

1. An assay method comprising
 - (a) partitioning a sample into a plurality of sub-samples, wherein said sample comprises a plurality of nucleic acid molecules, and wherein at least two sub-samples comprise at least one nucleic acid molecule;
 - (b) providing sufficient reagents in each sub-sample to amplify a target sequence or sequences;
 - (c) amplifying the target sequence(s) in the sub-sample(s) containing target sequence(s) thereby producing amplicons in the sub-sample;
 - (d) distributing the amplicons into a plurality of aliquots; and,
 - (e) for each aliquot, determining a property of amplicons in the aliquot.
 2. An assay method comprising
 - (a) partitioning a sample into a plurality of sub-samples, wherein said sample comprises a plurality of nucleic acid molecules, and wherein at least two sub-samples comprise at least one nucleic acid molecule;
 - (b) providing sufficient reagents in each sub-sample to amplify at least two different target sequences;
 - (c) amplifying target sequence(s) in at least two sub-sample(s) thereby producing amplicons in the sub-sample(s);
 - (d) combining the amplicons from said at least two sub-samples to create an amplicon pool;
 - (e) dividing the amplicon pool into a plurality of aliquots; and,
 - (f) for each aliquot, determining a property of amplicons in the aliquot.
 3. The method of claim 2 wherein the sample is partitioned into at least 10^4 sub-samples.
 4. The method of claim 3 wherein each subsample has a volume of less than 1 nanoliter.
 5. The method of claim 2 wherein said nucleic acid molecules comprise RNA.
 6. The method of claim 2 wherein sufficient reagents are provided to amplify at least 10, 20, or 50 different target sequences, if present.
 7. The method of claim 2 wherein said amplification is by PCR or RT-PCR.
 8. The method of claim 2 wherein the amplicon pool is divided into at least 10, 20, 50 or 100 aliquots.
 9. The method of claim 2 wherein the sample comprises a plurality of cells comprising nucleic acid molecules, and wherein partitioning the sample comprises partitioning intact cells into a plurality of sub-samples.
 10. The method of claim 2 wherein the sample comprises only one cell.
 11. A method for conducting an analysis, comprising:
 - (a) partitioning a sample comprising a plurality of separable cells into at least 1000 separate reaction chambers in a MPD, wherein after partitioning at least two reaction chambers each comprise exactly one cell;
 - (b) providing in each reaction chamber one or more reagents for determining a property or properties of a cell, wherein the same reagents are provided in each chamber; and
 - (c) determining at least two different properties of a single cell in a chamber and/or determining at least one property for at least two different cells in different chambers.
 12. The method of claim 11 wherein at least 99% of the reaction chambers contain zero or one cell.
 13. The method of claim 11 wherein the cells are bacterial cells.
 14. The method of claim 11 wherein said reagents comprise reagents for nucleic acid amplification.
 15. The method of claim 11 wherein at least one property is the presence or absence in the cell of a nucleic acid having a specified sequence.
 16. The method of claim 11 wherein at least one property is other than the presence or absence in the cell of a nucleic acid having a specified sequence.
 17. A method for amplification and detection of multiple target DNA sequences in a sample, said method comprising
 - a) providing a sample containing
 - i) multiple target DNA sequences,
 - ii) a primer pair corresponding to each of said multiple target DNA sequences, each pair consisting of a first primer comprising U_1 , B_1 and F domains in the order 5'- U_1 - B_1 -F-3' and a second primer comprising U_2 and R domains in the order 5'- U_2 -R-3', wherein each pair of F and R primers is capable of annealing specifically to a different target DNA sequence under stringent annealing conditions;
 - iii) a universal primer pair capable of amplifying a double stranded DNA molecule with the structure

$$5'U_1\text{-----}U_2\text{'-}3'$$

$$3'U_1'\text{-----}U_2\text{'-}3'$$
- where U_1' is the sequence complementary to U_1 and U_2' is the sequence complementary to U_2 ;
- b) subjecting the sample to multiple cycles of melting, reannealing, and DNA synthesis thereby producing amplicons for each of said multiple target DNA sequences, and
 - c) detecting the amplicons using a probe that anneals to sequence of the amplicon having the sequence of the B_1 domain or its complement.
18. The method of claim 17 wherein the sample also contains a second set of multiple target sequences, a primer pair corresponding to to each of the target sequences in the second set, each pair consisting of a first primer comprising U_1 , B_2 and F domains in the order 5'- U_1 - B_2 -F-3' and a second primer comprising U_2 and R domains in the order 5'- U_2 -R-3', wherein each pair of F and R oligonucleotides is capable of annealing specifically to a different target DNA sequence in the second set of multiple target sequences under stringent annealing conditions; and wherein amplicons for each of the multiple target DNA sequences of the second set are produced; and detecting the amplicons for each of the multiple target DNA sequences using a probe that anneals to sequence of the amplicon having the sequence of the B_2 domain or its complement.
19. The method of claim 17 wherein U_1 , B_1 , F_1 , U_2 and R_1 domains are between 6 and 25 nucleotides in length and the probe is a molecular beacon.
20. A microfluidic device, comprising
 - (a) a first region comprising
 - (i) a flow channel formed within an elastomeric material and having a first end and a second end in fluid com-