E-06	1.12E-05	9.309
hsa-miR-30a	3.40E-06	3.37E-05	8.505
hsa-miR-221	0.0026	0.010097	8.481
hsa-miR-208	0.001589	0.007033	8.479
hsa-miR-16	7.06E-05	0.000485	7.541
hsa-miR-19b	0.001988	0.008071	7.143
hsa-miR-147	0.005475	0.017466	7
hsa-miR-23a	3.55E-05	0.000273	6.982
hsa-miR-101	0.008741	0.024658	6.783
hsa-miR-192*	1.00E-07	1.40E-06	6.629
hsa-miR-146a	0.009857	0.027516	6.582
hsa-miR-133b	0.004106	0.014109	6.491
hsa-miR-30d	3.56E-05	0.000273	6.075
hsa-miR-122*	0.00168	0.007262	5.967
hsa-miR-133a	0.000748	0.003932	5.75
hsa-miR-138–1*	< 1e-07	< 1e-07	5.474
hsa-miR-23b	3.78E-05	0.000281	5.058
hsa-miR-181a-2*	0.008702	0.024658	4.222
hsa-miR-29a	0.000786	0.003975	3.788
hsa-let-7i	0.00121	0.005689	3.346
hsa-miR-320	0.002071	0.008283	2.537
hsa-miR-342–3p	0.00793	0.022851	2.332
hsa-miR-29c	0.003373	0.012596	2.293
hsa-let-7e*	0.005727	0.017846	2.027
Down Regulated in MM PCs			
hsa-miR-23a*	< 1e-07	< 1e-07	0.026
hsa-miR-223	0.007363	0.021447	0.035
hsa-miR-106b*	2.30E-06	2.37E-05	0.05
hsa-miR-125b-2*	< 1e-07	< 1e-07	0.091
hsa-miR-188–5p	0.003548	0.012848	0.117

miRNA	Parametric *P* value	FDR	Fold change
hsa-miR-323–3p	7.00E-07	8.20E-06	0.127
hsa-miR-135b*	0.004367	0.014448	0.164
hsa-miR-194*	1.17E-05	0.000112	0.202
hsa-miR-193a-5p	0.000141	0.000902	0.204
hsa-miR-335	0.004307	0.014427	0.204
hsa-miR-219–2-3p	0.00582	0.017927	0.221
hsa-miR-125a-3p	0.003838	0.013683	0.226
hsa-miR-196b	0.005648	0.017809	0.229
hsa-miR-302a	8.73E-05	0.000585	0.236
hsa-miR-374a*	1.52E-05	0.000131	0.247
hsa-miR-26a-1*	0.000311	0.001894	0.26
hsa-miR-217	0.004802	0.015694	0.274
hsa-miR-181a*	0.000765	0.003944	0.275
hsa-miR-324–3p	0.001126	0.005389	0.291
hsa-miR-135a*	0.000396	0.002358	0.315
hsa-miR-299–3p	0.00388	0.013683	0.316
hsa-miR-140–5p	0.000523	0.002918	0.333
hsa-miR-296–3p	0.006647	0.019795	0.333
hsa-miR-198	0.001776	0.007442	0.345
hsa-let-7e	0.003039	0.011634	0.391
hsa-miR-367*	0.003384	0.012596	0.415
hsa-miR-30b*	0.000627	0.003363	0.416
hsa-miR-328	0.004222	0.014321	0.476
hsa-let-7f-1*	0.000552	0.003019	0.5
hsa-miR-301a	0.0019	0.007833	0.5
hsa-miR-139–3p	0.003448	0.012657	0.515
hsa-miR-137	0.007088	0.020874	0.516
hsa-miR-21*	0.001585	0.007033	0.533
hsa-miR-335*	0.004037	0.014052	0.585
hsa-miR-302c	0.006068	0.01848	0.593
hsa-miR-323–5p	0.006495	0.019558	0.621

MiRNAs are sorted by *P* value of the univariate test (BRB tools). The first 96 genes are significant at the nominal 0.01 level of the univariate test.
*miR-34b was not detected in any of MM samples analyzed by q-RT-PCR[B]

Table S5. miRNAs differentially expressed between PCs from MM patients versus healthy PCs

