

Clone #	microRNA	Length(bp)	% Identity
1	miR-517b	183	99.2
10	miR-519d	510	99.4
11	miR-519a-2	511	99.4
12	miR-519b	509	99.4
13	miR-519d	510	99.4
14	miR-519a-2	510	99.4
15	miR-519a-2	331	98.7
16	miR-526a-1	329	99.7
18	miR-519a-2	331	99.1
19	miR-526a-1	329	97.7
20	miR-519c	268	97.6
21	miR-522	331	98.2
22	miR-519c	268	98.8
23	miR-519c	260	98.4
24	miR-526a-1	327	98.2
25	miR-519c	267	98.8
26	miR-519b	279	98.2
27	miR-519c	172	100
28	miR-519a-1	330	97.6
29	miR-519a-1	332	97.8
51	miR-520b	476	98.7
53	miR-520b	476	98.5
54	miR-519b	470	99.4

SupplementaryTable 2. Identification of C19MC ESTs. Reverse transcription of RNA harvested from 293Ts was performed at 65° C using a C19MC pre-miRNA degenerate primer. PCRs using the initial degenerate primer (reverse) based on pre-miRNA alignments and a degenerate miR-517 or -519 primer (forward) based on sequences 5' of these pre-miR families were cloned in batch, and individual colonies sequenced (Clone #). In all, 23 clones (representing nine distinct C19MC miRNA loci) corresponded to a C19MC transcript terminating (3') within a C19MC pre-miRNA and originating (5') of the pre-miRNA. Length and % Identity refer to an alignment between an individual clone and the specific miR locus indicated. The % Identity was calculated as # identical basepairs / alignment length.