What is Claimed is:

1. A method for detecting one or more disease or condition-specific markers in a sample obtained from a subject for identifying the presence of said disease or condition, or the risk of developing said disease or condition, or the prognosis of said disease or condition, the method comprising:

a) preparing a first profile of one or more markers of the disease or condition by detecting the one or more markers from a cell-free bodily fluid sample from the subject;

b) preparing a second profile of at least one of the one or more markers by detecting at least one of the one or more markers from a population of non-phagocytic cells obtained from the subject; and

c) identifying a difference between the first and second profiles of at least one or more of said markers, wherein the difference is indicative of the presence of said disease or condition, or the risk of developing said disease or condition, or the prognosis of said disease or condition, in the subject, wherein the one or more markers are nucleic acids, proteins, or combinations thereof, and wherein the profile is a nucleic acid profile, a protein profile, or a combination thereof.

2. A method for assessing the efficacy of a treatment for a disease or condition, or monitoring the progression or regression of the disease or condition, or identifying a compound capable of ameliorating or treating the disease or condition, by detecting one or more disease or condition-specific markers in a sample obtained from a subject comprising:

a) preparing a first profile of one or more markers of the disease or condition by detecting the one or more markers from a cell-free bodily fluid sample from the subject before the treatment, or at a first time point, or before administration of the compound, respectively; preparing a second profile of at least one of the one or more markers by detecting at least one of the one or more markers from a population of non-phagocytic cells obtained from the subject before the treatment, or at the first time point, or before administration of the compound, respectively; identifying a first difference between the first and second profiles of at least one or more of said markers;

b) preparing a third profile of at least one of the one or more markers by detecting at least one of the one or more markers from a cell-free bodily fluid sample from the subject after the treatment, or at a second time point, or after administration of the compound, respectively; preparing a fourth profile of at least one of the one or more markers by detecting at least one of the one or more markers from a population of non-phagocytic cells obtained from the subject after the treatment, or at the second time point, or after administration of the compound, respectively; identifying a second difference between the third and fourth profiles of at least one or more of said markers; and

c) identifying a difference between the first difference and the second difference, wherein the identified difference is indicative of the efficacy of the treatment for said disease or condition, or the progression or regression of said disease or condition, or indicates that the compound is capable of ameliorating or treating said disease or condition, in the subject, wherein the one or more markers are nucleic acids, proteins, or combinations thereof, and

wherein the profile is a nucleic acid profile, a protein profile, or a combination thereof.

3. The method of claim 1 or 2, wherein the nucleic acid profile is a genotypic profile, a single nucleotide polymorphism profile, a gene mutation profile, a gene copy number profile, a DNA methylation profile, a DNA acetylation profile, a chromosome dosage profile, a gene expression profile, or a combination thereof.

4. A method for identifying one or more markers for a disease or condition in a sample obtained from a subject comprising:

a) preparing a first profile of analytes by detecting said analytes from a cell-free bodily fluid sample from a subject having said disease or condition; preparing a second profile of said analytes by detecting said analytes from the subject's non-phagocytic cells;

identifying a first set of differences between the first and second profiles, wherein the first set of differences is specific to the first profile relative to the second profile;

b) preparing a third profile of analytes by detecting said analytes from a cell-free bodily fluid sample from a control subject not having said disease or condition;

preparing a fourth profile of said analytes by detecting said analytes from the control subject's non-phagocytic cells;

identifying a second set of differences between the third and fourth profiles, wherein the second set of differences is specific to the third profile relative to the fourth profile;

c) identifying one or more analytes specific to the first set of differences relative to the second set of differences, the identified analytes being markers of said disease or condition;

optionally wherein the method further comprises:

d) obtaining a fifth profile of said analytes from cells or tissues affected by said disease or condition in the subject having said disease or condition;

obtaining a sixth profile of said analytes from cells or tissues not affected by said disease or condition in the subject having said disease or condition;

identifying a third set of differences between the fifth and sixth profiles, wherein the third set of differences is specific to the fifth profile relative to the sixth profile; and

e) identifying at least one of the one or more markers of c) present in the third set of differences, wherein the one or more markers are nucleic acids, proteins, or combinations thereof, and wherein the profile is a nucleic acid profile, a protein profile, or a combination thereof.

