

ERRATUM

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Numerous microRNPs in neuronal cells containing novel microRNAs

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We wish to revise the designation of the microRNAs (miRNAs) reported in Tables 1 and 2 of the original manuscript. The simultaneous publication of numerous new miRNA sequences in the same issue of *RNA* (Lagos-Quintanas, M., Rauhut, R., Meyer, J., Borkhardt, A., and Tuschl, T. 2003. New microRNAs from mouse and human. *RNA* 9: 175–179), and the report of several miRNA sequences which were not available at the time of submission of our manuscript resulted in an extensive overlap in the designation of many of the miRNAs we reported. To rectify this, we changed the designations of many of the miRNAs included in Tables 1 and 2 and adopted the designation used by others. The novel miRNAs—those not included in publications by others—are numbered sequentially beginning with miRNA 224. In addition, many of the miRNAs we

Table 1. miRNA and miRNA-like sequences associated with miRNPs in the Weri human neuronal cell line

miRNA	Number of	miRNA sequence clones	Size	Source (nt)	Predicted Precursors							
					Hs (Chr.)	Dr	Fr	Dm	Ce	Mm	Rn	
let-7a	1	UGAGGUAGUAGGUUGUUAUGUU	22	Hs	+	(9, 11, 22)	-	+	+	+	+	+
miR-15a	1	UAGCAGCACAUAAUGGUUUGUGA	23	Hs	+	(13)	+	+	-	-	-	-
miR-15b	1	UAGCAGCACAUCAUGGUUUAC	21	Hs, Mm	+	(3)	-	-	-	-	+	-
miR-19a	4	UGUGCAAAUCUAUGCAAAACUGA	23	Hs	+	(13)	-	+	-	+	-	+
miR-19b	4	UGUGCAAAUCCAUUGCAAAACUGA	23	Hs	+	(13, X)	-	+	-	-	-	+
miR-20	8	UAAAGUGCUUAUAGUGCAGGUAG	23	Hs	+	(13)	-	+	-	-	-	+
miR-21	1	AGUUAGCUUAUCAGACUGAUGUUUA	25	Hs	+	(13)	-	+	-	-	-	+
miR-27b	1	GUUCACAGUGGCUAAGUUCUG	21	Hs, Mm	+	(9)	-	+	-	-	+	+
miR-29a	1	UAGCACCAUCUGAAAUCGGUUA	22	Hs	+	(7.1, 7.2)	-	-	-	-	+	+
miR-29c	1	UAGCACCAUUAUGAAAUCGGUUA	22	Hs	+	(1)	-	+	-	-	-	+
miR-34	2	UGGCAGUGUCUUAUGCGGUUGUU	23	Hs	+	(1)	-	+	-	-	+	-
miR-91	5	CAAAGUGCUUACAGUGCAGGUAG	23	Hs	+	(13)	-	+	-	-	-	+
miR-92	3	UAUUGCACUUGUCCGCGCCUGU	22	Hs	+	(13, X)	-	+	+	-	-	+
miR-93	1	AAAGUGCUGUUCGUGCAGGUAG	22	Hs	+	(7.1, 7.2)	-	+	-	-	+	-
miR-94	1	UAAAGUGCUGACAGUGCAGAU	22	Hs	+	(7.1, 7.2)	-	-	-	-	+	-
miR-106	1	AAAAGUGCUUACAGUGCAGGUAGC	24	Hs	+	(X)	-	+	-	-	-	-
miR-124a	3	UAAGGCACGCGGUGAAUGCCAA	22	Hs	+	(8.1, 8.2, 20)	-	+	+	+	-	-
miR-181	1	AACAUUAACGCUGUCGGUGAGUU	25	Hs, Mm	+	(1, 9)	-	+	-	-	+	+
miR-183	1	UAUGGCACUGGUAGAAUUCACU	22	Hs	+	(7)	+	+	+	-	-	-
miR-224	1	CAAGUCACUAGUGGUUCCGUUUA	23	Hs	+	(X)	-	-	+	-	+	-
miR-Lk-1	1	GGACUGCCUCAGCUGUGC	18	Hs	+	(2)	-	-	-	-	-	-
miR-Lk-2	1	GUGUCCUAAAGGUGAGCUCAG	20	Hs	+	(8)	-	-	-	+	+	+
miR-Lk-3	1	GGUUGAUAGGUCGGGGUGUGAA	22	Hs, Mm	-	-	-	-	-	-	-	-
miR-Lk-4	1	AUUUCAGGUGAAGUUUCAAGAGUC	24	Hs, Mm	-	-	-	-	-	-	-	-
miR-Lk-5	1	GUGCUGAGGGAUUGGGGCUUG	20	Hs, Mm	-	-	-	-	-	-	+	+
miR-Lk-6a	1	CAAAGUGCUGUUAUGGUCAGGUAG	23	Hs	-	-	-	+	-	-	-	+
miR-Lk-6b	-	CAAAGUGCUGUUAUUGCAGG	20	-	+	(11)	-	-	-	-	-	+
miR-Lk-7	2	ACUACGAAUGAUAAACUCCGUGG	23	Hs	-	-	-	-	-	-	-	-
miR-Lk-8	1	AUGCAAGUCGAGCUUGAAGUUUC	23	Hs	-	-	-	-	-	-	-	-
miR-Lk-9	1	AUCGUUAUUUAUCGAGGCGUGA	22	Hs	-	-	-	-	-	-	-	-
miR-Lk-10	1	CGGCCUUAGUCGUCGGGGUGAUU	23	Hs	-	-	-	-	-	-	-	-
miR-Lk-11	1	AGGAGCACAGCUGGGUUAUCUAAGU	24	Hs	-	-	-	-	-	-	-	-
miR-Lk-12	1	CAACCUUGGGAUACCAACCCUGUA	23	Hs	-	-	-	-	-	-	-	-
miR-Lk-13	1	CGUAGACCCGAAACCGGGUGAC	22	Hs	-	-	-	-	-	-	-	-
miR-Lk-14	1	UACCGCAUAAUGUUGAAAGAUGG	23	Hs	-	-	-	-	-	-	-	-
miR-Lk-15	1	CGGUUCAUACCCGAAGGGUGCCAA	24	Hs	-	-	-	-	-	-	-	-
miR-Lk-16	1	AUAACGUUGAAAGAUGGCAUC	21	Hs	-	-	-	-	-	-	-	-
miR-Lk-17	1	CGAGCCGUCGUAGACCACGACGUU	24	Hs	-	-	-	-	-	-	-	-
miR-Lk-18	1	GCCGUCGUCGACGAGUGCAUU	22	Hs	-	-	-	-	-	-	-	-
miR-Lk-19	1	CAAAGUGCUUACAGUUCAGGUAG	23	Hs	-	-	-	-	-	-	-	-

