We claim:

1. A method for determining the presence of a plurality of nucleotide sequences of interest in a plurality of samples while preserving the identity of each sample, comprising the steps of:

(a) contacting each sample with a plurality of probe sets, each probe set comprising:

a first probe having a first identification sequence and a first hybridization sequence complementary to a first portion of a sequence of interest, and

a second probe having a second identification sequence and a second hybridization sequence complementary to a second portion of the same sequence of interest; wherein each of the first and the second identification sequence comprises a separate subsequence for identifying the sample and a separate subsequence for identifying the sequence of interest;

(b) joining the first and second probes of a probe set if the first hybridization sequence is hybridized to the first portion of the sequence of interest, and the second hybridization sequence is hybridized to the second portion of the same sequence of interest;

(c) decoding the identification sequences for a plurality of joined probes, wherein decoding the identification sequences comprises paired-end sequencing of the first and second identification sequences and whereby the identity of each sample is preserved; and

(d) determining the presence of the sequence of interest and the identity of the sample containing the sequence of interest based on identification sequence codes present in each joined probe, wherein said determining comprises an error detection step of:

(i) detecting joint probes having mismatched or unexpected combinations of first and second identification sequence codes; and

(ii) discarding the information obtained from those joined probes having mismatched or unexpected combinations of first and second identification sequence codes.

2. The method of claim 1, wherein the sequences of interest comprise at least one methylation polymorphism.

3. The method of claim 1, wherein the first or the second identification sequence is a single undivided identification sequence.

4. The method of claim 1, wherein the probe set further comprises a third probe having a third identification sequence and a third hybridization sequence complementary to an alternate allele of the sequence of interest.

5. The method of claim 1, wherein joining the first and second probes of at least one probe set further comprises extending the first probe with a polymerase and ligating the extended first probe to the second probe.

6. The method of claim 1, wherein the first probe further comprises a first universal primer sequence and the second probe further comprises a second universal primer sequence.

7. The method of claim 6, further comprising the step of hybridizing the joined probe to a substrate comprising oligonucleotide sequences complementary to the first universal primer sequence.

8. The method of claim 7, wherein the substrate further comprises oligonucleotide sequences complementary to the second universal primer sequence.

9. The method of claim 1, further comprising combining the joined probes of step (b) to form a plurality of joined probe sets from a plurality of samples.