

Supplementary Data

Supplementary Materials and Methods

Identification of conserved sequences in novel MicroRNAs

Sequences of the mature forms of putative MicroRNAs were assessed for conservation in the genomes of other

species using NCBI blast. Conserved sequences were converted into a FASTA format and aligned using MultAlin (<http://multalin.toulouse.inra.fr/multalin/multalin.html>).

SUPPLEMENTARY TABLE S1. SUMMARY OF CLONED SMALL RNAs IN HUMAN MESENCHYMAL STEM CELLS

ID	Sequence of small RNA	Size	Chromosomal location	Stem-loop	Strand	Location	Start	End
hms-smR-1	CAGAGAAUCCCCGCCCGC	19	2q21.1	X	-	Intergenic	132416452	132416470
hms-smR-2	GCCGACCGCCGCCCGCCUCC	21	10q24.1	X	+	Intergenic	98592169	98592189
hms-smR-3-1	GGGGUGCAGGAGCGUGUG	18	11q13.3	X	-	Intron	68454908	68454925
hms-smR-3-2			1936.33	X	+	Intron	2104184	2104201
hms-smR-4	GCCGCCGCCGCCGUCUCCC	19	13q33.3	X	+	Exon	108518522	108518540
hms-smR-5	CCGUUCCUCCUCCUGAGA	19	Xp22.31	X	+	Intergenic	6250786	6250804
hms-smR-6	CGGAGGAAAAGAAGGGACGG	20	8q24.22	X	+	Intron	134094593	134094612
hms-smR-7	GGCGGCGGCGGCGGAGGAGC	22	5p12	X	-	Exon	45695967	45695988
hms-smR-8	AGACGAGAGAGAAGGGCA	18	10p13	X	+	Intron	13660217	13660234
hsa-miR-6086-1	GGAGGUUGGGAAGGGCAGAG	20	Xp22.2	O	+	Intron	13518333	13518352
hsa-miR-6086-2			3q21.2	X	-	Intron	124914709	124914728
hms-smR-10	ACCGCUCUCCGACCCGCC	19	19p13.3	X	+	Intron	2211048	2211066
hms-smR-11	GGGAGGACGGCGGGGCGC	18	10q22.3	X	+	Intergenic	79398465	79398482
hms-smR-12	Redundant of hms-smR-8							
hms-smR-13	GAGCGAGAGAUAGCCUGG	18	7q34	X	+	Intergenic	141616367	141616384
hms-smR-14	CUCUCCCCCGCCCCACCCCG	20	4p16.3	X	+	Exon	750087	750106
hms-smR-15	UCAAUCCUGAGUCCUGCC	18	7p14.1	X	+	Intron	37899317	37899334
hms-smR-16	Redundant of hms-smR-4							
hms-smR-17	GCCCCCGCCCCGCCUCGCC	20	9q33.3	X	+	Intergenic	128812593	128812612
hms-smR-18-1	GCAAUGGCGUGAUCUCGGCUCA	22	1q44	X	+	Intron	247806425	247806446
hms-smR-18-2			2q37.3	X	+	Intron	242507589	242507610
hms-smR-18-3			3q29	X	+	Intron	196768399	196768420
hms-smR-18-4			4q35.1	X	+	Intergenic	184548731	184548752
hms-smR-18-5			5q35.3	X	+	Intergenic	177601903	177601924
hms-smR-18-6			6q26	X	+	Intergenic	163803341	163803362
hms-smR-18-7			7q36.3	X	+	Intergenic	157887055	157887076
hms-smR-18-8			8q24.3	X	+	Exon	145172572	145172593
hms-smR-18-9			9q34.3	X	+	Intron	140152008	140152029
hms-smR-18-10			10q26.3	X	+	Intergenic	133343173	133343194
hms-smR-18-11			11q25	X	+	Intron	133947313	133947333
hms-smR-18-12			12q24.33	X	+	Intron	130977913	130977934
hms-smR-18-13			13q34	X	+	Intergenic	114069044	114069065
hms-smR-18-14			14q32.33	X	+	Intergenic	104362150	104362171
hms-smR-18-15			15q26.3	X	+	Intron	101044502	101044523
hms-smR-18-16			16q24.3	X	+	Intron	89815674	89815695
hms-smR-18-17			17q25.3	X	+	Intron	80152240	80152261
hms-smR-18-18			18q23	X	+	Intron	74762556	74762577
hms-smR-18-19			19q13.43	X	+	Intergenic	58809449	58809470
hms-smR-18-20			20q13.32	X	+	Intron	57374404	57374425
hms-smR-18-21			21q22.3	X	+	Intergenic	47915235	47915256
hms-smR-18-22			Xq28	X	+	Intron	153375275	153375296
hms-smR-18-23			Yq11.21	X	+	Intergenic	15092235	15092256
hms-smR-19	GGGAACAGAGUGCAGGGGGC	20	19p13.3	X	+	Intron	4943326	4943345
hms-smR-20	AAGAUGGUGGAGUAAGGAG	19	3q22.3	X	+	Intron	136068565	136068583
hms-smR-21	Redundant of hms-smR-18							
hms-smR-22	GCCUGCCCCGCGCCCCGCC	20	22q11.21	X	+	Intergenic	20307669	20307688
hms-smR-23-1	GGCGGCGGGGCGCGGGACG	19	14q32.2	X	-	Exon	100438315	100438333