5. A method for identifying one or more markers of a disease or condition in a sample obtained from a subject comprising:

a) preparing a first profile of analytes by detecting said analytes from a cell-free bodily fluid sample from a subject having said disease or condition; preparing a second profile of said

analytes by detecting said analytes from a cell-free bodily fluid sample from a control subject not having said disease or condition;

identifying a first set of differences between the first and second profiles, wherein the first set of differences is specific to the first profile relative to the second profile;

b) preparing a third profile of said analytes by detecting said analytes from said subject's non- phagocytic cells; preparing a fourth profile of said analytes by detecting said analytes from the control subject's non-phagocytic cells;

identifying a second set of differences between the third and fourth profiles, wherein the second set of differences is specific to the third profile relative to the fourth profile;

c) identifying one or more analytes specific to the first set of differences relative to the second set of differences, the identified analytes being markers of said disease or condition;

optionally wherein the method further comprises:

d) obtaining a fifth profile of analytes from cells or tissues affected by said disease or condition in the subject having said disease or condition;

obtaining a sixth profile of analytes from cells or tissues not affected by said disease or condition in the subject having said disease or condition;

identifying a third set of differences between the fifth and sixth profiles, wherein the third set of differences is specific to the fifth profile relative to the sixth profile; and

e) identifying at least one of the one or more markers of c) present in the third set of differences, wherein the one or more markers are nucleic acids, proteins, or combinations thereof, and wherein the profile is a nucleic acid profile, a protein profile, or a combination thereof.

6. A method for identifying one or more markers of a disease or condition in a sample obtained from a subject comprising:

a) preparing a first profile of analytes by detecting said analytes from a cell-free bodily fluid sample from a subject having said disease or condition;

obtaining a second profile of analytes from a cell-free bodily fluid sample from a control subject not having said disease or condition by data mining;

identifying a first set of differences between the first and second profiles, wherein the first set of differences is specific to the first profile relative to the second profile;

b) preparing a third profile of said analytes by detecting said analytes from said subject's non-phagocytic cells;

obtaining a fourth profile of analytes from the control subject's non-phagocytic cells by data mining;

identifying a second set of differences between the third and fourth profiles, wherein the second set of differences is specific to the third profile relative to the fourth profile; and

c) identifying one or more analytes specific to the first set of differences relative to the second set of differences, the identified analytes being markers of said disease or condition;

optionally wherein the method further comprises

d) obtaining a fifth profile of said analytes from cells or tissues affected by said disease or condition by data mining;

obtaining a sixth profile of said analytes from cells or tissues not affected by said disease or condition by data mining;

identifying a third set of differences between the fifth and sixth profiles, wherein the third set of differences is specific to the fifth profile relative to the sixth profile; and

e) identifying at least one of the one or more markers of c) present in the third set of differences, wherein the one or more markers are nucleic acids, proteins, or combinations

thereof, and wherein the profile is a nucleic acid profile, a protein profile, or a combination thereof.

7. A method for identifying one or more markers of a disease or condition in a sample obtained from a subject comprising:

a) preparing a first profile of analytes by detecting said analytes from a cell-free bodily fluid sample from a subject having said disease or condition;

preparing a second profile of said analytes by detecting said analytes from the subject's non-phagocytic cells;

identifying a first set of differences between the first and second profiles, wherein the first set of differences is specific to the first profile relative to the second profile;

b) preparing a third profile of said analytes by detecting said analytes from the subject's cells or tissues affected by said disease or condition;

preparing a fourth profile of said analytes by detecting said analytes from the subject's cells or tissues not affected by said disease or condition;

identifying a second set of differences between the third and fourth profiles, wherein the second set of differences is specific to the third profile relative to the fourth profile;

c) identifying one or more analytes present in both the first set of differences and the second set of differences, the identified analytes being markers of said disease or condition;

optionally wherein the method further comprises:

d) preparing a fifth profile of said analytes by detecting said analytes from a cell-free bodily fluid sample from a control subject not having said disease or condition;

identifying a third set of differences between the first and fifth profiles, wherein the third set of differences is specific to the first profile relative to the fifth profile;

e) identifying at least one of the one or more markers of c) present in the third set of differences, wherein the one or more markers are nucleic acids, proteins, or combinations thereof, and wherein the profile is a nucleic acid profile, a protein profile, or a combination thereof.

8. The method of any one of claims 1-7, wherein the nucleic acids are nucleotides, oligonucleotides, DNAs, RNAs, or DNA-RNA hybrids; and

wherein the proteins are amino acids, peptides, enzymes, antigens, antibodies, cytokines, lipoproteins, glycoproteins, or hormones.

