Claims

1. A method for detecting an analyte in a pathogen-comprising sample comprising:

    i) Inactivation of the pathogen within the sample without isolation of RNA and/or DNA from the pathogen or the sample;

    ii) Detecting the analyte by spatial transcriptomics.

2. The method according to claim 1, wherein the pathogen-comprising sample is selected from the group consisting of a solid, a fluidic sample, a smear and a surface comprising pathogenic material and wherein the pathogen-comprising sample is a biological sample, preferably comprising biological tissue, further preferably comprising biological cells and/or extracts and/or part of cells containing a pathogen.

3. The method according to claim 1, wherein the pathogen-comprising sample comprise eukaryotic, archaea, prokaryotic organisms, and/or viruses.

4. The method according to of any one of claims 1 to 2, wherein the pathogen-comprising sample comprises formalin-fixed, paraffin-embedded tissues containing a pathogen and/or wherein the pathogen-comprising sample is frozen or alcoholic stabilized.

5. The method according to of any one of claims 1 to 2, wherein the pathogen is inactivated by a physical, chemical, biochemical and/or biological treatment.

6. The method according to claim 5, wherein the physical inactivation treatment is selected from the group consisting of temperature change, electromagnetic waves and light including visible and invisible light like UV irradiation, temperature treatment with a temperature higher than 30°C, 40°C, 50°C, 60°C, 70°C, 80°C, 90°C, 100°C or 110°C, treatment by X-ray, radioactivity, UV-light, blue light red light and/or infrared light, or combinations thereof.

7. The method according to claim 5, wherein the pathogen is inactivated by a chemical inactivation treatment, wherein the chemical inactivation treatment is selected from the group consisting of pH change, salt treatment, treatment with a fraction of a polar or non-polar solvent, treatment with an oxidative or reductive reagent, treatment with a reagent that

perform covalent or non-covalent linkage to the pathogen and treatment with a degenerative reagent that cleaves at least parts of the pathogen, or combinations thereof.

8. The method according to claim 5, wherein the biochemical inactivation treatment is a treatment with enzymes and/or biomolecules.

9. The method according to of any one of claims 1 to 8, wherein the spatial transcriptomics detecting comprises a multiplex method for detecting different analytes in the pathogen-comprising sample by sequential signal-encoding of said analytes, comprising an inactivation of the pathogen within the sample without isolation of RNA and/or DNA from the pathogen or the sample, and

(A) contacting the sample with at least twenty (20) different sets of analyte-specific probes for encoding of at least 20 different analytes, each set of analyte-specific probes interacting with a different analyte, wherein if the analyte is a nucleic acid each set of analyte-specific probes comprises at least five (5) analyte-specific probes which specifically interact with different sub-structures of the same analyte, each analyte-specific probe comprising

(aa) a binding element (S) that specifically interacts with one of the different analytes to be encoded, and

(bb) an identifier element (T) comprising a nucleotide sequence which is unique to the analyte to be encoded (unique identifier sequence),

wherein the analyte-specific probes of a particular set of analyte-specific probes differ from the analyte-specific probes of another set of analyte-specific probes in the nucleotide sequence of the identifier element (T),

wherein the analyte-specific probes in each set of analyte-specific probes binds to the same analyte and comprises the same nucleotide sequence of the identifier element (T) which is unique to said analyte; and

(B) contacting the sample with at least one set of decoding oligonucleotides per analyte, wherein in each set of decoding oligonucleotides for an individual analyte each decoding oligonucleotide comprises:

(aa) an identifier connector element (t) comprising a nucleotide sequence which is essentially complementary to at least a section of the unique identifier sequence of the identifier element (T) of the corresponding analyte-specific probe set, and

(bb) a translator element (c) comprising a nucleotide sequence allowing a specific hybridization of a signal oligonucleotide;

wherein the decoding oligonucleotides of a set for an individual analyte differ from the decoding oligonucleotides of another set for a different analyte in the first connect element (t); and

(C) contacting the sample with at least a set of signal oligonucleotides, each signal oligonucleotide comprising:

(aa) a translator connector element (C) comprising a nucleotide sequence which is essentially complementary to at least a section of the nucleotide sequence of a translator element (c) comprised in a decoding oligonucleotide, and

(bb) a signal element.

(D) Detecting the signal caused by the signal element;

(E) Selectively removing the decoding oligonucleotides and signal oligonucleotides from the sample, thereby essentially maintaining the specific binding of the analyte-specific probes to the analytes to be encoded;

(F) Performing at least three (3) further cycles comprising steps B) to E) to generate an encoding scheme with a code word per analyte, wherein in particular the last cycle may stop with step (D).

10. The method according to claim 9, wherein all steps are automated, in particular wherein steps B) to F) are automated, in particular by using a robotic system.

11. The method according to of any one of claims 9 to 10, wherein the code words obtained for the individual analytes in the performed cycles comprise the detected signals and additionally at least one element corresponding to no detected signal.

12. The method according to of any one of claims 9 to 11, wherein no signal is detected for at least one analyte within at least one cycle.

13. The method according to of any one of claims 9 to 12, wherein for at least for one individual analyte a position of the code word is zero (0).

14. The method according to of any one of claims 9 to 13, wherein the code word zero (0) is generated by using no decoding oligonucleotides having an identifier connector element (t) comprising a nucleotide sequence which is essentially complementary to at least a section of the unique identifier sequence of the identifier element (T) of a corresponding analyte-specific probe for an individual analyte.

15. The method according to of any one of claims 9 to 14, wherein if at least for one individual analyte a position of the code word is zero (0) in this cycle no corresponding decoding oligonucleotides having an identifier connector element (t) comprising a nucleotide sequence which is essentially complementary to at least a section of the unique identifier sequence of the identifier element (T) of a corresponding analyte-specific probe for an individual analyte are used.