miRNA	Parametric *P* value	FDR	Fold change
Up-regulated in MM patients			
hsa-miR-25	3e-07	3.18e-05	71.396
hsa-miR-32	< 1e-07	< 1e-07	51.4
hsa-miR-95	0.0012682	0.0137588	25.706
hsa-miR-20a	0.0016298	0.0143821	18.113
hsa-miR-27a	0.0046673	0.025371	14.952
hsa-miR-26b	0.0013192	0.0137588	14.922
hsa-miR-93	0.0002066	0.0043799	14.819
hsa-miR-208	3.89e-05	0.0017202	14.2
hsa-miR-23a	5.2e-05	0.0017202	13.685
hsa-miR-221	0.0003123	0.0055173	12.475
hsa-miR-106b	0.0019293	0.0157312	11.793
hsa-miR-106a	0.004788	0.0253764	11.249
hsa-miR-15b	0.0043757	0.0244118	10.19
hsa-miR-181a	0.0116724	0.0475875	9.34
hsa-miR-100	0.0023116	0.0169783	9.114
hsa-miR-21	0.0436926	0.1186381	9.109
hsa-miR-376c	0.0009224	0.0115029	9.03
hsa-miR-107	0.001696	0.0143821	8.79
hsa-miR-192*	0.0015374	0.0143821	8.631
hsa-miR-130a	0.0379689	0.1045378	8.21
hsa-miR-214	0.0083197	0.0367453	8.005
hsa-miR-16–2*	0.0040342	0.023757	7.754
hsa-miR-23b	4.83e-05	0.0017202	7.722
hsa-miR-103	0.0026865	0.0183722	7.448
hsa-miR-15a	0.0295121	0.0893795	7.257
hsa-miR-26a	0.0071042	0.0334687	7.022
hsa-miR-19b	0.0126398	0.0505592	5.976
hsa-miR-30a	0.0279578	0.0893795	5.797
hsa-miR-125b	0.0490095	0.1267075	5.563
hsa-miR-181b	0.0024624	0.017401	5.43
hsa-miR-92a	5.68e-05	0.0017202	4.662
hsa-miR-191	0.0204731	0.0711524	4.426
hsa-miR-30a*	0.0078035	0.0351988	4.284
hsa-miR-146a	0.0133744	0.0525069	4.026
hsa-miR-223	0.0372938	0.1040301	2.509
hsa-miR-138–1*	0.0055909	0.0282207	2.107
hsa-miR-30d	0.0443574	0.1186381	2.079
Down-regulated in MM patients			
hsa-miR-323–5p	0.0447691	0.1186381	0.583
hsa-miR-149	0.0364549	0.1030459	0.558
hsa-miR-335*	0.0030646	0.0191087	0.462
hsa-miR-30b*	0.0013629	0.0137588	0.461
hsa-miR-190	0.0075634	0.0348574	0.457
hsa-miR-328	0.0177072	0.0636259	0.421
hsa-miR-346	0.0001791	0.0042188	0.373
hsa-miR-373*	0.0011776	0.0137588	0.371
hsa-miR-198	0.0028464	0.0188574	0.279
hsa-miR-101*	0.0149276	0.0565116	0.262
hsa-miR-200c*	0.0467811	0.1224394	0.244
hsa-miR-202	0.0111322	0.046275	0.242
hsa-miR-302d*	0.0322366	0.0949189	0.24
hsa-miR-125a-3p	0.0360108	0.1030459	0.219
hsa-miR-188–5p	0.0334685	0.0971962	0.215
hsa-miR-19b-1*	0.0257773	0.0840737	0.212
hsa-miR-25*	0.0226938	0.0774264	0.196
hsa-miR-181c*	0.0246223	0.0815614	0.192
hsa-miR-129–3p	0.0286576	0.0893795	0.186
hsa-miR-302b	0.0294565	0.0893795	0.184
hsa-miR-148a*	0.0023225	0.0169783	0.168
hsa-miR-92a-1*	0.0099747	0.0422927	0.161
hsa-miR-218	0.0069806	0.0334687	0.16
hsa-miR-338–3p	0.0198039	0.0699738	0.16
hsa-miR-30c-1*	0.0094994	0.0410994	0.153

miRNA	Parametric *P* value	FDR	Fold change
hsa-miR-33b	0.002048	0.0160806	0.127
hsa-miR-7	0.0155802	0.0579474	0.123
hsa-miR-105*	0.0006145	0.0093053	0.121
hsa-miR-187	0.0030122	0.0191087	0.115
hsa-miR-26a-1*	4.25e-05	0.0017202	0.11
hsa-miR-186	0.0004738	0.0077266	0.109
hsa-miR-23a*	0.0016261	0.0143821	0.108
hsa-miR-335	8.59e-05	0.0022763	0.107
hsa-miR-200b	0.0068521	0.0334687	0.102
hsa-miR-196b	0.0032343	0.0195906	0.096
hsa-miR-193a-5p	0.0049147	0.0254126	0.096
hsa-miR-339–5p	0.0043508	0.0244118	0.091

MiRNAs are sorted by *P* value of the univariate test (BRB tools). The first 74 genes are significant at the nominal 0.01 level of the univariate test.[C]

Table S6. Common miRNAs expressed between MM PCs and MM patients

miRNA	Fold change MM patients	Fold change MM PCs
Common up-regulated		
hsa-miR-25	71.396	224.3
hsa-miR-32	51.4	288.98
hsa-miR-95	25.706	201.69
hsa-miR-20a	18.113	72.32
hsa-miR-27a	14.952	54.417
hsa-miR-26b	14.922	18.38
hsa-miR-93	14.819	48.17
hsa-miR-208	14.2	8.47
hsa-miR-23a	13.685	6.98
hsa-miR-221	12.475	8.48
hsa-miR-106b	11.793	38.49
hsa-miR-106a	11.249	67.06
hsa-miR-15b	10.19	12.9
hsa-miR-181a	9.34	25.47
hsa-miR-100	9.114	25.2
hsa-miR-21	9.109	24.14
hsa-miR-376c	9.03	11.29
hsa-miR-107	8.79	20.1
hsa-miR-192*	8.631	6.62
hsa-miR-130a	8.21	12.72
hsa-miR-214	8.005	13.38
hsa-miR-16–2*	7.754	13.46
hsa-miR-23b	7.722	5.05
hsa-miR-103	7.448	15.33
hsa-miR-26a	7.022	10.08
hsa-miR-19b	5.976	7.14
hsa-miR-30a	5.797	8.50
hsa-miR-125b	5.563	27.95
hsa-miR-181b	5.43	13.73
hsa-miR-92a	4.662	11.60
hsa-miR-191	4.426	15.67
hsa-miR-146a	4.026	6.58
hsa-miR-138–1*	2.107	5.47
hsa-miR-30d	2.079	6.0
Common down-regulated		
hsa-miR-323–5p	0.583	0.621
hsa-miR-335*	0.462	0.58
hsa-miR-30b*	0.461	0.416
hsa-miR-328	0.421	0.476
hsa-miR-198	0.279	0.345
hsa-miR-125a-3p	0.219	0.226
hsa-miR-23a*	0.108	0.027
hsa-miR-335	0.107	0.201
hsa-miR-196b	0.096	0.240
hsa-miR-193a-5p	0.096	0.204

[D]