9. The method of any one of claims 4-8, wherein the analytes are nucleic acids, proteins, or combinations thereof;

wherein the nucleic acids are nucleotides, oligonucleotides, DNAs, RNAs, or DNA-RNA hybrids; and

wherein the proteins are amino acids, peptides, enzymes, antigens, antibodies, cytokines, lipoproteins, glycoproteins, or hormones.

10. The method of any one of claims 1-9, wherein the nucleic acid profile is a genotypic profile, a single nucleotide polymorphism profile, a gene mutation profile, a gene copy number profile, a DNA methylation profile, a DNA acetylation profile, a chromosome dosage profile, a gene expression profile, or a combination thereof; and

wherein the protein profile is a protein expression profile, a protein activation profile, or a combination thereof; and further optionally wherein the protein activation profile comprises determining a phosphorylation state, an ubiquitination state, a myristoylation state, or a conformational state of the one or more markers.

11. The method of any one of claims 1-10, wherein the profile is determined by a qualitative assay, a quantitative assay, or a combination thereof;

optionally wherein the quantitative assay uses sequencing, direct sequencing, random shotgun sequencing, Sanger dideoxy termination sequencing, whole-genome sequencing, sequencing by hybridization, pyrosequencing, capillary electrophoresis, gel electrophoresis, duplex sequencing, cycle sequencing, single-base extension sequencing, solid-phase sequencing, high-throughput sequencing, massively parallel signature sequencing, emulsion PCR, sequencing by reversible dye terminator, paired-end sequencing, near-term sequencing, exonuclease sequencing, sequencing by ligation, short-read sequencing, single-molecule sequencing, sequencing-by-synthesis, real-time sequencing, reverse-terminator sequencing, nanopore sequencing, 454 sequencing, Solexa Genome Analyzer sequencing, SOLiD® sequencing, MS-PET sequencing, mass spectrometry, matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry, electrospray ionization (ESI) mass spectrometry, surface- enhanced laser desorption/ionization-time of flight (SELDI-TOF) mass spectrometry, quadrupole- time of flight (Q-TOF) mass spectrometry, atmospheric pressure photoionization mass spectrometry (APPI-MS), Fourier transform mass spectrometry (FTMS), matrix-assisted laser desorption/ionization-Fourier transform-ion cyclotron resonance (MALDI-FT-ICR) mass spectrometry, secondary ion mass spectrometry (SIMS), polymerase chain reaction (PCR) analysis, quantitative PCR, real-time PCR, fluorescence assay, colorimetric assay, chemiluminescent assay, or a combination thereof.

12. The method of any one of claims 1-10, wherein the profile is a nucleic acid profile detected by polymerase chain reaction (PCR) analysis, sequencing analysis, electrophoretic analysis, restriction fragment length polymorphism (RFLP) analysis, Northern blot analysis, reverse-transcriptase-PCR analysis (RT-PCR), quantitative PCR, quantitative RT-PCR, allele-specific oligonucleotide hybridization analysis, comparative genomic hybridization, heteroduplex mobility assay (HMA), single strand conformational polymorphism (SSCP), denaturing gradient gel electrophoresis (DGGE), RNAase mismatch analysis, mass spectrometry, matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry, electrospray ionization (ESI) mass spectrometry, surface-enhanced laser desorption/ionization-time of flight (SELDI-TOF) mass spectrometry, quadrupole-time of flight (Q-TOF) mass spectrometry, atmospheric pressure photoionization mass spectrometry (APPI-MS), Fourier transform mass spectrometry (FTMS), matrix-assisted laser desorption/ionization-

Fourier transform-ion cyclotron resonance (MALDI-FT-ICR) mass spectrometry, secondary ion mass spectrometry (SIMS), Southern blot analysis, in situ hybridization, fluorescence in situ hybridization (FISH), chromogenic in situ hybridization (CISH), immunohistochemistry (IHC), microarray, comparative genomic hybridization, karyotyping, multiplex ligation-dependent probe amplification (MLPA), Quantitative Multiplex PCR of Short Fluorescent Fragments (QMPSF), microscopy, methylation specific PCR (MSP) assay, Hpaii tiny fragment Enrichment by Ligation-mediated PCR (HELP) assay, radioactive acetate labeling assays, colorimetric DNA acetylation assay, chromatin immunoprecipitation combined with microarray (ChiP-on-chip) assay, restriction landmark genomic scanning, Methylated DNA immunoprecipitation (MeDIP), molecular break light assay for DNA adenine methyltransferase activity, chromatographic separation, methylation-sensitive restriction enzyme analysis, surface plasmon resonance, bisulfite-driven conversion of non-methylated cytosine to uracil, methyl-binding PCR analysis, or a combination thereof;

