

THAT WHICH IS CLAIMED:

1. A method of assaying for presence of a viral infection in a subject comprising:
obtaining a methylation pattern for a set of DNA methylation sites from a sample derived from the subject; and
analyzing the methylation pattern for the set of DNA methylation sites with an infection positive methylation classifier and/or an infection negative methylation classifier,
wherein presence of a viral infection in the subject is indicated when a score derived from the infection positive classifier exceeds a cutoff and/or threshold value indicating the presence of a viral infection.
2. The method of claim 1, wherein the viral infection is a SARS-CoV-2 infection.
3. The method of claim 2, wherein the SARS-CoV-2 infection causes COVID-19.
4. The method of any one of claims 1–3, wherein the sample is a blood sample from the subject.
5. The method of any one of claims 1–4, wherein the subject is a human subject.
6. The method of any one of claims 1–5, wherein obtaining the methylation pattern for the set of DNA methylation sites is performed on a methylation bead array.
7. The method of claim 6, wherein the methylation bead array comprises a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.
8. The method of any one of claims 1–7, wherein analyzing the methylation pattern for the set of DNA methylation sites with an infection positive methylation classifier and/or an infection negative methylation classifier comprises analyzing methylation of a set of genes

comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

9. The method of claim 8, wherein an infection positive methylation signature comprises hypomethylation of one or more genes selected from a group consisting of IFI27, ARID5B, ANLN, PARP9, MX1, CBX3B2, EPSTI1, CHSY1, MX1, and GPX1, or any subset thereof, and/or hypermethylation of one or more genes selected from a group consisting of LINC01429, CALHM2, LINC00428, OAS1, RAB40C, TSEN15, PEPD, PPL, ARID3B, ZDHHC6, TNFRSF8, DDX60, OAS2, and FGFR1, or any subset thereof.

10. The method of claim 9, wherein the infection positive methylation signature comprises hypomethylation of IFI27.

11. A method for determining likelihood of a viral infection producing acute respiratory distress syndrome in a subject comprising:

obtaining a methylation pattern for a set of DNA methylation sites from a sample derived from the subject; and

analyzing the methylation pattern for the set of DNA methylation sites with an acute respiratory distress syndrome positive methylation classifier and/or an acute respiratory distress syndrome negative methylation classifier,

wherein likelihood the subject will exhibit acute respiratory distress syndrome is indicated when a score derived from the acute respiratory distress syndrome positive classifier exceeds a cutoff and/or threshold value indicating likelihood of a viral infection producing acute respiratory distress syndrome.

12. The method of claim 11, wherein the viral infection is a SARS-CoV-2 infection.

13. The method of claim 12, wherein the SARS-CoV-2 infection causes COVID-19.

14. The method of any one of claims 11–13, wherein the sample is a blood sample from the subject.
15. The method of any one of claims 11–14, wherein the subject is a human subject.
16. The method of any one of claims 11–15, wherein obtaining the methylation pattern for the set of DNA methylation sites is performed on a methylation bead array.
17. The method of claim 16, wherein the methylation bead array comprises a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.
18. The method of any one of claims 11–17, wherein analyzing the methylation pattern for the set of DNA methylation sites with an infection positive methylation classifier and/or an infection negative methylation classifier comprises analyzing methylation of a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.
19. The method of claim 18, wherein an acute respiratory distress syndrome positive methylation signature comprises hypomethylation of one or more genes selected from a group consisting of IFI27, ARID5B, ANLN, PARP9, MX1, CBX3B2, EPSTI1, CHSY1, MX1, and GPX1, or any subset thereof, and/or hypermethylation of one or more genes selected from a group consisting of LINC01429, CALHM2, LINC00428, OAS1, RAB40C, TSEN15, REPD, PPL, ARID3B, ZDHHC6, TNFRSF8, DDX60, OAS2, and FGFR1, or any subset thereof.
20. The method of claim 19, wherein the infection positive methylation signature comprises hypomethylation of IFI27.

