

cartridge data (e.g. a schematic of a printer); an icon to email a data report of biochip cartridge data (e.g. an envelope icon); an icon to export a data report of biochip cartridge data to another computer device; and an icon to display a virtual keyboard. Again, these secondary icons are generally selected to be “language neutral”, such that they are easily comprehended by operators that speak different languages.

**[0268]** Alternatively, the panel of options is displayed by selecting and touching one of the bay icons without the need to load a cartridge.

**[0269]** Once an assay is complete, the bay icon can be pressed to result in the display of an assay report, detailing the results of the assay (which virus present, SNP status, etc.). This report can be printed by icon, emailed by icon, downloaded to an external memory device (e.g. flash memory device), etc.

#### IV. Assays

##### General Methods

**[0270]** The detection methods are based on capture binding ligands (capture probes when the target is nucleic acid) to bind the target analytes and solution binding ligands (label probes when the target is nucleic acid) that carry electron transfer moiety (ETM) electrochemical labels to form “sandwich hybridization complexes”. See for example FIG. 2B of U.S. Pat. No. 7,935,481, incorporated by reference (as are all of the Figures, accompanying legends and the associated specification descriptions). That is, only in the presence of the target analyte will the ETM(s) be present at the surface of the detection electrode, thus giving rise to a signal. Suitable ETMs are outlined in the cited cases, and all discussions relating to ETMs are specifically incorporated independently and optionally by reference.

**[0271]** These techniques are generally described in U.S. Pat. Nos. 4,887,455; 5,591,578; 5,705,348; 5,770,365; 5,807,701; 5,824,473; 5,882,497; 6,013,170; 6,013,459; 6,033,601; 6,063,573; 6,090,933; 6,096,273; 6,180,064; 6,190,858; 6,192,351; 6,221,583; 6,232,062; 6,236,951; 6,248,229; 6,264,825; 6,265,155; 6,290,839; 6,361,958; 6,376,232; 6,431,016; 6,432,723; 6,479,240; 6,495,323; 6,518,024; 6,541,617; 6,596,483; 6,600,026; 6,602,400; 6,627,412; 6,642,046; 6,655,010; 6,686,150; 6,740,518; 6,753,143; 6,761,816; 6,824,669; 6,833,267; 6,875,619; 6,942,771; 6,951,759; 6,960,467; 6,977,151; 7,014,992; 7,018,523; 7,045,285; 7,056,669; 7,087,148; 7,090,804; 7,125,668; 7,160,678; 7,172,897; 7,267,939; 7,312,087; 7,381,525; 7,381,533; 7,384,749; 7,393,645; 7,514,228; 7,534,331; 7,560,237; 7,566,534; 7,579,145; 7,582,419; 7,595,153; 7,601,507; 7,655,129; 7,713,711; 7,759,073; 7,820,391; 7,863,035; 7,935,481; 8,012,743; 8,114,661, all of which are incorporated by reference in their entirety.

**[0272]** As outlined herein, the systems of the invention are used to detect the presence or absence of a target (e.g. viruses or bacteria) and/or the elucidation of a specific sequence such as a single nucleotide polymorphism (SNP). As is known in the art, there are a number of techniques that can be used to detect or determine the identity of a base at a particular location in a target nucleic acid, including, but not limited to, the use of temperature, competitive hybridization of perfect and imperfect probes to the target sequence, sequencing by synthesis, for example using single base extension techniques (sometimes referred to as “mini-sequencing”), the oligonucleotide ligase amplification (OLA) reaction, rolling circle

amplification (RCA), allelic PCR, competitive hybridization and Invader™ technologies. In addition, the present invention is directed to a novel invention that capitalizes on novel properties of surface-bound arrays, and uses “competimers” to reduce non-specific binding.

**[0273]** These techniques in the present invention rely on the formation of assay complexes on a detection electrode surface, as a result of hybridization of a target sequence (either the target sequence of the sample or an amplicon sequence generated in the assay) to a capture probe on the surface. As is more fully outlined herein, this may be direct or indirect (e.g. through the use of sandwich type systems) hybridization. The assay complex further comprises at least one electron transfer moiety (ETM) that is also either directly or indirectly attached to the target. Once the assay complexes are formed, the presence or absence of the ETMs are detected as is described below and in U.S. Pat. Nos. 5,591,578; 5,824,473; 5,770,369; 5,705,348 and 5,780,234; U.S. Ser. Nos. 08/911,589; 09/135,183; 09/306,653; 09/134,058; 09/295,691; 09/238,351; 09/245,105 and 09/338,726; and PCT Pub Nos. WO 98/20162; WO 00/16089; and PCT Application Nos. PCT/US99/01705; PCT/US99/01703; PCT/US00/10903 and PCT/US99/10104, all of which are expressly incorporated herein by reference in their entirety. Specific reference is made to the structures of the ETMs, the different assay methods and assay components, the methods of making the PCB component/detection electrodes, etc.

**[0274]** Specific SNP detection generally requires one or two primer nucleic acids (which may include the ETM labels as well as the use of nucleic acid analogs) that is hybridized to the target sequence to form a hybridization complex, and an enzyme is added that in some way modifies the primer to form a modified primer; generally, the occurrence of the modification depends on the presence or absence of a particular sequence, thus allowing sequence differentiation. For example, OLA requires two primers that hybridize (either directly adjacently or separated by one or more bases) to the target sequence and a ligase; Invader® requires two primers and a cleavage enzyme; etc. Thus, in general, a target nucleic acid is added to a reaction mixture that comprises the necessary amplification components, and a modified primer is formed, which is then either detected as an indication that the variation is present, or queried to determine the identity of the base at the position of interest.

**[0275]** In general, the modified primer (which can be an amplicon in the case of traditional PCR as is generally outlined herein) is incorporated into an assay complex that comprises a label, such as an electron transfer moiety (ETM), which is either incorporated by an enzyme, present on the original primer, or added via a label probe. As required, the unreacted primers can be removed in a variety of ways, as will be appreciated by those in the art, although in many embodiments this is not required. The hybridization complex is then optionally disassociated, and the modified primer is added to an electrode as is generally described herein and in the cited applications. Usually, the electrodes comprise capture probes that will hybridize to the modified primers although as outlined herein, a variety of configurations, including sandwich assays, can be used. Detection proceeds via detection of the ETM label as an indication of the presence, absence or amount of the target sequence.

**[0276]** The methods of the invention find particular use in genotyping assays, i.e. the detection of particular nucleotides at specific positions, although as will be appreciated by those