The short (22–25 nt) RNAs associated with miRNPs in Weri cells were cloned as previously described (Elbashir et al., 2001), and a total of 64 clones were sequenced. **miRNAs** in bold letters were previously shown to associate with miRNPs in HeLa cells. miR-Lk-number represents small RNA sequences, identified in the miRNP complexes, that cannot be classified as miRNAs under the novel classification code for miRNAs. The sequences are shown 5' to 3'. The source (Hs; *Homo sapiens*, Mm; *Mus musculus*) indicates the species of the cell line from which the RNAs were identified. In this column, - indicates RNAs identified by sequence homology in the human genome. (Chr.); chromosomal localization of the miRNA in the human genome. Dr; *Danio rerio*, Fr; *Fugu rubripes*, Dm; *Drosophila melanogaster*, Ce; *Caenorhabditis elegans*, Mm; *Mus musculus*, Rn; *Rattus norvegicus*. + indicates fully conserved RNAs, and + represents conserved RNAs containing one or two mismatches.

reported do not, in the absence of additional data, fulfill the stringent criteria suggested as guidelines for classification of newly discovered RNAs as miRNAs as was recently published (Ambros, V., Bartel, B., Bartel, D.P., Burge, C.B., Carrington, J.C., Chen, X., Dreyfuss, G., Eddy, S.R., Griffiths-Jones, S., Marshall, M., et al. 2003. A uniform system for microRNA annotation. *RNA* **9**: 277–279). However, we are confident in the authenticity of these RNAs as assessed by co-immunoprecipitation with anti-Gemin3 antibodies and sequence determination often from multiple clones. In light of this, we refer to these RNAs as miRNA-like (miRNA-Lk-#) in the revised Tables. Four RNAs—miR-173, miR-196a, miR-196b, and miR-196c—were deleted from the Tables because their relevance to the corresponding genome could not be confirmed by additional criteria. The new designations of the novel miRNAs will be corrected in the NCBI database. We regret any potential confusion in nomenclature that our original publication may have caused. All the conclusions of the paper remain.

Table 2. miRNA and miRNA-like sequences associated with miRNPs in the MN-1 mouse neuronal cell line