21. A method of determining the nature of a viral infection in a subject comprising:
obtaining a methylation pattern for a set of DNA methylation sites from a sample derived from the subject; and

analyzing the methylation pattern for the set of DNA methylation sites with a SARS-CoV-2 positive methylation classifier and/or a SARS-CoV-2 negative methylation classifier,

wherein presence of a SARS-CoV-2 infection in the subject is indicated when a score derived from the SARS-CoV-2 positive methylation classifier exceeds a cutoff and/or threshold value indicating presence of a SARS-CoV-2 infection.

22. The method of claim 21, wherein the sample is a blood sample from the subject.

23. The method of claim 1 or 2, wherein the subject is a human subject.

24. The method of any one of claims 21–23, wherein obtaining the methylation pattern for the set of DNA methylation sites is performed on a methylation bead array.

25. The method of claim 24, wherein the methylation bead array comprises a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

26. The method of any one of claims 21–25, wherein analyzing the methylation pattern for the set of DNA methylation sites with an infection positive methylation classifier and/or an infection negative methylation classifier comprises analyzing methylation of a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

27. The method of claim 26, wherein an acute respiratory distress syndrome positive methylation signature comprises hypomethylation of one or more genes selected from a group consisting of IFR7, ARID5B, ANLN, PARP9, MX1, CBX3P2, EPSTI1, CHSY1, MX1, and GPX1, or any subset thereof, and/or hypermethylation of one or more genes selected from a group consisting of LINC01429, CALHM2, LINC00428, OAS1, RAB40C, TSEN15, PEPD, PPL, ARID3B, ZDHHC6, TNFRSF8, DDX60, OAS2, and FGFR1, or any subset thereof.

28. The method of claim 27, wherein the infection positive methylation signature comprises hypomethylation of IFR7.

29. A computer-implemented method for executing the method of any one of claims 1–28.

30. A methylation bead array of DNA methylation sites comprising a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

31. A method of treating COVID-19 in a subject comprising:
obtaining a methylation pattern for a set of DNA methylation sites from a sample derived from the subject suspected of having COVID-19;
analyzing the methylation pattern for the set of DNA methylation sites with a SARS-CoV-2 positive methylation classifier and/or a SARS-CoV-2 negative methylation classifier, wherein presence of a SARS-CoV-2 infection in the subject is indicated when a score derived from the SARS-CoV-2 positive methylation classifier exceeds a cutoff and/or threshold value indicating presence of a SARS-CoV-2 infection; and
treating the subject for COVID-19 if the presence of a SARS-CoV-2 infection in the subject is indicated.

32. The method of claim 31, wherein the sample is a blood sample from the subject.

33. The method of claim 31 or 32, wherein the subject is a human subject.
34. The method of any one of claims 31–33, wherein obtaining the methylation pattern for the set of DNA methylation sites is performed on a methylation bead array.
35. The method of claim 34, wherein the methylation bead array comprises a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.
36. The method of any one of claims 1–7, wherein analyzing the methylation pattern for the set of DNA methylation sites with an SARS-CoV-2 positive methylation classifier and/or an SARS-CoV-2 negative methylation classifier comprises analyzing methylation of a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.
37. The method of claim 36, wherein an SARS-CoV-2 positive methylation signature comprises hypomethylation of one or more genes selected from a group consisting of IFI27, ARID5B, ANLN, PARP9, MX1, CBX3B2, EPSTI1, CHSY1, MX1, and GPX1, or any subset thereof, and/or hypermethylation of one or more genes selected from a group consisting of LINC01429, CALHM2, LINC00428, OAS1, RAB40C, TSEN15, REPD, PPL, ARID3B, ZDHHC6, TNFRSF8, DDX60, OAS2, and FGFR1, or any subset thereof.
38. The method of claim 37, wherein the SARS-CoV-2 positive methylation signature comprises hypomethylation of IFI27.

