CLAIMS

1. A method for use in diagnosing a disease or disorder associated with a damaged cell or a pathogen based on an identified symptom experienced by a subject and based on a first biological sample obtained from the subject, the first biological sample including nucleic acids, the method being executed by a device, the method comprising:

based on the symptom that has been identified, preselecting a first set of the nucleic acids for analysis;

capturing by the device a first plurality of the nucleic acids of the first set that are present in the first biological sample;

for each of the captured nucleic acids of the first plurality:

quantifying by the device an amount of that captured nucleic acid that is present in the first biological sample;

sequencing by the device that captured nucleic acid; and

based on the sequence and amount of that captured nucleic acid, identifying by the device a pathogen or cell of origin of that captured nucleic acid; and

outputting by the device an indication of the quantified amount and the identified pathogen or cell of origin of at least one captured nucleic acid that is present in the first biological sample,

wherein the identifying by the device the pathogen or cell of origin of the captured nucleic acid comprises comparing the sequence of that nucleic acid to sequences stored in a library stored in a computer-readable medium of the device;

optionally wherein the library stores nucleic acid sequences for a human and for a plurality of pathogens.

2. The method of claim 1, wherein preselecting the first set of the nucleic acids for analysis comprises receiving by the device a first symptom-specific cartridge comprising a first set of complementary nucleic acids configured to capture the first set of the nucleic acids for analysis;

optionally further comprising, after the outputting step, removing the first symptom-specific cartridge from the device and receiving by the device a second symptom specific cartridge comprising a second set of complementary nucleic acids;

optionally wherein the first set of complementary nucleic acids is different than the second set of complementary nucleic acids.

3. The method of any one of claims claim 1 or 2, further comprising outputting by the device an indication of the quantified amount of each of the captured nucleic acids of the first plurality.

4. The method of any one of claims 1-3, wherein:

the capturing comprises separating extracellular nucleic acids in the first biological sample from intracellular nucleic acids in the first biological sample; and

the quantifying and sequencing steps are performed separately on the separated extracellular nucleic acids and on the intracellular nucleic acids;

optionally further comprising outputting by the device an indication of the quantified amount of at least one of the extracellular nucleic acids and an indication of the quantified amount of at least one of the intracellular nucleic acids.

5. The method of any one of claims 1-4, wherein the output indicates the relative number of a pathogen per human cell.

6. The method of any one of claims 1-5, further comprising:

receiving by the device a second biological sample obtained from the subject, the second biological sample being different from the first biological sample;

capturing by the device a second plurality of the nucleic acids of the first set that are present in the second biological sample;

for each of the captured nucleic acids of the second plurality:

quantifying by the device an amount of that captured nucleic acid that is present in the second biological sample;

sequencing by the device that captured nucleic acid; and

based on the sequence and amount of that captured nucleic acid, identifying by the device a pathogen or cell of origin of that captured nucleic acid; and

wherein the outputting by the device further includes an indication of the quantified amount and the identified pathogen or cell of origin of at least one captured nucleic acid that is present in the second biological sample.

7. The method of any one of claims 1-8, further comprising outputting by the device an indication of at least one potential diagnosis for the subject and an indication of the likelihood of the at least one potential diagnosis based on the quantified amount and the identified pathogen or cell of origin of at least one captured nucleic acid that is present in the first

biological sample.

8. A device for use in diagnosing a disease or disorder associated with a damaged cell or a pathogen based on an identified symptom experienced by a subject and based on a first biological sample obtained from the subject, the first biological sample including nucleic acids, the device comprising:

a first set of complementary nucleic acids configured to capture a first set of the nucleic acids, the first set of the nucleic acids being selected based on the symptom that has been identified, the first set of complementary nucleic acids being configured to capture a first plurality of the nucleic acids of the first set that are present in the first biological sample;

a nucleic acid quantifier configured to quantify an amount of each of the captured nucleic acids that is present in the first biological sample;

a nucleic acid sequencer configured to sequence each captured nucleic acid that is present in the first biological sample;

a processor coupled to the quantifier and to the sequencer and being suitably programmed to identify a pathogen or cell of origin of each captured nucleic acid based on the sequence and amount of that captured nucleic acid; and

an output module coupled to the processor, the processor further being suitably programmed to cause the output module to output an indication of the quantified amount and the identified pathogen or cell of origin of at least one captured nucleic acid that is present in the first biological sample,

wherein the processor further is programmed to identify the pathogen or cell of origin of the captured nucleic acid based on comparing the sequence of that nucleic acid to sequences stored in a library stored in the computer-readable medium,

optionally wherein the library stores nucleic acid sequences for a human and for a plurality of pathogens.

9. The device of claim 8, wherein the device comprises a receptacle configured to receive the first set of complementary nucleic acids within a first symptom-specific cartridge or a second symptom-specific cartridge comprising a second set of complementary nucleic acids;

optionally wherein the first set of complementary nucleic acids is different that the second set of complementary nucleic acids.

10. The device of any one of claim 8 or 9, wherein the processor further is suitably

programmed to cause the output module to output an indication of the quantified amount of each of the captured nucleic acids of the first plurality.

11. The device of any one of claims 8-10, further comprising a separator configured to separate extracellular nucleic acids in the first biological sample from intracellular nucleic acids in the first biological sample; and

wherein the nucleic acid quantifier and nucleic acid sequencer separately operate on the separated extracellular nucleic acids and on the intracellular nucleic acids.

12. The device of claim 11, wherein the processor further is suitably programmed to cause the output module to output an indication of the quantified amount of at least one of the extracellular nucleic acids and an indication of the quantified amount of at least one of the intracellular nucleic acids.

13. The device of any one of claims 8-12, further comprising a computer-readable medium coupled to the processor,

optionally wherein the output indicates the relative number of a pathogen per human cell.

14. The device of any one of claims 8-13,

the first set of complementary nucleic acids further being configured to capture a second plurality of the nucleic acids of the first set that are present in a second biological sample obtained from the subject, the second biological sample being different from the first biological sample;

the nucleic acid quantifier further being configured to quantify an amount of each of the captured nucleic acids that is present in the second biological sample;

the nucleic acid sequencer further being configured to sequence each of the captured nucleic acids that is present in the second biological sample; and

the processor further being suitably programmed to identify a pathogen or cell of origin of each captured nucleic acid based on the sequence and amount of the captured nucleic acid that is present in the second biological sample; and

the processor further being suitably programmed to cause the output module to output an indication of quantified amount and the identified pathogen or cell of origin of at least one captured nucleic acid that is present in the second biological sample.

15. The device of any one of claims 8-14, wherein the processor further is suitably

programmed to cause the output module to output an indication of at least one potential diagnosis for the subject and an indication of the likelihood of the at least one diagnosis based on the quantified amount and the identified pathogen or cell of origin of at least one captured nucleic acid that is present in the first biological sample.