optionally wherein the sequencing analysis is selected from the group consisting of direct sequencing, random shotgun sequencing, Sanger dideoxy termination sequencing, whole-genome sequencing, sequencing by hybridization, pyrosequencing, capillary electrophoresis, gel electrophoresis, duplex sequencing, cycle sequencing, single-base extension sequencing, solid-phase sequencing, high-throughput sequencing, massively parallel signature sequencing, emulsion PCR, sequencing by reversible dye terminator, paired-end sequencing, near-term sequencing, exonuclease sequencing, sequencing by ligation, short-read sequencing, single-molecule sequencing, sequencing-by-synthesis, real-time sequencing, reverse-terminator sequencing, nanopore sequencing, 454 sequencing, Solexa Genome Analyzer sequencing, SOLiD® sequencing, MS-PET sequencing, mass spectrometry, and a combination thereof;

or wherein the profile is a protein profile detected by an immunohistochemistry assay, an enzyme-linked immunosorbent assay (ELISA), chromatography, liquid chromatography, size exclusion chromatography, high performance liquid chromatography (HPLC), gas chromatography, mass spectrometry, tandem mass spectrometry, matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometry, electrospray ionization (ESI) mass spectrometry, surface-enhanced laser desorption/ionization-time of flight (SELDI-TOF) mass spectrometry, quadrupole-time of flight (Q-TOF) mass spectrometry, atmospheric

pressure photoionization mass spectrometry (APPI-MS), Fourier transform mass spectrometry (FTMS), matrix-assisted laser desorption/ionization-Fourier transform-ion cyclotron resonance (MALDI-FT-ICR) mass spectrometry, secondary ion mass spectrometry (SIMS), radioimmunoassays, surface plasmon resonance, microfluidic chip-based assays, Western blotting assay, or a combination thereof.

13. The method of any one of claims 1-12, wherein the disease or condition is a cardiovascular disease or condition, a kidney-associated disease or condition, a prenatal or pregnancy-related disease or condition, a neurological or neuropsychiatric disease or condition, an autoimmune or immune-related disease or condition, a cancer, an infectious disease or condition, a mitochondrial disorder, a respiratory-gastrointestinal tract disease or condition, a reproductive disease or condition, an ophthalmic disease or condition, a musculo-skeletal disease or condition, or a dermal disease or condition.

14. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of AKT2, BAKl, EGFR, ERBB2, ETS2, FOS, JUN, MAP2Kl, MMP2, PDGFB, RBI, SERPINB2, SNCG, and SPPl.

15. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of AKTl, AKT2, BAK2, CDC25A, E2Fl, EGFR, ERBB2, FOS, JUN, MAP2Kl, MMP2, NFKBl, PDGFB, PIK3Rl, PNN, RBI, SERPINB2, SERPINB5, SNCG, SPPl, TERT, TIMP3, and TP53.

16. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of CASP8, CASP9, COL18Al, ETS2, HTATIP2, MMP9, SRC, and TWISTl.

17. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of AKTl, APAFl, ATM, CDC25A, CDKNlA, ETS2, FOS, IL8, ITGA4, ITGA6, ITGAV, JUN, MAP2Kl, NFKBIA, PLAU, PLAUR, RAFl, SERPINB2, SYK, TIMPl, TNF, TNFRSFlOB, and TNFRSFlA.

18. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of ACP2, AK2, AKT3, ARL5B, ATP2B3, BGN, BRAF, BTG2, CAMKK2, CAPG, CAPN12, CPLX2, DENND5A, DNA2, FAM104A, FNIPl, GFRA4, GLUDl, GNAQ, GPlBB, HNRPLL, HOXA2, HPS3, INPP4A, ITGAV, KLHL23, LANCL2, LYPD6, MAPKAPK3, MEF2A (includes, EG:4205), MEF2C, NVL, PCYTlA, PGLYRP4, PLOD I, PPPlCB, PRKAB2, PROS I, PTPRE, RASA4 (includes,EG:10156), RBMS2, RBPJ, STAT5B, THBSl, TRIBl, TRIM2, TSPAN6, and ZDHHC21.

19. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of B4GALT5, BOPl, CCL2, CCL3, CCL3Ll, CCRL2, CD83, CLEC4G, CLIC4, CTSC, CTSO, CXCLlO, FCGR3A, FPR3, HBAl, HBB, LRMP, MAP1LC3B2, MS4A4A, MSRl, MYADML, NIDI, PF4, PION, RNF217, SAMD9L, SERPING1, and SPARC.

20. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of ACOT9, AMPD2, ARHGAP15, BATF2, C3AR1, C5orf41, CCL3, CCL3Ll, CD63, CHSTll, CHSYl, CLEC4G, CTSZ, CXorf21, CYTH4, CYTIP, DLEU2, DNAJAl, DOCK8, DTX3L, DUSP6, EPSTil, ERF, F2RL1, FYB, GABRB2, GBP5, GLRX, GNB4, ICAMl, IFI35, IFIHl, IFNAR2, ILlRl, IRFl, ITGA5, LAP3, LAPTM5, LCP2, MAP1LC3B, MAP1LC3B2, MICAL2, MTlDP, MTlJP, MTlM, MT2A, MYADML, NEK6, NINJ2, NNMT, NT5C3L, NUBl, PDE4B, PLODl, PML, PRKCB, PSMB9, RCN3, RGS4, RNASE6, RTP4, SAMD9L, SELlL, SERPINGl, SETX, SIGLEClO, SKIL, SLC7A7, SNORA21, SPlOO, SPllO, SP140, SSFA2, STAT2, STK17B, STK3, TDRD7, TMCCl, TMPRSS11E2, TNFRSFlB, TPMl, TRIM21,TXNDC4, UBE2L6, UBE2W, USP18, VAVl, WARS, WIPFl, and WIPil.

21. The method of claim 1 or 2, wherein the one or more markers comprise at least one gene selected from the group consisting of ADAR, ADM, ALAS I, ANKRD22, ARHGAP27, B3GNT5, BCLlO, C12orf35, C15orf29, C2orf59, CD177, CEACAMl, CPEB2, DDX58, F2RL1, GDPD3, GNAB, HIST2H3A, HIST2H3D, HIST2H4A, HMGCR, HSPA6, HSPC159, IL4R, IMPA2, KPNBl, KREMENl, KRT23, LDLR, LOC100130904, LTB4R, MAEA, MARK2, MBOAT2, MPZL3, N4BP1, NBEAL2, NMI, NPEPPS, PARP14, PGM2, PPIF, PXN,

RALBPl, RODl, RPS6KA1, SlOOP, SERTAD2, SLC9Al, SLPI, SPllO, SPINTl, ST14, TBC1D3, TNFRSF9, TRIM21, UPPl, VPS24, ZBTB34, and ZNF256.

22. The method of any one of claims 1-7, further comprising extracting the one or more markers from the cell-free bodily fluid sample; optionally wherein the cell-free bodily fluid sample comprises viable diseased cells, dead diseased cells, apoptotic diseased cells, circulating tumor cells, infectious agents, fetal cells, trophoblasts, or fragments thereof.

23. The method of any one of claims 1-7, further comprising extracting the cellular contents from the non-phagocytic cells before a).

24. The method of any one of claims 1-7, wherein the non-phagocytic cells are T cells, B cells, null cells, basophils, or mixtures thereof;

optionally wherein the non-phagocytic cells are isolated from a bodily fluid sample, tissues, or cells of the subject; optionally wherein the bodily fluid sample is blood, urine, stool, saliva, lymph fluid, cerebrospinal fluid, synovial fluid, cystic fluid, ascites, pleural effusion, fluid obtained from a pregnant woman in the first trimester, fluid obtained from a pregnant woman in the second trimester, fluid obtained from a pregnant woman in the third trimester, maternal blood, amniotic fluid, chorionic villus sample, fluid from a preimplantation embryo, maternal urine, maternal saliva, placental sample, fetal blood, lavage and cervical vaginal fluid, interstitial fluid, or ocular fluid;

optionally wherein the cell-free bodily fluid sample is separated from a bodily fluid sample; optionally wherein the bodily fluid sample is blood, urine, stool, saliva, lymph fluid, cerebrospinal fluid, synovial fluid, cystic fluid, ascites, pleural effusion, fluid obtained from a pregnant woman in the first trimester, fluid obtained from a pregnant woman in the second trimester, fluid obtained from a pregnant woman in the third trimester, maternal blood, amniotic fluid, chorionic villus sample, fluid from a preimplantation embryo, maternal urine, maternal saliva, placental sample, fetal blood, lavage and cervical vaginal fluid, interstitial fluid, or ocular fluid; and optionally wherein the cell-free bodily fluid is serum or plasma.