39. A method of treating acute respiratory distress syndrome (ARDS) in a subject suspected of having COVID-19 comprising:

obtaining a methylation pattern for a set of DNA methylation sites in a sample derived from the subject;

analyzing the methylation pattern for the set of DNA methylation sites to an ARDS positive methylation classifier and/or an ARDS negative methylation classifier, wherein likelihood the subject will exhibit acute respiratory distress syndrome is indicated when a score derived from the ARDS positive classifier exceeds a cutoff and/or threshold value indicating likelihood of a COVID-19 infection producing ARDS; and

treating the subject for ARDS.

40. The method of claim 39, wherein the sample is a blood sample from the subject.

41. The method of claim 39 or 40, wherein the subject is a human subject.

42. The method of any one of claims 39–41, wherein obtaining the methylation pattern for the set of DNA methylation sites is performed on a methylation bead array.

43. The method of claim 42, wherein the methylation bead array comprises a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

44. The method of any one of claims 31–43, wherein analyzing the methylation pattern for the set of DNA methylation sites with an ARDS positive methylation classifier and/or an ARDS negative methylation classifier comprises analyzing methylation of a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

45. The method of claim 44, wherein an ARDS positive methylation signature comprises hypomethylation of one or more genes selected from a group consisting of IFR7, ARID5B, ANLN, PARP9, MX1, CBX3P2, EPSTI1, CHSY1, MX1, and GPX1, or any subset thereof, and/or hypermethylation of one or more genes selected from a group consisting of LINC01429, CALHM2, LINC00428, OAS1, RAB40C, TSEN15, PEPD, PPL, ARID3B, ZDHHC6, TNFRSF8, DDX60, OAS2, and FGFR1, or any subset thereof.

46. The method of claim 45, wherein the ARDS positive methylation signature comprises hypomethylation of IFR7.

47. A method of treating multisystem inflammatory syndrome in children (MIS-C) in a subject suspected of having COVID-19 comprising:

obtaining a methylation pattern for a set of DNA methylation sites in a sample derived from the subject;

analyzing the methylation pattern for the set of DNA methylation sites to an MIS-C positive methylation classifier and/or an MIS-C negative methylation classifier, wherein likelihood the subject will exhibit MIS-C is indicated when a score derived from the MIS-C positive classifier exceeds a cutoff and/or threshold value indicating likelihood of a COVID-19 infection producing MIS-C; and

treating the subject for MIS-C.

48. The method of claim 47, wherein the sample is a blood sample from the subject.

49. The method of claim 47 or 48, wherein the subject is a human subject.

50. The method of claim 49, wherein the human subject is a juvenile human subject.

51. The method of any one of claims 47–50, wherein obtaining the methylation pattern for the set of DNA methylation sites is performed on a methylation bead array.

52. The method of claim 51, wherein the methylation bead array comprises a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

53. The method of any one of claims 31–43, wherein analyzing the methylation pattern for the set of DNA methylation sites with an MIS-C positive methylation classifier and/or an MIS-C negative methylation classifier comprises analyzing methylation of a set of genes comprising ANLN, ARID3B, ARID5B, CALHM2, CBX3B2, CD38, CHSY1, CMPK2, DDX60, DTX3L, EPSTI1, FAM38A, FGFR1, GPX1, GTPBP2, IFI27, IFIT3, IRF7, LINC00428, LINC01429, MX1, OAS1, OAS2, PARP9, PHOSPHO1, PPL, RAB40C, REPD, TNFRSF8, TRIM22, TSEN15, and ZDHHC6, or any subset thereof.

54. The method of claim 53, wherein an MIS-C positive methylation signature comprises hypomethylation of one or more genes selected from a group consisting of IFR7, ARID5B, ANLN, PARP9, MX1, CBX3P2, EPSTI1, CHSY1, MX1, and GPX1, or any subset thereof, and/or hypermethylation of one or more genes selected from a group consisting of LINC01429, CALHM2, LINC00428, OAS1, RAB40C, TSEN15, PEPD, PPL, ARID3B, ZDHHC6, TNFRSF8, DDX60, OAS2, and FGFR1, or any subset thereof.

55. The method of claim 54, wherein the infection positive methylation signature comprises hypomethylation of IFR7.

56. An array for detecting the presence of a respiratory virus in a sample comprising a plurality of oligonucleotide probes attached to a solid support; wherein the plurality of oligonucleotide probes detect a methylation signature of the sample.

