CLAIMS

What is claimed is:

1. A method of determining cell type or cell states comprising:

providing a methylation profile of cell-free DNA (cfDNA) from a sample comprising plasma, wherein the methylation profile comprises co-associated CpG methylation patterns and/or methylation haplotype blocks (MHBs);

detecting cell types from the methylation profile;

assigning the detected cell types to cell states based on reference CpG values or reference MHB values determined from reference cell types or reference cell states, wherein each reference CpG value or reference MHB value corresponds to a cell type or a cell state and wherein at least one detected cell type is assigned a tumor infiltrating leukocyte (TIL) cell state; and

counting DNA molecules assigned to each reference CpG value or reference MHB value to thereby profile tumor cell states and TILs of a tumor microenvironment.

2. The method of claim 1, further comprising counting known *single* CpG methylation profiles.

3. The method of claim 1, wherein reference values are differentially methylated CpGs derived from DNA originating from known cell types and known cell states, optionally of bacterial, viral, fungal, or eukaryotic parasitic origin.

4. The method of claim 1, wherein the sample is a blood or plasma sample.

5. The method of claim 1, further comprising determining cell state-specific signatures.

6. The method of claim 1, further comprising:

profiling the TILs according to methylation signatures; and

determining the proportions of distinct TIL subsets from a cell type-specific methylation profile identified in the cell-free DNA.

7. The method of claim 1, wherein DNA is classified as originating from a normal leukocyte cell, a tumor-associated cell, or a tumor infiltrating leukocyte.

8. The method of claim 1, wherein the methylation profile for the DNA in the sample is generated using microarrays or bisulfite sequencing.