(continued)

SUPPLEMENTARY TABLE S1. (CONTINUED)

<i>ID</i>	<i>Sequence of small RNA</i>	<i>Size</i>	<i>Chromosomal location</i>	<i>Stem-loop</i>	<i>Strand</i>	<i>Location</i>	<i>Start</i>	<i>End</i>
hms-smR-23-2			16p13.13	X	+	Exon	11349938	11349956
hms-smR-24	GCCGAGAGAGGGGGGUAGGGA	21	11q23.3	X	+	Intron	119073121	119073141
hms-smR-25	UCCGGUGAGCUCUCGCGUGGCC	21	5q13.2	X	+	Intergenic	71182646	71182666
hms-smR-26-1	CAGUGGUGGCGGCGGCGGC	19	1	X	-	Exon	172628512	172628530
hms-smR-26-2			7q22.1	X	-	Intron	101459624	101459642
hms-smR-26-3			11q21	X	-	Exon	93276460	93276478
hms-smR-26-4			14q32.12	X	+	Exon	93214856	93214874
hms-smR-26-5			16p11.2	X	+	Exon	31196396	31196414
hms-smR-26-6			19q13.12	X	+	Exon	36124656	36124674
hms-smR-27	Redundant of hms-smR-14							
hsa-miR-6087	UGAGGCGGGGGGGCGAGC	18	Xq22.3	O	+	Intergenic	108297774	108297791
hsa-miR-6088	AGAGAUGAAGCGGGGGGGCG	20	19q13.33	O	+	Intergenic	50631752	50631771
hms-smR-30	AAGAGGGACGAGAAGACCCC	20	16p13.3	X	+	Exon	1664776	1664795
hms-smR-31	GGAAGAGGAAGCAGAAGAAUG	21	2q32.3	X	+	Intergenic	192644315	192644335
hms-smR-32	GAGAUGGGCGAGCAGAGG	18	3p21.31	X	+	Intergenic	46512001	46512018
hms-smR-33-1	CUGGCACGGUGAAGAGAC	18	2p12	X	+	Intergenic	78928772	78928789
hms-smR-33-2			Xq22.3	X	+	Intergenic	108297623	108297640
hms-smR-35	CCGCCGCCCGGACCCGCGC	22	16p13.3	X	+	Exon	765212	765233
hms-smR-36	Redundant of hms-smR-30							
hms-smR-37	CUCGCGGCCAGCCCCUC	18	17q24.3	X	+	Intron	67323096	67323113
hms-smR-38	CUUCCACCGCUCGCCGCC	20	4q31.21	X	+	Intron	146449094	146449113
hms-smR-39	Redundant of hms-smR-17							
hms-smR-40-1	UGAGCCGAGAUCACGCCAUUGCC	23	1q42.12	X	+	Intergenic	227006474	227006496
hms-smR-40-2			2p14	X	+	Intron	65912635	65912657
hms-smR-40-3			3q28	X	+	Intergenic	190551934	190551956
hms-smR-40-4			5q14.1	X	+	Intergenic	79394748	79394770
hms-smR-40-5			6p25.1	X	+	Intron	5342928	5342950
hms-smR-40-6			7q11.23	X	+	Intergenic	77093414	77093436
hms-smR-40-7			8q24.13	X	+	Intergenic	123185062	123185084
hms-smR-40-8			9q31.3	X	+	Intergenic	114587185	114587207
hms-smR-40-9			11q14.1	X	+	Intron	77814617	77814639
hms-smR-40-10			12p13.33	X	+	Intron	1548231	1548253
hms-smR-40-11			14q22.1	X	+	Intron	52109197	52109219
hms-smR-40-12			15q15.2	X	+	Intergenic	43407689	43407711
hms-smR-40-13			16q12.1	X	+	Intergenic	51291589	51291611
hms-smR-40-14			17p11.2	X	+	Intron	20942820	20942842
hms-smR-40-15			18q22.2	X	+	Intergenic	67887764	67887786
hms-smR-40-16			19q13.42	X	+	Intergenic	54850863	54850885
hms-smR-40-17			20q13.12	X	+	Intergenic	44602306	44602328
hms-smR-41-1	GGAGAAGCCGGCGGGAGC	18	1p36.22	X	-	Intergenic	11968901	11968918
hms-smR-41-2			5q13.2	X	+	Intergenic	71146768	71146785
hms-smR-42	CGGGCGGCGGCGGGCGGGGC	22	18p11.22	X	+	Exon	8599682	8599703
hms-smR-43	AGACUCUACAGCGGGGA	18	3p24.1	X	+	Intron	28440463	28440480
hms-smR-44	GCGAGGGUCCUCCUGCUC	20	14q32.2	X	+	Exon	100194816	100194835
hms-smR-45	Redundant of hms-smR-4							
hms-smR-46	Redundant of hms-smR-31							
hms-smR-47-1	GGUCUAGUGGUUAGGAUUC GGCGC	24	1q44	X	+	Exon	249168455	249168478
hms-smR-47-2			2p13.3	X	-	Exon	71273529	71273552
hms-smR-47-3			6p22.1	X	+	Intergenic	28949984	28950007
hms-smR-48	CCCCCCCCGUCCCCCU	18	1p36.13	X	+	Intron	17336579	17336596
hms-smR-49	Redundant of hms-smR-28							
hms-smR-50	Redundant of hms-smR-26							
hms-smR-51	CCCCCGCCCUACCUUCCAC	20	11p15.5	X	+	Intron	620004	620023
hms-smR-52	Redundant of hms-smR-28							
hms-smR-53	Redundant of hms-smR-43							
hms-smR-54-1	CCCCGCGCCCCGCCCCGGC	20	2q37.3	X	+	Exon	240322129	240322148
hms-smR-54-2			17q21.31	X	+	Integenic	42836454	42836473
hms-smR-55	GCGGCGGCUCCGUCCCCG	18	20p11.23	X	+	Exon	18038341	18038358
hms-smR-56	GGAUGGGGCCUGAGAGAAGA	20	4q32.1	X	+	Intergenic	161763057	161763076
hms-smR-58	GGGCGGCGGAGAGGGAG	18	6p12.1	X	+	Intron	56886638	56886655

