

miR-200 family

a

chr1 (+) — miR-200b — miR-200a — miR-429 —

Name	Sequence	isomiR/canonical miRNA Ratio
hsa-miR-200b-5p 0 0 #	CATCTTACTGGGCAGCATTGGA	
hsa-miR-200b-3p 0 0	TAATACTGCCTGGTAATGATGA	
hsa-miR-200b-3p 0 +1	TAATACTGCCTGGTAATGATGAC	3.384096919
hsa-miR-200b-3p 0 +1(+1U)	TAATACTGCCTGGTAATGATGACT	2.493702431
hsa-miR-200b-3p +1 +1(+1U)	- AATACTGCCTGGTAATGATGACT	1.058009474
hsa-miR-200a-5p 0 0 #	CATCTTACCGACAGCTGTGGA	
hsa-miR-200a-3p 0 0	TAACACTGTCTGGTAACGATGT	
hsa-miR-200a-3p 0 -1	TAACACTGTCTGGTAACGATG -	0.796067898
hsa-miR-200a-3p 0 +1	TAACACTGTCTGGTAACGATGTT	1.26819602
hsa-miR-429 0 0 #	TAATACTGTCTGGTAAACCGT	
hsa-miR-429 0 -1	TAATACTGTCTGGTAAACCG -	

chr12 (+) — miR-200c — miR-141 —

Name	Sequence	isomiR/canonical miRNA Ratio
hsa-miR-200c-5p 0 0 #	CGTCTTACCCAGCAGTGTGTTGG	
hsa-miR-200c-3p 0 0	TAATACTGCCGGGTAATGATGGA	
hsa-miR-200c-3p 0 -1	TAATACTGCCGGGTAATGATGG -	0.516753753
hsa-miR-141-5p 0 0 #	CATCTTCCAGTACAGTGTGTTGGA	
hsa-miR-141-3p 0 0	TAACACTGTCTGGTAAAGATGG	
hsa-miR-141-3p 0 -1	TAACACTGTCTGGTAAAGATG -	23.15295859
hsa-miR-141-3p 0 +1	TAACACTGTCTGGTAAAGATGGC	1.946459168
hsa-miR-141-3p 0 +2	TAACACTGTCTGGTAAAGATGGCT	0.779214083

b