57. An array for determining the clinical outcome of a respiratory viral infection in a patient comprising a plurality of oligonucleotide probes attached to a solid support; wherein the plurality of oligonucleotide probes detect a methylation signature of a sample from the patient.

58. The array of claim 56 or 57, wherein the methylation signature comprises detecting a methylation status of at least one gene selected from the group consisting of: A_24_P561165, AA455656, ABCF1, ACBD5, AGL, AGPAT1, AID, AIF1, AIM2, ANLN, ANKRD28, APE1, APOBEC3G, APOL2, APOL3, APOL6, APPBP2, ARID3B, ARID5B, ASK1, ASPM, ATAT1, ATF2, ATP2C1, B2M, BATF, BATF2, BCL2L14, BRD2, C10orf81, C1orf68, C1R, C1S, C2, C3, C4A, C4B, C5, C6, C6orf136, C6orf15, C7, C8, C9, CALHM2, CALR, CASP1, Caspase-3, Caspase-8, CATSPER2, CATSPER2P1, CATSPERG, CBX3B2, CCDC66, CCHCR1, CCRL1, CD19, CD27-AS1, CD4, CD38, CD40, CD74, CD8, CDKN1A, CELF4, CEP162, CFB, CFH, CFHR1, CFHR2, CFHR3, CFHR4, CHSY1, CHTOP, CIITA, CIITA BX117479, c-Jun, CLIC5, CMPK2, CSNK2B, CTNND1, CTSS ZBP1, CUTA, CX3CL1 A_24_P912985, CXCL10, CXCL11, CXCL2, CYP21A2, DAG1, DDR1, DDX60, DENND2B, DEXI, DTNB, DTX3L, DYSE, E2F5, EGFL8, EHMT2, eIF-2, eIF2B, ELAVL2, EPSTI1, ERP27, ETV7, FADD, FAM26F, FAM38A, FAM49B, FGFR1 GPX1, FKBP5, FLG, FLG-AS1, FRMD3, FZD5, GAPVD1, GPANK1, GPX5, GTPBP2, GTF2H4, HCG17, HCG18, HCG20, HCG22, HCG24, HCG25, HCG27, HCG4, HCG4B, HCP5, HCP5 NNMT, HLA-A, HLA-B, HLA-C, HLA-DMB, HLA-DOA, HLA-DPA1, HLA-DPB1, HLA-DPB2, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB1-AS1, HLA-DRA, HLA-DRB3, HLA-DRB4, HLA-DRB5, HLA-E, HLA-F, HLA-F-AS1, HLA-G, HLA-H, HLA-V, HRNR, HSD17B8, HSPA1B, ICAM1, IFI16, IFI27, IFI35, IFI44, IFI44L, IFIH1, IFIT2, IFIT3, IFIT5, IFITM1, IFNL1, IFNL2, IFNL3, IFNL4, IFN- α , IFN- β , IFN- γ , IFN- γ , IFN- ϵ , IFN- κ , IFN- ω , IGH, IGK, IGL, IKK- α , IKK- β , IKK- γ , IKK ϵ , IL-10, IL-11, IL-12, IL12A, IL-13, IL-15, IL-17, IL-18, IL18BP, IL-1ra, IL-1 α , IL-1 β , IL-2, IL-3, IL-33, IL-36 α , IL-36 β , IL-36 γ , IL-37, IL-38, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IRF1, IRF3, IRF7, IVL, JAK2, JNK, KCTD16, KDM4C, KIFC1, KPRP, LAP3, LCE1D, LCE1E, LCE2B, LCE2C, LCE2D, LCE3C, LCE4A, LELP1, LGP2, LINC00302, LINC00428, LINC01429, LINC01185, LOC100129636, LOC100294145, LOC100507547, LOC101929006, LOC105375690, LRBA, LST1, LTA, LTBR, LT- α , LY6G6F-LY6G6D, LYRM4-AS1, M27126, MAVS, MCCD1, MDA5, MDC1, MEF2C, MEKK1, MICA, MICA-AS1, MICAB, MICB, MICB-DT, MIR219A1, MIR4479, MKK7, MMP25, MOG, MPIO6B, MSH5, MUCL3, MX1, NA, NAIP, NBP18P, NELFE, NFKB1, NFKB2, NFKBIA, NLRC3, NLRC4, NLRC5, NLRP1, NLRP10, NLRP11, NLRP12, NLRP13, NLRP14, NLRP2, NLRP3, NLRP4, NLRP5, NLRP6, NLRP7, NLRP8,

