

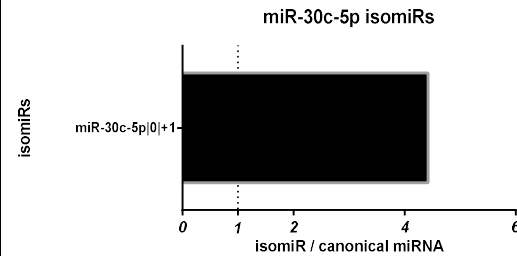
miR-30 family

a

chr1 (+) — miR-30e — miR-30c-1 —

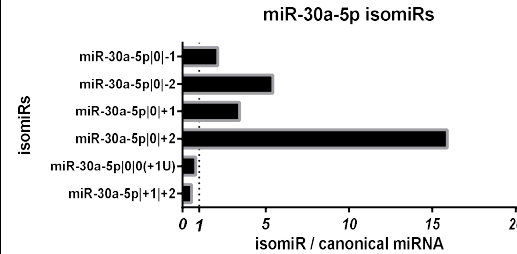
Name	Sequence	isomiR/canonical miRNA Ratio
hsa-miR-30e-5p 0 0 #	TGTAACATCCTTGACTGGAAG	
hsa-miR-30e-5p 0 -1	TGTAACATCCTTGACTGGAA -	
hsa-miR-30e-5p 0 -2	TGTAACATCCTTGACTGGA - -	
hsa-miR-30e-5p 0 +1	TGTAACATCCTTGACTGGAAGC	
hsa-miR-30e-5p 0 +2	TGTAACATCCTTGACTGGAAGCT	
hsa-miR-30e-5p 0 +2(+1U)	TGTAACATCCTTGACTGGAAGCTT	
hsa-miR-30e-5p +1 +2	- GTAAACATCCTTGACTGGAAGCT	
hsa-miR-30e-3p 0 0	CTTTCAGTCGGATGTTACAGC	
hsa-miR-30c-5p 0 0	TGTAACATCCTACACTCTCAGC	
hsa-miR-30c-5p 0 +1	TGTAACATCCTACACTCTCAGCT	4.419753371

b



chr6 (-) — miR-30a — miR-30c-2 —

Name	Sequence	isomiR/canonical miRNA Ratio
hsa-miR-30a-5p 0 0	TGTAACATCCTCGACTGGAAG	
hsa-miR-30a-5p 0 -1	TGTAACATCCTCGACTGGAA -	2.11398921
hsa-miR-30a-5p 0 -2	TGTAACATCCTCGACTGGA - -	5.411779755
hsa-miR-30a-5p 0 +1	TGTAACATCCTCGACTGGAAGC	3.427772113
hsa-miR-30a-5p 0 +2	TGTAACATCCTCGACTGGAAGCT	15.90352778
hsa-miR-30a-5p 0 0(+1U)	TGTAACATCCTCGACTGGAAGT	0.788466371
hsa-miR-30a-5p +1 +2	- GTAAACATCCTCGACTGGAAGCT	0.546994708
hsa-miR-30a-3p 0 0	CTTTCAGTCGGATGTTGCAGC	
hsa-miR-30c-2-3p 0 0 #	CTGGGAGAAGGCTGTTACTCT	



chr8 (-) — miR-30b — miR-30d —

Name	Sequence	isomiR/canonical miRNA Ratio
hsa-miR-30b-5p 0 0	TGTAACATCCTACACTCAGCT	
hsa-miR-30b-5p 0 -1	TGTAACATCCTACACTCAGC -	0.552310527
hsa-miR-30b-3p 0 0 #	CTGGGAGGTGGATGTTACTTC	
hsa-miR-30d-5p 0 0	TGTAACATCCCCGACTGGAAG	
hsa-miR-30d-5p 0 -1	TGTAACATCCCCGACTGGAA -	2.00625
hsa-miR-30d-5p 0 -2	TGTAACATCCCCGACTGGA - -	1.745275673
hsa-miR-30d-5p 0 +1	TGTAACATCCCCGACTGGAAGC	3.38984638
hsa-miR-30d-5p 0 +2	TGTAACATCCCCGACTGGAAGCT	10.08834175
hsa-miR-30d-5p 0 0(+1U)	TGTAACATCCCCGACTGGAAGT	0.351083754
hsa-miR-30d-5p 0 +2(+1U)	TGTAACATCCCCGACTGGAAGCTT	0.251441498
hsa-miR-30d-3p 0 0 #	CUUUCAGUCAGAUUUUGCUGC	

