

Table 7. Prediction of only 5' or 3' end

miRNA/cluster	Chromosome (Strand)	Genomic coordinates of the miRNA cluster	Approximate 5' boundary of the primary transcript	Approximate 3' boundary of the primary transcript	Approximate length (bp) of the primary transcript	Supporting evidences
hsa-mir-143~145	X (-)	148788674-148790489	133511337	-	-	TSS,CpG,5'CAGE
hsa-mir-424~503	X (-)	133508024-133508407	26910311	-	-	TSS,CpG,5'CAGE
hsa-mir-193a	17 (+)	26911128-26911215	61279194	-	-	TSS,CpG,5'CAGE
hsa-mir-124a-3	20 (+)	61280297-61280383	98581691	-	-	TSS,CpG,5'CAGE
hsa-mir-607	10 (-)	98578416-98578511	44079213	-	-	TSS,5'CAGE
hsa-mir-196a-1	17 (-)	44064851-44064920	103653207	-	-	TSS,CpG
hsa-mir-203	14 (+)	103653495-103653604	1901236	-	-	TSS,CpG
hsa-mir-212-132	17 (-)	1899952-1900424	133506262	-	-	CpG,Ditags
hsa-mir-542~450-2~450-1	X (-)	133502037-133503133	20336451	-	-	TSS,CpG,5'CAGE
hsa-mir-130b	22 (+)	20337593-20337674	86948918	-	-	TSS,5'CAGE
hsa-mir-7-2	15 (+)	86956060-86956169	219574684	-	-	TSS,CpG
hsa-mir-375	2 (-)	219574611-219574674	43557309	-	-	TSS,CpG,5'CAGE
hsa-mir-129-2	11 (+)	43559520-43559609	45705764	-	-	TSS,CpG
hsa-mir-565	3 (-)	45705468-45705564	44014642	-	-	TSS,CpG,5'CAGE
hsa-mir-10a	17 (-)	44012199-44012308	99842787	-	-	TSS,CpG,5'CAGE
hsa-mir-345	14 (+)	99843949-99844046	16863701	-	-	TSS,CpG,5'CAGE
hsa-mir-648	22 (-)	16843634-16843727	65305876	-	-	TSS,CpG,5'CAGE
hsa-mir-101-1	1 (-)	65296705-65296779	24081832	-	-	TSS,5'CAGE
hsa-mir-573	4 (-)	24130913-24131011	57162485	-	-	TSS,5'CAGE
hsa-mir-130a	11 (+)	57165247-57165335	28842178	-	-	TSS,5'CAGE
hsa-mir-801	1 (+)	28847698-28847793	-	-	-	ESTs,polyA
hsa-mir-614	12 (+)	12960030-12960119	-	12962140	-	ESTs,polyA
hsa-let-7b	22 (+)	44888230-44888312	-	44888453	-	ESTs