WHAT IS CLAIMED IS:

1. A method for screening cells for a trait, the method comprising:

(a) obtaining a plurality of barcoded cells, wherein each barcoded cell comprises a single, unique barcode;

(b) performing a first sequencing of RNA and/or DNA on a subset of the plurality of barcoded cells;

(c) culturing the plurality of barcoded cells in the presence of a selection pressure for a first period of time, thereby forming a first plurality of cells;

(d) performing a second sequencing of RNA and/or DNA on a subset of the first plurality of cells;

(e) culturing the first plurality of cells in the presence of the selection pressure for a second period of time, thereby forming a second plurality of cells;

(f) performing a third sequencing of RNA and/or DNA on at least a subset of the second plurality of cells; and

(g) determining a level of a barcode sequenced in the first sequencing, second sequencing, and/or third sequencing

wherein steps (e) and (f) are repeated for one or more iterations thereby forming one or more subsequent pluralities of cells and thereby performing one or more subsequent sequencing on a subset of said pluralities of cells.

2. A method for screening cells for a response trait to a therapeutic agent, the method comprising:

(a) obtaining a plurality of barcoded cells, wherein each barcoded cell comprises a single, unique barcode;

(b) performing a first sequencing of RNA and/or DNA on a subset of the plurality of barcoded cells;

(c) culturing the plurality of barcoded cells in the presence of the therapeutic agent for a first period of time, thereby forming a first plurality of cells;

(d) performing a second sequencing of RNA and/or DNA on a subset of the first plurality of cells;

(e) culturing the first plurality of cells with the therapeutic agent for a second period of time, thereby forming a second plurality of cells;

(f) performing a third sequencing of RNA and/or DNA on a subset of the second plurality of cells; and

(g) determining a level of a barcode sequenced in the first sequencing, second sequencing, and/or third sequencing

wherein steps (e) and (f) are repeated for one or more iterations thereby forming one or more subsequent pluralities of cells and thereby performing one or more subsequent sequencing on a subset of said pluralities of cells.

3. A method for comparing responses to selective pressures, the method comprising:

(a) obtaining a first plurality of barcoded cells, wherein each barcoded cell comprises a single, unique barcode;

(b) obtaining a second plurality of barcoded cells that is substantially similar to the first plurality of barcoded cells;

(c) performing a first sequencing of RNA and/or DNA from the first plurality of barcoded cells and/or the second plurality of barcoded cells;

(d) culturing the first plurality of barcoded cells in the presence of a first selection pressure, thereby forming a first plurality of cells;

(e) culturing the second plurality of barcoded cells in the presence of a second selection pressure, thereby forming a second plurality of cells;

(f) performing a second sequencing of RNA and/or DNA from the first plurality of cells and/or the second plurality of cells;

(g) culturing the first plurality of cells in the presence of the first selection pressure, thereby forming a third plurality of cells;

(h) culturing the second plurality of cells in the presence of the second selection pressure, thereby forming a fourth plurality of cells;

(i) performing a third sequencing of RNA and/or DNA from the third plurality of cells and/or the fourth plurality of cells; and

(j) determining a level of one or more barcodes sequenced in the first sequencing, second sequencing, and/or third sequencing

wherein steps (g) to (i) are repeated for one or more iterations, thereby forming one or more subsequent pluralities of cells and one or more subsequent sequencings.

4. The method of claim 3, wherein step (j) further comprises determining a level of one or more barcodes in the one or more subsequent sequencing steps.

5. The method of claim 3 or 4, wherein the first plurality of barcoded cells and the second plurality of barcoded cells comprise a plurality of clonal populations, wherein each cell within a single clonal population comprises the same single, unique barcode.

6. The method of any one of claims 3 to 5, wherein the single, unique barcode is a unique combination of barcodes.

7. The method of claim 5, wherein the relative abundance of cells in each clonal population is approximately equal to the number of cells in each other clonal population in steps (a) and (b).

8. The method of claim 7, wherein from the first sequencing step the relative abundance of cells in a clonal population is determined relative to the number of cells comprising the barcode(s).

9. The method of any one of claims 3 to 8, further comprising identifying a barcode(s) that is enriched in the first plurality of cells and/or the second plurality of cells.

10. The method of claim 9, further comprising identifying one or more genes having higher levels of expression in cells comprising the enriched barcode(s).

11. The method of any one of claims 3 to 10, further comprising determining a first level of expression of a gene in cells having a barcode(s) enriched in the first plurality of cells and/or third plurality of cells and/or one or more subsequent pluralities of cells based on the second sequencing and/or third sequencing and/or one or more subsequent sequencings, and a second level of expression of the gene in the second plurality of barcoded cells, and/or fourth plurality of cells and/or one or more subsequent pluralities of cells based on the first sequencing, second sequencing, and/or third sequencing and/or one or more subsequent sequencings.

12. The method of claim 11, further comprising comparing the first level of expression of the gene to the second level of expression of the gene.

