patogenesis penyakit tertentu langkah selanjutnya adalah diwakili oleh validasi hasil yang diperoleh dalam fase pertama melalui metode alternatif sebagai QRT-PCR (jika kita awalnya digunakan microarray atau sebaliknya) atau Northern Blotting. Setelah terfokus pada sejumlah calon beberapa miRs maka dimulai "in silico", target miRs disregulasi diendapkan pada database line dan untuk menguraikan hipotesis patogenesis. Akhirnya, ada perkembangan in vitro dan in vivo model overekspresi atau *downregulation* dari miRs yang dipilih. [7]

Tabel 3 : Metode Profilling miRNA [7]

	Advantages	Disadvantages	Requires Retro Transcript.	High-through-out
Northern Blotting	Supplies both qualitative and quantitative information High specificity	Laborious Low sensibility	No	No
qRT-PCR	High sensibility Requires low starting amount of total RNA Allows discrimination between miRs that differ only by few nucleotides	Requires sample manipulation (retro transcription) Technically challenging	Yes	Yes
MicroRNA microarray	Specificity Ease of automation It is able to study hundred of miRs in a single experiment	Low sensibility Requires high starting amount of total RNA	Optional	Yes
Bead based methode	Specificity Requires high starting amount of total RNA	Requires a flow cytometer Requires both amplification and hybridization steps	Yes	Yes
MIRAGE	Allows identification of new miRs	Requires both amplification and hybridization steps Requires sequencing	Yes	Yes
RAKE	High sensibility Allows discrimination between miRs that differ only by few nucleotides No sample manipulation	Requires an amplification step to magnify the signal	No	Yes

qRT-PCR : Quantitative Real Time PCR
MIRAGE : MicroRNA serial Analysis of Gene Expression
RAKE : RNA primed-Array-based Klenow Enzyme assay

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