WHAT IS CLAIMED IS:

1. A method of analyzing a blood sample of a mammal, the method comprising:

detecting a first number of methylated or unmethylated DNA fragments in a cell-free mixture of the blood sample at one or more differentially-methylated regions based on signals obtained from an assay, the cell-free mixture including cell-free DNA from a plurality of cell lineages, each of the one or more differentially-methylated regions specific to a particular hematological cell lineage by being hypomethylated or hypermethylated relative to other cell lineages;

determining a methylation level using the first number;

comparing the methylation level to one or more cutoff values;

measuring a hemoglobin level of the blood sample;

comparing the hemoglobin level to a hemoglobin threshold; and

determining a classification of a blood cancer in the mammal based on the comparing of the methylation level to the one or more cutoff values and the comparing of the hemoglobin level to the hemoglobin threshold.

2. The method of claim 1, wherein the blood cancer is leukemia.

3. The method of claim 1, wherein the blood cancer is lymphoma.

4. The method of claim 1, wherein the blood cancer is polycythemia rubra vera.

5. The method of claim 1, wherein the blood cancer is myelodysplastic syndrome.

6. The method of claim 1, further comprising:

determining a total number of DNA fragments in the cell-free mixture at the one or more differentially-methylated regions; and

determining the methylation level using the first number and the total number.

7. The method of claim 1, further comprising:

determining a volume of the cell-free mixture, wherein the methylation level is determined using the first number and the volume of the cell-free mixture.

8. The method of claim 1, further comprising identifying the one or more differentially-methylated regions by:

obtaining methylation indexes of a plurality of sites for each of the plurality of cell lineages, including the particular hematological cell lineage and the other cell lineages;

at each site of the plurality of sites, comparing the methylation indexes of the plurality of cell lineages;

identifying one or more sites of the plurality of sites that have a methylation index in the particular hematological cell lineage that is below/above a first methylation threshold and methylation indexes in each of the other cell lineages that are above/below a second methylation threshold; and

identifying a differentially-methylated region that contains the one or more sites.

9. The method of claim 1, further comprising determining the one or more cutoff values, including:

obtaining a plurality of samples, each sample known to have a particular classification of blood cancer, the plurality of samples having at least two classifications of blood cancer;

determining a methylation level of the one or more differentially-methylated regions for each of the plurality of samples;

identifying a first set of samples that have a first classification of blood cancer;

identifying a second set of samples that have a second classification of blood cancer, the first set of samples collectively having a statistically different methylation level than the second set of samples; and

determining a cutoff value that discriminates between the first set of samples and the second set of samples within a specified specificity and sensitivity.

10. The method of claim 1, further comprising:

determining that the blood cancer exists based on comparing the methylation level to the one or more cutoff values; and

performing a bone marrow biopsy in response to determining that the blood cancer exists.

11. The method of claim 1, wherein the one or more differentially-methylated regions comprise CpG sites.

12. The method of claim 11, wherein a first region of the one or more differentially-methylated region comprises a plurality of CpG sites that are within 100 bp of each other, and wherein the plurality of CpG sites are all hypomethylated or hypermethylated.

13. The method of claim 1, wherein the one or more differentially-methylated regions are hypomethylated.

14. The method of claim 1, wherein one of the one or more differentially-methylated regions is in the FECH gene.

15. The method of claim 1, wherein one of the one or more differentially-methylated regions is in chromosome 12 at genomic coordinates 48227688 – 48227701.

16. The method of claim 1, wherein one of the one or more differentially-methylated regions is in chromosome 12 at genomic coordinates 48228144 – 48228154.

17. A computer product comprising a computer readable medium storing a plurality of instructions for controlling a system to perform the method of any one of claims 1-16.

18. A system comprising:

the computer product of claim 17; and

one or more processors for executing instructions stored on the computer readable medium.

19. A system configured to perform the method of any one of claims 1-16.