

CLAIMS

1. A method for trapping discrete biological units in a hydrogel, said method comprising the steps of:
 - a) contacting a plurality of biological units with a plurality of barcode units to form biological unit/barcode unit complexes, wherein each barcode unit comprises a unique barcode, and wherein said barcode units comprise at least one means involved with binding said biological units,
 - b) contacting said biological unit/barcode unit complexes with a hydrogel solution,
 - c) polymerizing the hydrogel solution to embed said biological unit/barcode unit complexes in a hydrogel matrix, and
 - d) barcoding, within each of said biological unit/barcode unit complexes, the biological unit's nucleic acid with unique barcode of the barcode unit in the hydrogel matrix, wherein each barcode unit comprises a unique barcode.

2. A method for analyzing gene expression in discrete biological units, said method comprising the steps of:
 - a) contacting a plurality of biological units with a plurality of barcode units to form biological unit/barcode unit complexes, wherein each barcode unit comprises a unique barcode, and wherein said barcode units comprise at least one means involved with binding said biological units,
 - b) contacting said biological unit/barcode unit complexes with a hydrogel solution,
 - c) polymerizing the hydrogel solution to embed said biological unit/barcode unit complexes in a hydrogel matrix,
 - d) releasing nucleic acids from each biological unit in the hydrogel matrix,
 - e) barcoding said nucleic acids from each biological unit with the unique barcode of the barcode unit of a given biological unit/barcode unit complex in the hydrogel matrix,
 - f) synthesizing a cDNA library from the nucleic acids from each biological unit,
 - g) amplifying said cDNA library from each biological unit, wherein amplification of said cDNA library from each biological unit incorporates clonal copies of said unique barcode into the amplification products from each biological unit

3. A method for analyzing gene expression in discrete biological units according to claim 2, wherein said method further comprise a further step of sequencing the amplification products after step g).
4. A method for analyzing the genotype in discrete biological units, said method comprising the steps of:
 - a) contacting a plurality of biological units with a plurality of barcode units to form biological unit/barcode unit complexes, wherein each barcode unit comprises a unique barcode, and wherein said barcode units comprise at least one means involved with binding said biological units,
 - b) contacting said biological unit/barcode unit complexes with a hydrogel solution,
 - c) polymerizing the hydrogel solution to embed said biological unit/barcode unit complexes in a hydrogel matrix,
 - d) releasing genomic DNA from each biological unit in the hydrogel matrix,
 - e) barcoding said genomic DNA from each biological unit with the unique barcode of the barcode unity of a given biological unit/barcode unit complex in the hydrogel matrix, and
 - f) amplifying said genomic DNA from each biological unit, wherein amplification of said genomic DNA from each biological unit incorporates clonal copies of said unique barcode into the amplification products from each biological unit.
5. A method for analyzing the genotype in discrete biological units according to claim 4, wherein said method comprising a further step of synthesizing a DNA library from the nucleic acids from each biological unity between steps e) and f), and wherein step f) comprises amplifying said DNA library.
6. The method for analyzing the genotype in discrete biological units according to claim 4 or 5, wherein said method comprises a further step of sequencing the amplification products after step f).
7. A method for analyzing the haplotype in discrete biological units, said method comprising the steps of:
 - a) contacting a plurality of biological units with a plurality of barcode units to form biological unit/barcode unit complexes, wherein each barcode unit comprises a

