oral cavity cancer, an esophagus cancer, a stomach cancer, a small intestine cancer, a colon cancer, a rectum cancer, an anal cancer, an anorectum cancer, a liver cancer, an intrahepatic bile duct cancer, a gallbladder cancer, a biliary cancer, a digestive organ cancer, a larynx cancer, a bronchus cancer, a respiratory organ cancer, a bone cancer, a joint cancer, a soft tissue cancer, a heart cancer, a melanoma, a nonepithelial skin cancer, a uterine cancer, a cervical cancer, a vulva cancer, a vagina cancer, a penis cancer, a genital cancer, a testis cancer, a kidney cancer, a renal pelvis cancer, a ureter cancer, a urinary organ cancer, an eye cancer, an orbit cancer, a nervous system cancer, an endocrine cancer, a thyroid cancer, a Hodgkin lymphoma, a non-Hodgkin lymphoma, a myeloma, an acute lymphocytic leukemia, a chronic lymphocytic leukemia, an acute myeloid leukemia, a chronic myeloid leukemia, or a leukemia.

[0003a] In another aspect, there is a provided method for identifying a biomarker as associated with a disease state, the method comprising: (a) isolating a first plurality of analytes in a first biological sample of an individual known to have the disease state using an electrode array configured to generate an AC dielectrophoretic field; (b) isolating a second plurality of analytes in a second biological sample of healthy individual using an electrode array configured to generate an AC dielectrophoretic field; and (c) identifying a subset of the first plurality of analytes, wherein the subset is quantitatively different in the first biological sample compared with the second biological sample, wherein the subset is identified as associated with the disease state.

[0004] In another aspect, there are provided methods of analysis comprising (a) measuring an amount of an analyte in a biological sample from an individual; and (b) identifying the individual as being at risk of developing a disease when the amount of the analyte is greater than or less than the amount observed in a control sample, wherein the analyte comprises one or more biomarker identified in any of the method provided herein. In some cases, measuring comprises isolating the analytes in the biological sample using an electrode array configured to generate an AC dielectrophoretic field. In some cases, isolating comprises using electrodes configured to generate a dielectrophoretic low field region and a dielectrophoretic high field region. In some cases, isolating comprises capturing the first plurality of analytes or the second plurality of analytes on one or more electrode. In some cases, measuring comprises mass spectrometry analysis of the analyte. In some cases, the analyte comprises a protein or a polypeptide. In some cases, the analyte comprises a nucleic acid. In some cases, the analyte comprises an exosome. In some cases, the disease is a cancer, a neurological disease, an infection, or an inflammatory disease. In some cases, the cancer is a pancreatic cancer, an ovarian cancer, a bladder cancer, a colorectal cancer, a lung cancer, a brain cancer, a prostate cancer, a breast cancer, a skin cancer, a lymphoma, or a leukemia.

[0004a] In another aspect, there is a provided method of analysis comprising: (a) measuring an amount of an analyte in a biological sample from an individual; and (b) identifying the individual as being at risk of developing a disease when the amount of the analyte is greater than or less than the amount observed in a control sample.

[0005] A further aspect, there are provided methods of identifying a therapeutic target, the method comprising: (a) isolating a first plurality of analytes in a first biological sample of an individual known to have the disease state using an electrode array configured to generate an AC dielectrophoretic field; (b) isolating a second plurality of analytes in a second biological sample of healthy individual using an electrode configured to generate an AC dielectrophoretic field; and (c) identifying a subset of the first plurality of analytes, wherein the subset is quantitatively different in the first biological sample compared with the second biological sample, wherein the subset is identified as the therapeutic target for drug discovery or drug development.

[0005a] In another aspect, there is a provided method of identifying a therapeutic target, the method comprising: (a) isolating a first plurality of analytes in a first biological sample of an individual known to have the disease state using an electrode array configured to generate an AC dielectrophoretic field; (b) isolating a second plurality of analytes in a second biological sample of healthy individual using an electrode configured to generate an AC dielectrophoretic field; and (c) identifying a subset of the first plurality of analytes, wherein the subset is quantitatively different in the first biological sample compared with the second biological sample, wherein the subset is identified as the therapeutic target.

INCORPORATION BY REFERENCE

[0006] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0007] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings(s) will be provided by the Office upon request and payment of the necessary fee.

[0008] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0009] **FIG. 1** shows (left) a tilted top view of an assay cartridge; (center) a visualization of blood cells separated from the sample away from the electrodes; and (left) a visualization of DNA and extracellular vesicles on the electrode.

[0010] **FIG. 2** shows a workflow for biomarker analysis: (left) biomarkers isolated on an electrode, (center) various biomarkers to be analyzed; and (right) modalities for downstream analysis either off chip or on chip.

[0011] **FIG. 3** shows an example of a method for isolating nucleic acids from cells.

[0012] **FIG. 4** shows an example of a method for isolating extra-cellular nucleic acids from a fluid comprising cells.

[0013] **FIG. 5** shows a flow diagram for biomarker discovery.

[0014] **FIG. 6** shows (left) a cluster diagram of exosomal proteins isolated from pancreatic cancer patients (right) a heat map of biomarkers over expressed and under expressed in pancreatic cancer compared with healthy control.

[0015] **FIG. 7** shows the subjects used in a multi-cancer test using samples from known cancer patients and healthy controls.

[0016] **FIG. 8** shows results of a multicancer test using samples from known cancer patients and healthy controls.

[0017] **FIGS. 9A-9C** show an experimental outline. **FIG. 9A** shows a workflow diagram. **FIG. 9B** shows a statistical approach to develop and evaluate performance of the EXPLORE test: 100 iterations of randomly selected subjects were used for development (training set, 67% of subjects) and performance evaluation (test set, 33% of subjects). **FIG. 9C** shows relative concentration of 13 exoproteins used in the EXPLORE test by subject ID. The concentration levels were normalized to