(continued)

SUPPLEMENTARY TABLE S1. (CONTINUED)

<i>ID</i>	<i>Sequence of small RNA</i>	<i>Size</i>	<i>Chromosomal location</i>	<i>Stem-loop</i>	<i>Strand</i>	<i>Location</i>	<i>Start</i>	<i>End</i>
hms-smR-59	Redundant of hms-smR-22							
hms-smR-60	CCUCCAGUUUCUUCUCCUC	19	18q12.3	X	+	Intergenic	41497631	41497649
hms-smR-61	GGGGCGGAGGCCGCGCGCCG	19	21q22.3	X	+	Exon	44496014	44496032
hms-smR-62	CGAGCGGCGCGCGCGGGG	18	9p13.3	X	+	Intergenic	35791654	35791671
hsa-miR-6090	GGGGAGCGAGGGGCGGGGC	19	11q24.3	O	+	Intron	128392325	128392343
hms-smR-64	UCGGGGCGGCGCGCGCGGGC	20	13q12.11	X	+	Intron	21277876	21277895
hms-smR-65	CAAUGGGCCGCGCGCUCGCGC	22	21q22.3	X	+	Intron	45285368	45285389
hms-smR-66	CGCCCGCCGCGCGCGCGCCG	23	16p13.3	X	+	Exon	2264782	2264804
hms-smR-67	CCCCCCCCCGUUCUUCCC	21	6p25.3	X	+	Intron	2231177	2231197
hms-smR-68	GGACAGGGAGGACAGGGAGGA	21	20p12.2	X	+	Intergenic	10969595	10969615
hms-smR-69	ACUAGGACAGCCGAGAGGGG	20	15q25.1	X	+	Intergenic	78700317	78700336
hms-smR-70	CCUUCUGAACCCGGGACC	18	7p12.2	X	+	Intron	49904347	49904364
hms-smR-71	Redundant of hms-smR-55							
hms-smR-72	Redundant of hms-smR-44							
hms-smR-73	Redundant of hms-smR-35							
hms-smR-75	Redundant of hms-smR-54							
hms-smR-76	GAACCCGACUCCCUUUCG	18	2q36.3	X	+	Intron	230045521	230045538
hms-smR-77	Redundant of hms-smR-61							
hms-smR-78	Redundant of hms-smR-63							
hms-smR-79	GAAGGGCAGGCCCGCAGGA	19	17q25.3	X	+	Intron	79290083	79290101
hms-smR-80	Redundant of hms-smR-26							
hms-smR-82	Redundant of hms-smR-65							
hms-smR-83	Redundant of hms-smR-35							
hms-smR-84	Redundant of hms-smR-10							
hms-smR-85	Redundant of hms-smR-58							
hms-smR-86	GCCCGUCCCUACACAAGCC	19	2q36.3	X	+	Intron	227603351	227603369
hms-smR-87	CACGUCUGAUCUGAGGUCGCG	21	17q12	X	+	Intron	33478255	33478275
hms-smR-88	CCCUUCUCCCCCAACUCU	19	16q21	X	+	Intergenic	58024643	58024661
hsa-miR-6089	GGAGGCCGGGUGGGGCGG GGCGG	24	Xp22.33	O	+	Intergenic	2537270	2537293
hms-smR-90	Redundant of hms-smR-64							
hms-smR-91	GGCGGCGGGGGAGAAGG	18	22	X	+	Intron	43924317	43924331
hms-smR-92	CCCCCGCCUCAGUCUUUC	19	17p11.2	X	+	Intergenic	16934869	16934887
