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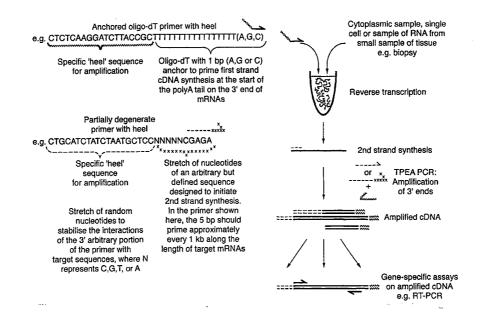
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(57) Abstract

A method is provided for the expression profiling of single cells. The method employs a first heeled primer for reverse transcription of mRNA in a sample to provide first strand cDNA species, and then a second heeled primer population to generate second strand cDNAs. The non-heeled portion of the second heeled primers are capable of hybridizing to the reverse transcribed first strands of cDNA species, at least one along the lengths thereof. Due to the presence of random and preselected sequences in the second primers a qualitatively more uniform and therefore representative cDNA profile is produced from cellular mRNAs.

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