miRNA	Number of clones	miRNA sequence	Size (nt)	Source	Predicted Precursors							
					Hs (Chr.)	Dr	Fr	Dm	Ce	Mm	Rn	
miR-16	1	UAGCAGCAGCUAAAUUUGGCG	22	Mm	+	(3, 13)	-	+	-	-	+	-
miR-19a	1	UGUGCAAUUCUAUGCAAAACUGA	23	Mm	+	(13)	-	+	-	+	-	+
miR-19b	2	UGUGCAAUCCAUUGCAAAACUGA	23	Mm	+	(13, X)	-	+	-	-	-	+
miR-21	1	UAGCUUAUCAGACUGAUGUUGAC	22	Mm	+	(13)	-	+	-	-	-	+
miR-22	1	AAGCUGCCAGUUGAAGAACUG	21	Mm	+	(17)	-	-	-	-	+	+
miR-23b	2	AUCACAUUGCCAGGGAUUUACCAC	23	Mm	+	(9)	-	+	-	-	-	-
miR-24	2	UGGCUAGUUCAGCAGGAACAGA	23	Mm	+	(9, 19)	-	+	-	-	+	+
miR-26b	1	UUCAAGUAAUUCAGGAUAGGUUU	23	Mm	+	(2)	-	+	-	-	+	+
miR-27	2	UUCACAGUGGCUAAGUUCGCG	21	Mm	+	(19)	-	+	-	-	+	+
miR-30d	1	UGUAAACAUCGCCGACUGGAA	22	Mm	+	(8)	-	+	-	-	+	-
miR-103	1	AGCAGCAUUGUACAGGGCUAUGA	23	Mm	+	(5, 10, 20)	-	+	-	-	+	+
miR-130	1	CAGUGCAAUGUUAAAAGGGCAU	22	Mm	+	(11)	-	+	-	-	-	+
miR-186	1	CAAAGAAUUCUCCUUUUGGGCUU	23	Mm	+	(1)	-	-	-	-	-	-
miR-199-as	1	ACAGUAGUCUGCACAUUGGUUA	22	Mm	+	(1, 9, 19)	-	+	-	-	+	+
miR-20	1	ACUGGACUUGGAGUCAAAAGG	21	Mm	+	(4)	-	-	-	-	-	-
miR-21	1	CCUGGGUGCCAAGUUUUGAC	20	Mm	+	(4)	-	-	-	-	-	-
miR-Lk-22a	1	UGAUUCGGUGGUGGUGGUGC	21	Mm	-	-	-	-	-	-	-	-
miR-Lk-22b	-	UGAUUCCGUGGUGGUGGUGC	21	-	+	(19)	-	-	-	-	-	+
miR-Lk-22c	-	UGAUUCUGUGGUGGUGGUGC	21	-	+	(11, 17)	-	-	-	-	+	+
miR-Lk-23	1	GUGCUAGGAUUGGGGCU	17	Mm	+	(4)	-	-	-	-	-	+
miR-Lk-24	1	AGCCAAUGGUGCGAAGCUA	19	Mm	+	(8, 11, 17)	-	-	-	-	+	-
miR-Lk-25	1	UGUUGAAAAAGCAUGGGAUG	20	Mm	+	(13)	-	-	-	-	+	+
miR-Lk-26	1	UAAAGUGCUGACAGCUCAGAU	22	Mm	-	-	-	-	-	-	-	-
miR-Lk-27	1	CCGUAGGCCGUGAAGCGAUC	21	Mm	-	-	-	-	-	-	-	-
miR-Lk-28	1	UUAGUAUGGUUGCCUCCAA	20	Mm	-	-	-	-	-	-	-	+
miR-Lk-29	1	UCGUCCGAGACCGAUUAUUU	21	Mm	-	-	-	-	-	-	-	-
miR-Lk-30	1	GACCUGAGAGGGUGAUCGGCCAC	23	Mm	-	-	-	-	-	-	-	-
miR-Lk-31	1	AGGCAUGGCCAGGUUGAAGCGAGG	24	Mm	-	-	-	-	-	-	-	-
miR-Lk-32	1	GUACUUAGUAGAGCAGCCAC	20	Mm	-	-	-	-	-	-	-	-
miR-Lk-33	1	GGCGUAAAGGGAGCGUACGCGGAU	24	Mm	-	-	-	-	-	-	-	-
miR-Lk-34	1	AGACCCACCAGGCGUUCGGCC	21	Mm	-	-	-	-	-	-	-	-
miR-Lk-35	1	UUAGAUGAGAUACAGGUUUUCU	22	Mm	-	-	-	-	-	-	-	-
miR-Lk-36	1	CAAAGCAGCAGUAUCGCCU	19	Mm	-	-	-	-	-	-	-	-
miR-Lk-37	1	AUGCCUGUCGGUUAUCUGCCUGCU	23	Mm	-	-	-	-	-	-	-	+
miR-Lk-38	2	CAGACAGGGUGUACAUGACCUU	22	Mm	-	-	-	-	-	-	+	-

The short (22–25 nt) RNAs associated with miRNPs in MN-1 cells were cloned as previously described (Elbashir et al., 2001), and a total of 43 clones were sequenced. **miRNAs** in bold letters were previously shown to associate with miRNPs in HeLa cells. miR-Lk-number represents small RNA sequences, identified in the miRNP complexes, that cannot be classified as miRNAs under the novel classification code for miRNAs. The sequences are shown 5' to 3'. The source (Hs; *Homo sapiens*, Mm; *Mus musculus*) indicates the species of the cell line from which the RNAs were identified. In this column, - indicates RNAs identified by sequence homology in the human genome. (Chr.); chromosomal localization of the miRNA in the human genome. Dr; *Danio rerio*, Fr; *Fugu rubripes*, Dm; *Drosophila melanogaster*, Ce; *Caenorhabditis elegans*, Mm; *Mus musculus*, Rn; *Rattus norvegicus*. + indicates fully conserved RNAs, and + represents conserved RNAs containing one or two mismatches.



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