

Supplementary Table 8. Overlap of mammal/bird-specific miRNA families with genomic elements

# families overlapping with genomic element ^a (expected number ^b)							
species	transposable						total
	exon	intron	element	repetitive DNA	pseudogene	none	
human	4 (3)	91 (53)	69 (69)	6 (9)	3 (0)	33 (44)	146
macaque	9 (2)	86 (48)	41 (65)	5 (11)	1 (0)	55 (57)	161
mouse	11 (3)	63 (47)	18 (53)	11 (10)	0 (0)	63 (48)	142
opossum	10 (2)	84 (44)	30 (41)	43 (82)	0 (0)	56 (55)	169
platypus	1 (1)	16 (10)	15 (21)	2 (8)	0 (0)	32 (27)	59
chicken	8 (2)	39 (29)	13 (7)	3 (2)	0 (0)	33 (46)	84

^aMulti-member miRNA families were considered as overlapping only if all members overlap the same genomic element.

^bBased on the fraction of the genome that corresponds to the considered genomic element.

Supplementary Table 9. Number of miRNA duplication and *de novo* emergence events

species	# miRNA	# family	# events		# hit ^a	corrected # events ^b	
			<i>de novo</i>	duplication		<i>de novo</i>	duplication
human	344	239	239	105	78	184	160
macaque	345	256	256	89	73	195	150
mouse	317	234	234	83	75	183	134
opossum	417	266	266	151	60	217	200
platypus	233	143	143	90	30	116	117
chicken	231	172	172	59	29	146	85

^aNumber of blast hits between two miRNA families (see main text, Methods).

^bNumber of events assuming that cross-family blast hits reflect ancient duplication events.

Supplementary Table 10. Comparison of 1:1 orthologous mature miRNA sequences

Species comparison	N ^a	% with substitution(s)		% with shift(s)	
		seed	mature	5'	3'
human-macaque	112	0.9	4.7	6.2	13.4
human-mouse	83	2.6	8.0	13.3	27.7
human-opossum	41	0	25.6	4.9	26.8
human-platypus	30	0	29.6	10.0	36.7
human-chicken	25	0	24.0	4.0	40.0
macaque-mouse	84	1.3	6.5	11.9	17.9
macaque-opossum	47	2.2	28.9	6.4	21.3
macaque-platypus	32	0	34.4	12.5	28.1
macaque-chicken	25	0	32.0	4.0	28.0
mouse-opossum	43	0	25.0	9.3	30.2
mouse-platypus	33	0	24.1	18.1	48.5
mouse-chicken	25	0	25.0	12.0	32.0
opossum-platypus	32	0	20.0	6.2	31.2
opossum-chicken	26	0	23.1	3.8	34.6
platypus-chicken	22	0	9.5	9.1	31.8

^aSample size: number of 1:1 orthologous miRNAs.

Supplementary Table 11. Comparison of within-species paralogous mature miRNA sequences

Species	miRNA family age ^a	N ^b	% with substitution(s)		% with shift(s)	
			seed	mature	5'	3'
human	ancient	26	0.0	50.0	0.0	23.1
	recent	14	41.7	50.0	50.0	57.1
macaque	ancient	28	0.0	42.9	3.6	21.4
	recent	12	70.0	70.0	58.3	58.3
mouse	ancient	29	0.0	51.9	10.3	27.6
	recent	10	50.0	75.0	70.0	70.0
opossum	ancient	30	0.0	34.5	6.7	16.7
	recent	17	56.2	62.5	58.9	52.9
platypus	ancient	28	3.7	44.4	10.7	21.4
	recent	6	50.0	66.7	50.0	66.7
chicken	ancient	32	3.1	40.6	0.0	9.4
	recent	6	0.0	0.0	0.0	0.0

^aAncient: age > 310 MY; recent: age < 310MY.

^bSample size: number of miRNA families with within-species paralogs.

Supplementary Table 12. Previously unknown primate-specific miRNA genes with fast-evolving sites

Genomic coordinates (host gene)	# fast-evolving sites^a	tissue with highest expression	Species^d	biological process^b
18:11654884-11654940 –	7 (1)	testis ^c	Human	glucose import
1:67094135-67094189 + (<i>SGIP1</i>)	7 (3)	testis	Great apes, tarsier	macrophage differentiation
2:233415202-233415263 – (<i>TIGD1</i>)	10 (5)	cerebellum	Great apes	synaptic transmission
2:6114794-6114864 +	7 (1)	brain ^c	Human, chimp	endocytosis
3:184970998-184971058 – (<i>EHHADH</i>)	4 (1)	heart	Great apes	protein glycosylation
8:2024669-2024720 + (<i>MYOM2</i>)	7 (3)	heart ^c	Great apes	vascular permeability

^aNumber of fast-evolving sites in the precursor sequence with uncorrected $P < 0.05$ according to phyloP scores (corrected $P < 0.05$).

^bSee Methods for details of GO analysis.

^cExpression level is at least twice as high as in other tissues.

^dSpecies carrying human-orthologous precursor sequence with miRNA folding structure.

Supplementary Table 13. Genomic organization of autosomal and X(Z)-linked miRNAs

species	chromosome	count (density per Mb)			% miRNA genes	
		miRNA	family	cluster	in cluster	recent ^a
human	autosomal	292 (0.099)	206 (0.07)	35 (0.012)	43.5	54.5
	X-linked	52 (0.33*)	33 (0.21*)	8 (0.052*)	78.8 ⁺	86.5 ⁺
macaque	autosomal	292 (0.11)	218 (0.08)	38 (0.014)	42.5	51.7
	X-linked	45 (0.29*)	33 (0.21*)	9 (0.058*)	77.8 ⁺	86.7 ⁺
mouse	autosomal	267 (0.11)	198 (0.08)	37 (0.015)	45.3	47.9
	X-linked	49 (0.29*)	39 (0.23*)	7 (0.042*)	73.5 ⁺	85.7 ⁺
opossum	autosomal	260 (0.076)	221 (0.065)	35 (0.01)	32.3	49.2
	X-linked	142 (1.8*)	44 (0.55*)	11 (0.14*)	87.3 ⁺	94.4 ⁺
platypus	autosomal	40 (0.11)	38 (0.11)	7 (0.02)	40.0	22.5
	X1/X3/X5-linked	22 (0.26*)	13 (0.15)	1 (0.012)	50.0	63.6 ⁺
chicken	autosomal	193 (0.2)	151 (0.16)	24 (0.025)	30.6	37.8
	Z-linked	18 (0.24)	17 (0.23)	2 (0.027)	27.8	55.6

^aSpecific to therians, monotreme, or birds, respectively.

*Significantly higher density than in autosomes (two-sample binomial test; corrected $P < 0.05$).

⁺Significantly higher percentage than in autosomes (proportion test; corrected $P < 0.05$).