NLRP9, NLRX1, NMI, NOD1, NOD2, NRCAM, OAS1, OAS2, OR10C1, OR12D2, OR14J1, OR2H1, OR2H2, OR2J1, OR2J2, OSMR, PARP9, PCDH15, PDCD6IPP2, PDIA3, PGLYRP4, PHF1, PHOSPHO1, PKR, PMAIP1, PML, POMC, PPL, PPP1R11, PPP2R5A, PPP6R3, PPT2, PRR3, PRR9, PRRC2A, PRRT1, PSMB8, PSMB8-AS1, PSMB9, PSORS1C1, PSORS1C2, RAB40C, RALYL, REC8, REL, RELA, RELB, REPD, TNFRSF8, RIG-1, RING1, RIP, RNase L, RNF43, RNF5, RNF5P1, RPL13A, RPS18, RPS6KC1, RTP4, RXRB, S100A13, S100A7, S100A8, SAMD9L, SCNN1A, SECTM1, SEPX1, SERPINB7, SERPING1, SHMT1, SKIV2L, SLC44A4, SLC05A1, SMURF2P1-LRRC37BP1, SNAPC3, SNHG32, SNORD32B, SNX14, SOCS1, SP110, SPRR1A, SPRR1B, SPRR3, SPRR4, SPTLC3, SSTR2, STAT1, STAT4, STOML1, SUN1, SYNGAP1, TAP1, TAP2, TAPBP, TBC1D5, TBK1, TCF19, TGF β , THRB, TK2, TLR1, TLR10, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TMEM140, TMEM185A, TMEM62, TNF, TNFR1, TNFR2, TNFRSF14, TNFRSF14-AS1, TNFSF10, TNFSF13B, TP53, TPTE2P5, TRA, TRADD, TRAF2, TRAF3, TRB, TRD, TRG, TRIM10, TRIM15, TRIM22, TRIM25, TRIM27, TRIM33, TRIM37, TRIM39, TRIM40, TRIT1, TRPM4, TSBP1, TSBP1-AS1, TSEN15, UBB, UBE2K, UNG, USP8, VAMP5, VARS2, VEZT, VPS52, WARS, XAF1, XPOT, YY1AP1, ZC3HAV1, ZDHHC6, ZMYND11, ZNF248, ZNF512, ZNF610, and ZNRD1ASP.

59. The array of claim 56 or 57, wherein the plurality of oligonucleotide probes comprises at least one sequence selected from the group consisting of SEQ ID NOS:1–7,831.

60. The array of any one of claims 56 or 57, wherein the plurality of oligonucleotide probes comprises at least one sequence selected from the group consisting of SEQ ID NOS:42, 48, 49, 56, 60, 152, 153, 154, 155, 156, 160, 161, 170, 174, 175, 176, 192, 195, 196, 205, 206, 207, 208, 209, 210, 211, 217, 219, 220, 221, 222, 235, 255, 294, 295, 298, 299, 300, 310, 315, 322, 329, 330, 331, 337, 602, 607, 608, 668, 669, 677, 678, 738, 750, 751, 756, 757, 761, 762, 769, 770, 773, 776, 777, 779, 829, 830, 842, 843, 846, 847, 855, 856, 857, 858, 860, 864, 869, 870, 877, 882, 904, 905, 916, 922, 923, 924, 925, 933, 942, 943, 959, 964, 965, 966, 969, 981, 982, 999, 1000, 1002, 1003, 1004, 1005, 1035, 1036, 1046, 1047, 1048, 1049, 1062, 1063, 1090, 1095, 1096, 1097, 1122, 1123, 1138, 1145, 1146, 1155, 1156, 1158, 1165, 1173, 1174, 1180, 1181, 1185, 1210, 1211, 1216, 1217, 1219, 1220, 1225, 1237, 1238, 1247, 1248, 1249, 1250, 1254, 1255, 1256,