13. A method of screening cells for a trait in a cell, comprising:

(a) providing a mixture of cells comprising multiple clonal populations wherein each clonal population comprises an identifier that is unique to the respective clonal populations,

and wherein initial genetic, transcriptomic, and/or proteomic information of at least one representative member of each clonal population is known;

(b) culturing the mixture of cells in the presence of a first selective pressure for a first period of time, and at the end of the first period of time, obtaining second genetic, transcriptomic, and/or proteomic information for at least one member of a surviving clonal population from within the mixture of cells;

(c) subjecting the mixture of cells that were subjected to the first selective pressure to a second selective pressure for a second period of time, and at the end of the second period of time, obtaining third genetic, transcriptomic, and/or proteomic information of at least one member of a surviving clonal population from within the mixture of cells; and

(d) determining the level of a clonal population present in the final mixture of cells based upon the unique identifier for the clonal population.

14. The method of claim 13, wherein step (b) or (c) is repeated for one or more iterations.

15. The method of claim 13, wherein steps (b) and (c) are repeated for one or more iterations.

16. The method of any one of claims 13 to 15, further comprising identifying an adaptive trait, wherein the adaptive trait is a genetic and/or proteomic trait present in or absent from a clonal population in the final mixture of cells.

17. The method of claim 16, wherein the adaptive trait is a presence or absence of a gene, allele, genetic modification, transcript, or protein; or a change in a gene, allele, transcript, or protein when comparing the first, second and/or third and/or one or more subsequent genetic, transcriptomic, and/or proteomic information obtained.

18. The method of any one of claims 13 to 17, wherein step (b) comprises obtaining fourth genetic, transcriptomic, and/or proteomic information of at least one member of a second surviving clonal population from within the mixture of cells.

19. The method of any one of claims 13 to 18, wherein step (c) comprises obtaining fifth genetic, transcriptomic, and/or proteomic information of at least one member of a second surviving clonal population from within the mixture of cells.

20. The method of any one of claims 13 to 19, further comprising comparing information from the initial genetic, transcriptomic, and/or proteomic information, second genetic, transcriptomic, and/or proteomic information, and/or third genetic, transcriptomic, and/or proteomic information, and/or one or more subsequent genetic, transcriptomic, and/or proteomic information.

21. The method of any one of claims 13 to 20, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises RNA-seq, single cell RNA-seq, DNA sequencing, epigenetic sequencing, or protein sequencing.

22. The method of any one of claims 13 to 21, wherein the first selective pressure and/or the second selective pressure comprises treatment with a therapeutic agent, contact with a contaminant, genomic engineering, engraftment into a host, a culture condition, a growth condition, contact with a stimulus, or contact with other cells.

23. A method of identifying a cellular program that facilitates adaptation to a pressure, comprising:

a. transducing cells with a plurality of barcodes such that each cell contains a single, unique barcode;

b. expanding the cells in culture to create a starting cell pool of clones of cells containing each barcode;

c. obtaining first genetic, transcriptomic, and/or proteomic information from a first subset of the starting cell pool;

d. culturing a second subset of the starting cell pool in the presence of a selective pressure to expand the starting cell pool and form an intermediate cell pool;

e. obtaining second genetic, transcriptomic, and/or proteomic information from a first subset of the intermediate cell pool;

f. continuing to culture a second subset of the intermediate cell pool in the presence of the selective pressure to expand the intermediate cell pool and form a final cell pool;

g. obtaining third genetic, transcriptomic, and/or proteomic information from at least a subset of the final cell pool;

h. quantifying a level of each barcode in the final cell pool, intermediate cell pool, and/or starting cell pool;

i. assigning cells with barcodes enriched in the final cell pool as winning clones and/or assigning cells with barcodes depleted in the final cell pool as losing clones; and

j. determining a genetic mutation, transcription program, and/or protein expression associated with at least one winning clone and/or at least one losing clone

wherein approximately equal numbers of clones of cells containing each barcode are used to create the starting cell pool.

24. The method of claim 23, wherein the numbers of clones of cells are normalized relative to the numbers of cells comprising each barcode as obtained in step (c).

25. The method of claim 23 or 24, wherein steps (d) and (e) are repeated for one or more iterations thereby obtaining one or more additional intermediate cell pools and one or more additional intermediate genetic, transcriptomic, and/or proteomic information.

26. The method of claim 25, wherein step (h) further comprises quantifying a level of each barcode in the one or more additional intermediate cell pools.

27. The method of any one of claims 23 to 26, wherein the single, unique barcode is a unique combination of barcodes.

28. The method of any one of claims 23 to 26, wherein the selective pressure comprises treatment with a therapeutic agent, contact with a contaminant, genomic engineering, engraftment into a host, a culture condition, a growth condition, contact with a stimulus, or contact with other cells.

29. The method of any one of claims 23 to 28, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises RNA-seq, single cell RNA-seq, DNA sequencing, epigenetic sequencing, or protein sequencing.