**CLAIMS**

What is claimed is:

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

(a)(i) providing or having been provided a sample comprising DNA and generating a methylation profile for the DNA in the sample; or (ii) providing or having been provided a methylation profile of the DNA in the sample, wherein the methylation profile comprises co-associated CpG methylation patterns and/or methylation haplotype blocks (MHBs) (tightly coupled CpG sites) of the DNA; and

(b) detecting cell type or cell state comprising:

(i) counting co-associated CpG methylation patterns in the DNA , wherein co-associated CpG methylation patterns comprises two or more CpGs in the DNA; or

(ii) counting MHBs;

(c) assigning the DNA to a cell type or cell state based on reference CpG values or reference MHB values, wherein reference CpG values or reference MHB values are determined from reference cell types or reference cell states; and

(d) counting DNA molecules assigned to each reference CpG value or reference MHB value, wherein each reference CpG value or reference MHB value corresponds to a cell type or a cell state.

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

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 sample, plasma, urine, saliva, stool, tissue, or biopsy sample.

5. The method of claim 1, wherein the DNA is cell-free DNA and/or a rar cell type circulating DNA and is plasma-derived.

6. The method of claim 1, further comprising determining cell state-specific signatures by the method of claim 1 or providing or having been provided cell state-specific signatures of the sample.

7. The method of claim 1, wherein:

(a) the sample comprises cell-free DNA (cfDNA); and

(b) the sample is collected from a tumor microenvironment comprising tumor infiltrating leukocytes.

8. The method of claim 1, wherein the DNA is cell-free tumor ctDNA.

9. The method of claim 1, wherein the cell state measured is from DNA from a circulating, cell-free tumor infiltrating leukocyte (TIL) and, optionally, the sample is a sample from a tumor microenvironment (TME).

10. The method of claim 9, comprising:

profiling 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.

11. 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.

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

13. A computer-aided method for detecting at least one abundance of at least one cell identity in a biological sample, the sample comprising DNA, the method comprising:

providing a plurality of reads, each read comprising a sequence of the DNA and associated methylation status;

providing a CpG library comprising a plurality of entries, each entry comprising a CpG site and a corresponding cell identity, each CpG site comprising a co-associated CpG site, and each corresponding cell identity comprising a cell type or a cell state;

transforming, using a computing device, the plurality of reads into a plurality of read assignments according to at least one assignment rule, each read assignment comprising one of a cell identity, a cell-related identity, and an unrelated identity; and

transforming, using the computing device, the plurality of read assignments into the at least one abundance, each abundance corresponding to one cell identity, each abundance comprising a total number of read assignments comprising the one cell identity.

14. The computer-aided method of claim 13, wherein the at least one assignment rule comprises at least one of:

transforming, using the computing device, the read into the cell-related identity if the read comprises no more than one CpG site from the plurality of entries of the CpG library;

transforming, using the computing device, the read into the cell identity if the read comprises at least two CpG sites from the plurality of entries of the CpG library with the same corresponding cell identity; and

transforming, using the computing device, the read into the unrelated identity if the read does not comprise any CpG site from the plurality of entries of the CpG library.

15. The computer-aided method of any one of claims 13-14, further comprising transforming, using the computing device, each abundance into at least one of a relative abundance and an absolute abundance, wherein:

each relative abundance comprises the abundance of one cell identity normalized by the total of all abundances of all cell identities; and

each absolute abundance comprises the abundance of one cell identity normalized by a sum of the abundance and the total number of read assignments.

16. The computer-aided method of any one of claims 13-15, wherein providing the plurality of reads further comprises performing bisulfite sequencing or microarray methylation profiling on the DNA.

17. A computing device configured to detect at least one abundance of at least one cell identity in a biological sample, the sample comprising DNA, the computing device comprising at least one processor and a non-volatile computer-readable media, the non-volatile computer-readable media containing instructions executable on the at least one processor to:

receive a plurality of reads, each read comprising a sequence of the DNA and associated methylation status;

provide a CpG library comprising a plurality of entries, each entry comprising a CpG site and a corresponding cell identity, each CpG site comprising a co-associated CpG site, and each corresponding cell identity comprising a cell type or a cell state;

transform the plurality of reads into a plurality of read assignments according to at least one assignment rule, each read assignment comprising one of a cell identity, a cell-related identity, and an unrelated identity; and

transform the plurality of read assignments into the at least one abundance, each abundance corresponding to one cell identity, each abundance comprising a total number of read assignments comprising the one cell identity.

18. The computing device of claim 17, wherein the at least one assignment rule comprises at least one of:

transforming, using the computing device, the read into the cell-related identity if the read comprises no more than one CpG site from the plurality of entries of the CpG library;

transforming, using the computing device, the read into the cell identity if the read comprises at least two CpG sites from the plurality of entries of the CpG library with the same corresponding cell identity; and

transforming, using the computing device, the read into the unrelated identity if the read does not comprise any CpG site from the plurality of entries of the CpG library.

19. The computing device of any one of claims 17-18, wherein the non-volatile computer-readable media further contains instructions executable on the at least one processor to transform each abundance into at least one of a relative abundance and an absolute abundance, wherein:

each relative abundance comprises the abundance of one cell identity normalized by the total of all abundances of all cell identities; and

each absolute abundance comprises the abundance of one cell identity normalized by a sum of the abundance and the total number of read assignments.

20. The computing device of any one of claims 17-19, wherein each CpG site is differentially methylated within cells of one cell identity and each co-associated CpG site comprises a sequence position proximal to at least one additional CpG site with the same corresponding cell identity.