- unique barcode, and wherein said barcode units comprise at least one means involved with binding said biological units,
- b) contacting said biological unit/barcode unit complexes with a hydrogel solution,
 - c) polymerizing the hydrogel solution to embed said biological unit/barcode unit complexes in a hydrogel matrix,
 - d) barcoding said nucleic acids from each biological unit with the unique barcode of the barcode unit of a given biological unit/barcode unit complex in the hydrogel matrix, and
 - e) amplifying said nucleic acid from each biological unit, wherein amplification of said genomic DNA from each biological unit incorporates clonal copies of said unique barcode into the amplification products from each biological unit.
8. The method for analyzing haplotype of discrete biological units according to claim 7, wherein said method comprises a further step of releasing nucleic acids from each biological unit in the hydrogel matrix between steps c) and d).
 9. The method for analyzing haplotype of discrete biological units according to claims 7 or 8, wherein said method comprises a further step of synthesizing a DNA library from nucleic acids from each biological unit between steps d) and e), and wherein step e) comprises amplifying said DNA library.
 10. The method for analyzing haplotype of discrete biological units according to any one of claims 7 to 9, wherein said method comprises a further step of sequencing the amplification products after step e).
 11. A method for analyzing the epigenome in discrete biological units, said method comprising the steps of:
 - a) contacting a plurality of biological units with a plurality of barcode units to form biological unit/barcode unit complexes, wherein each barcode unit comprises a unique barcode, and wherein said barcode units comprise at least one means involved with binding said biological units,
 - b) contacting said biological unit/barcode unit complexes with a hydrogel solution,
 - c) polymerizing the hydrogel solution to embed said biological unit/barcode unit complexes in a hydrogel matrix,

- d) releasing non-nucleosome-bound-DNA from each biological unit in the hydrogel matrix,
 - e) barcoding said non-nucleosome-bound-DNA from each biological unit with the unique barcode of the barcode unit of a given biological unit/barcode unit complex in the hydrogel matrix, and
 - f) amplifying said non-nucleosome-bound-DNA from each biological unit, wherein amplification of said non-nucleosome-bound-DNA from each biological unit incorporates clonal copies of said unique barcode into the amplification products from each biological unit.
- 12.** The method for analyzing the epigenome in discrete biological units according to claim **11**, wherein said method comprises a further step of synthesizing a DNA library from the non-nucleosome bound DNA from each biological unit between steps e) and f), and wherein step f) comprises amplifying said DNA library.
- 13.** The method for analyzing the epigenome in discrete biological units according to claim **11** to **12**, wherein said method comprises a further step of sequencing the amplication products after step f).
- 14.** The method according to any one of claims **1** to **13**, wherein said biological units are immobilized on a support.
- 15.** The method according to any one of claims **1** to **13**, wherein said barcode units are immobilized on a support.
- 16.** The method according to claim **14** or **15**, wherein said biological units or said barcode units are immobilized on a support in a hydrogel layer.
- 17.** The method according to any one of claims **1** to **16**, wherein said unique barcode is present in multiple clonal copies on each barcode unit.
- 18.** The method of any one of claims **1** to **17**, wherein said unique barcode comprises a nucleic acid sequence barcode.
- 19.** The method according to any one of claims **1** to **18**, wherein said unique barcode further comprises a nucleic acid sequence primer.

20. The method of claim 19, wherein said nucleic acid sequence primer comprises random nucleic acid sequence primers and/or specific nucleic acid sequence primers.
21. The method according to any one of claims 1 to 20, wherein said at least a means involved with binding said biological unit comprises proteins, peptides and/or fragments thereof; antibodies and/or fragments thereof; nucleic acids; carbohydrates; vitamins and/or derivatives thereof; coenzymes and/or derivatives thereof; receptor ligands and/or derivatives thereof; and/or hydrophobic groups.
22. The method according to any one of claims 1 to 21, wherein said each barcode unit consists of a bead.
23. The method according to any one of claims 1 to 22, wherein the step of barcoding is carried out in the hydrogel matrix by primer template annealing, primer-directed extension and/or ligation.
24. The method according to any one of claims 1 to 23, wherein said discrete biological units comprise cells, groups of cells, viruses, nuclei, mitochondria, chloroplasts, biological macromolecules, exosomes, chromosomes, contiguity preserved transposition DNA fragments and/or nucleic acid fragments.
25. The method of claim 24, wherein said cells or groups of cells are selected from the group consisting of cells in *in vitro* culture, stem cells, tumor cells, tissue biopsy cells, blood cells and tissue section cells.