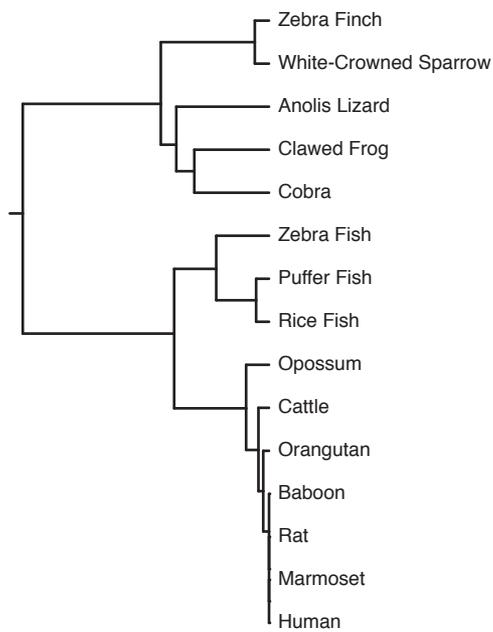


A



B

Callithrix jacchus	GCGCGTGGGCGTGTGCGGGGCGACCATGGCTGTAGACTGTTACCTC-----CAGTTCCACAGTAACAATCGAAAGCCACG-----
Pongo pygmaeus	GCGCGTGGGCGTGTGCGGGGCGACCATGGCTGTAGACTGTTACCTC-----CAGTTCCACAGTAACAATCGAAAGCCACG-----
Papio anubis	GCGCGTGGGCGTGTGCGGGGCGACCATGGCTGTAGACTGTTACCTC-----CAGTTCCACAGTAACAATCGAAAGCCACG-----
Bos taurus	GCGCGTGGGCGTGTGCGGGGCGACCATGGCTGTAGACTGTTACCTC-----CGGTCCACAGTAACAATCGAAAGCCACG-----
Rattus norvegicus	GAGCGTGGGCGTGTGCGGGGCGACCATGGCTGTAGACTGTTACCTC-----CGGTCCACAGTAACAATCGAAAGCCACG-----
Monodelphis domestica	CCGCGTGGGCGTGTGCGGGGCGACCATGGCTGTAGACTGTTACCTC-----TGGTCCACAGTAACAATCGAAAGCCACG-----
Fugu rubripes	-----TGCCCCCTAGCGACCATGGCTGTAGACTGTTACCTCAGTGGTGCAGTTGCTACAGTAACAATCTAATGCCACG-----
Oryzias latipes	-----TGCCCCCTAGCGACCATGGCTGTAGACTGTTACCTCAGTGGTGCAGTTGCTACAGTAACAATCTAATGCCACG-----
Danio rerio	-----TGCCCCCTGGCGACCATGGCTGTAGACTGTTACCTC-----GTGCCAACGCTACAGTAACAATCTAAAGCCACG-----
Anolis carolinensis	-CACGGCAACCGTCTCCAGGGCAACCGTGGCTTTAGATTGTTACTGTGC--GGACGTGGGTTTGGTAACAGTCTACAGCCATGGTTGGTCCGGCGGACGCAA-----
Ophiophagus hannah	--TCATCCTGCGTCTCCAGGGCAACCGTGGCTTTAGATTGTTACTGTGT--GGATGTGGGCT--GGTAACAGTCTACAGCCATGGTTGCCCGGACT-----
Zonotrichia leucophrys	-----GGCGACCGTGGCTTTAGATAGTTACTGTGC--CGCTGGGGG---AGTAACAGTCTACAGCCATGGTTCG-----
Taeniopygia guttata	----ATCCGACGCCCGCCGGGCGACCGTGGCTTTAGATAGTTACTGTTC--CACTGGGGG---AGTAACAGTCTACAGCCATGGTTCGCGGGGACAGGCAGACTCG---
Xenopus tropicalis	-----CTGTCTCCAGGGCAACCGTGGCTTTAGATTGTTACTGTA---GTTCTGCATT--GGTAACAGTCTACAGCCATGGTTCGCTCGGGCAAGATGC-----
Homo sapiens	-CCGCCCCCGCTCTCCAGGGCAACCGTGGCTTTGATTGTTACTGTG--GGAACGTGA---GGTAACAGTCTACAGCCATGGTTCGCCCCGCAGCACGCCACGCGC

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Figure S1. Confirmation of miR-132 sequence. A) Rooted phylogenetic tree based on the genomic miR-132 sequences of other closely related and distantly-related vertebrates. B) The genomic miR-132 sequence of white-crowned sparrows aligned with other species in ClustalW. The white-crowned sparrow miR-132 sequence was most similar to zebra finch miR-132 and more distantly related to mammalian miR-132 sequences. Asterisks indicate conservation of the given nucleotide across species. The mature region of the zlg-miR-132 sequence (highlighted in blue) had 100% homology with the human sequence hsa-miR-132.