hms-smR-94	GUUUCUCAAUCCUCUCCUC	20	Xq12	X	+	Intergenic	64803673	64803692
hms-smR-95	Redundant of hms-smR-4							
hms-smR-96	Redundant of hms-smR-43							
hms-smR-97	CUGUUUCUCACUGCUGUCCUC	22	8q12.3	X	+	Intron	65576653	65576674
hms-smR-98	GGAGGUCCGUAGCAGUCCUGA	22	1q21.1	X	+	Intron	145277363	145277383
hms-smR-99	UUCCCCACCGGCCAGCCCU	20	Xq26.2	X	+	Intergenic	132410986	132411005
hms-smR-100	CCCCCGCCCCGCGUCCUC	20	Xp22.2	X	-	Intergenic	9983089	9983108

SUPPLEMENTARY TABLE S2. THE SEQUENCES OF 5 NOVEL MICRORNAs ARE CONSERVED ACROSS SEVERAL SPECIES

<i>ID</i>		<i>hsa-miR-6086</i>																			
<i>Species</i>																					
Human	G G	A G G U U G G G A A G G G C A	G A G																		
Orangutan	G G	A G G U U G G G A A G G G C A	G A G																		
Chimpanzee	G	A G G U U G G G A A G G G C A	G																		
Monkey		A G G U U G G G A A G G G C A	G A G																		
Dog	G G	A G G U U G G G A A G G G C A																			

<i>ID</i>		<i>hsa-miR-6087</i>																	
<i>Species</i>																			
Human	U G	A G G C G G G G G G C G A G C																	
Orangutan	U G	A G G C G G G G G G C G A G C																	
Chimpanzee	U G	A G G C G G G G G G C G A G C																	
Monkey	U G	A G G C G G G G G G C G A G C																	
Dog	U G	A G G C G G G G G G C G A G C																	

<i>ID</i>		<i>hsa-miR-6088</i>																	
<i>Species</i>																			
Human	A G	A G A U G A A G C G G G G G G G	G C G																
Chimpanzee		A G A U G A A G C G G G G G G G	G C G																
Monkey	A G	A G A U G A A G C G G G G G G G																	
Cattle		A G A U G A A G C G G G G G G G	G C																
Zebrafish	A G	A G A U G A A G C G G G G G G G																	

<i>ID</i>		<i>hsa-miR-6089</i>																			
<i>Species</i>																					
Human	G G A	G G C C G G G G U G G G G C G G G G C G G	C G G																		
Orangutan	G G A	G G C C G G G G U G G G G C G G G G C G G																			
Monkey		G G C C G G G G U G G G G C G G G G C G G	C G G																		
Mouse		G G C C G G G G U G G G G C G G G G C G G	C G G																		
Cattle	G G A	G G C C G G G G C G G G G C G G G G C G G	C G G																		