1259, 1260, 1263, 1270, 1271, 1296, 1297, 1308, 1309, 1312, 1314, 1318, 1319, 1326, 1328, 1329, 1342, 1348, 1405, 1406, 1413, 1414, 1415, 1416, 1433, 1434, 1443, 1444, 1465, 1470, 1476, 1485, 1486, 1487, 1508, 1509, 1510, 1514, 1612, 1613, 1620, 1627, 1638, 1639, 1664, 1665, 1666, 1669, 1670, 1676, 1677, 1684, 1685, 1701, 1712, 1719, 1720, 1721, 1722, 1726, 1727, 1731, 1738, 1740, 1747, 1748, 1852, 1853, 1854, 1939, 2072, 2073, 2075, 2088, 2090, 2171, 2193, 2194, 2434, 2435, 2604, 2676, 2678, 2680, 2681, 2756, 2914, 2915, 2919, 2920, 3180, 3243, 3774, 3775, 3994, 3995, 3996, 3998, 3999, 4000, 4020, 4021, 4030, 4031, 4046, 4103, 4171, 4179, 4184, 4187, 4188, 4225, 4236, 4251, 4253, 4257, 4258, 4259, 4262, 4263, 4272, 4276, 4277, 4278, 4292, 4293, 4313, 4314, 4316, 4317, 4318, 4328, 4329, 4330, 4343, 4344, 4345, 4357, 4358, 4376, 4377, 4384, 4389, 4390, 4402, 4408, 4409, 4410, 4411, 4414, 4415, 4416, 4418, 4419, 4421, 4422, 4426, 4427, 4430, 4439, 4453, 4454, 4456, 4457, 4458, 4479, 4487, 4488, 4491, 4492, 4493, 4494, 4500, 4501, 4518, 4519, 4525, 4526, 4539, 4540, 4555, 4562, 4563, 4564, 4584, 4585, 4586, 4589, 4594, 4595, 4596, 4597, 4615, 4617, 4618, 4619, 4620, 4621, 4622, 4627, 4628, 4629, 4630, 4631, 4632, 4657, 4658, 4661, 4662, 4671, 4673, 4689, 4690, 4691, 4697, 4698, 4716, 4717, 4726, 4727, 4728, 4729, 4731, 4747, 4768, 4773, 4774, 4778, 4779, 4780, 4781, 4782, 4783, 4784, 4785, 4968, 4969, 4976, 4977, 4987, 4993, 4994, 4995, 4999, 5005, 5006, 5020, 5025, 5026, 5027, 5035, 5049, 5050, 5055, 5056, 5158, 5164, 5171, 5172, 5173, 5188, 5189, 5190, 5191, 5192, 5193, 5204, 5206, 5208, 5209, 5210, 5211, 5212, 5213, 5214, 5217, 5219, 5220, 5225, 5232, 5233, 5234, 5235, 5238, 5239, 5240, 5241, 5294, 5295, 5296, 5313, 5316, 5327, 5370, 5375, 5376, 5377, 5378, 5379, 5385, 5507, 5508, 5509, 5510, 5511, 5512, 5513, 5514, 5515, 5516, 5517, 5561, 5572, 5573, 5574, 5577, 5578, 5579, 5585, 5586, 5592, 5645, 5646, 5649, 5650, 5656, 5657, 5667, 5672, 5681, 5684, 5695, 5696, 5697, 5698, 5699, 5700, 5701, 5702, 5710, 5711, 5720, 5725, 5728, 5729, 5730, 5743, 5744, 5745, 5748, 5749, 5759, 5760, 5761, 5765, 5766, 5768, 5769, 5772, 5780, 5781, 5782, 5802, 5803, 5804, 5807, 5808, 5809, 5813, 5814, 5816, 5817, 5828, 5829, 5833, 5910, 5914, 5917, 5937, 5941, 5942, 5944, 5945, 5948, 5949, 5963, 6018, 6019, 6023, 6031, 6032, 6033, 6039, 6040, 6043, 6045, 6109, 6110, 6111, 6112, 6113, 6116, 6127, 6128, 6133, 6134, 6137, 6225, 6236, 6242, 6449, 6450, 6451, 6452, 6453, 6454, 6455, 6457, 6458, 6461, 6462, 6463, 6466, 6469, 6470, 6471, 6480, 6481, 6545, 6546, 6547, 6613, 6684, 6685, 6692, 6693, 6694, 6695, 6710, 6711, 6731, 6732, 6741, 6787, 6788, 6805, 6806, 6807, 6828, 6829, 6830, 6831, 6832, 6835, 6836, 6846, 6847, 6848, 6849, 6850, 6862, 6868, 6869, 6870, 6871, 6878, 6879, 6897, 6898, 6899, 6900, 6908, 6909, 6914, 6938, 6939, 6949, 6950, 6951, 6952, 6959, 6960, 6971, 6972, 6973, 6974, 6976, 6979, 7110, 7111, 7112, 7113, 7117, 7118, 7120, 7122,