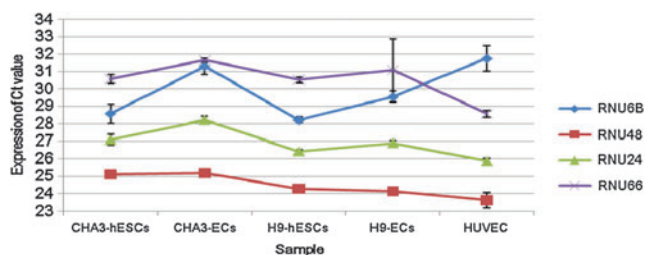
<i>ID</i>		<i>hsa-miR-6090</i>																	
<i>Species</i>																			
Human	G G G G	A G C G A G G G C G G G C																	
Orangutan	G G G G	A G C G A G G G C G G G C																	
Chimpanzee	G G G G	A G C G A G G G C G G G C																	
Monkey	G G G G	A G C G A G G G C G G G C																	
Dog	G G G G	A G C G A G G G C G G G C																	

Conserved sequence marked in gray.

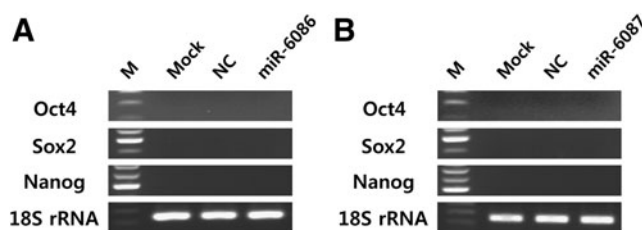
SUPPLEMENTARY TABLE S3. OLIGONUCLEOTIDE PRIMERS FOR RT-PCR OR POLY(A)-TAILED RT-PCR ANALYSIS ON MATURE MICRORNA

ID	Primer sequence (5'-3')
CDH5 3'UTR F	GCTCTAGAGCGGAAGAGCTGAGACCT
CDH5 3'UTR R	GCTCTAGAGCGTACTTGTTCATGCACC
ENG 3'UTR F	GCTCTAGAGCCTCCTCGGAGAGCAG
ENG 3'UTR R	GCTCTAGAGCTCATGGTCTGATTTATTGGT
CDH5 7mt F	CCCTGCCCTGCCGTTAAGATGTGGTCACCCATGC
CDH5 7mt R	GCATGGGTGACCACATCTTAACGGCAGGGCAGGG
ENG 7mt F	CGCGCCTACCCTTCGATAAGACCTCTCAGAGGCCTG
ENG 7mt R	CAGGCCTCTGAGAGGTCTTATCGAAGGGTAGGCGCG
Oct4 F	GACAACAATGAAAATCTTCAGGAG
Oct4 R	CTGGCGCCGGTTACAGAACCA
Sox2 F	GTGGAAACTTTTGTCCGAGAC
Sox2 R	TGGAGTGGGAGGAAGAGGTAAC
Nanog F	ATGCCTGTGATTTGTGGGCC
Nanog R	GCCAGTTGTTTTCTGCCAC
18S rRNA F	TACCTACCTGGTTGATCCTG
18S rRNA R	GGGTTGGTTTTGATCTGATA
hsa-miR-6088	AGAGATGAAGCGGGGGGGCG
hsa-miR-6089	GGAGCCCGGGTGGGGCGGGGCGG
hsa-miR-6090	GGGGAGCGAGGGGCGGGGC
RTQ-UNIr	CGAATTCTAGAGCTCGAGGCAGG
RTQ adaptor	CGAATTCTAGAGCTCGAGGCAGGCGACATGGCTGGCTAGTTAAGCTTGGTA CCGAGCTCGGATCCACTAGTCC(T) ₂₅ VN

In RTQ adaptor, V is A, G, or C; N is A, G, C, or T.
UTR, untranslated region; RT-PCR, reverse transcription-PCR.



SUPPLEMENTARY FIG. S1. Expression profile of 4 human snoRNAs as endogenous MicroRNA controls across 5 cell types.



SUPPLEMENTARY FIG. S2. hsa-miR-6086 and -6087 do not directly affect reprogramming factors, such as Oct4, Sox2, and Nanog. M (DNA size marker; Bionner D-1030).