7124, 7135, 7184, 7185, 7401, 7402, 7404, 7408, 7441, 7442, 7482, 7490, 7491, 7497, 7500, 7503, 7504, 7513, 7514, 7515, 7525, 7526, 7621, 7622, 7623, 7624, 7625, 7626, 7627, 7638, 7649, 7650, 7651, 7652, 7665, 7694, 7704, 7705, 7708, 7716, 7717, 7718, 7726, 7727, 7728, 7729, 7738, 7739, 7740, 7741, 7742, 7743, 7744, 7746, 7747, 7749, 7757, 7770, 7771, 7774, 7775, 7777, 7783, 7788, 7789, 7790, 7791, 7798, 7799, 7803, 7804, 7815, 7816, 7823, 7824, and 7825.

61. The array of claim 56 or 57, wherein the methylation signature comprises detecting a methylation status of at least one gene selected from the group consisting of: ABCF1, ABCF1, AIF1, APOBEC3G, APOL6, B2M, BCL2L14, BRD2, C2, C6orf136, C6orf15, C7, CALR, CD27-AS1, CD4, CD40, CFB, CFH, CHTOP, CIITA, CSNK2B, CUTA, CYP21A2, DDR1, DEXI, EGFL8, EHMT2, GPANK1, GPX5, GTF2H4, HCG17, HCG18, HCG20, HCG25, HCG27, HCG4, HCG4B, HLA-A, HLA-DPA1, HLA-DPB2, HLA-DQA2, HLA-E, HLA-F, HLA-F-AS1, HLA-G, HLA-V, ICAM1, IFI16, IFI35, IFI44, IFI44L, IFITM1, IVL, KIFC1, KPRP, LCE1D, LCE1E, LCE2C, LELP1, LINC00302, LOC100507547, LOC101929006, LY6G6F-LY6G6D, MICA-AS1, MICB, MICB-DT, MSH5, MX1, NA, NBP18P, NFKB1, NFKB2, NLRC5, NLRP11, NLRP3, NLRP5, NLRX1, OR2H1, OSMR, PDIA3, PHF1, PML, PPP1R11, PPT2, PRR9, PRRC2A, PSMB8-AS1, PSMB9, PSORS1C1, REC8, REL, RELB, RING1, RNF5, RPS18, RTP4, RXRB, S100A13, SCNN1A, SERPING1, SKIV2L, SLC44A4, SNORD32B, SPRR4, SPTLC3, SYNGAP1, TAP1, TBK1, TCF19, TLR3, TNF, TNFRSF14, TNFSF13B, TRAF2, TRAF3, TRIM15, TRIM27, TRIM39, TSBP1-AS1, TUBB, VARS2, VPS52, XAF1, and ZNRD1ASP.