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. The method of claim 1 or 2, wherein the plurality of barcoded cells of step (a) is expanded in culture prior to step (b) or step (c).~~

~~4. The method of claim 1 or 2, wherein the plurality of barcoded cells had been expanded in culture prior to step (a).~~

~~5. The method of any one of the above claims, 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 sequencings on a subset of said pluralities of cells.~~

~~6. The method of claim 5, wherein step (g) further comprises determining levels of barcodes sequenced in the one or more subsequent sequencings.~~

~~7. The method of any one of claims 1 to 6, wherein the plurality of barcoded cells comprises a plurality of clonal populations, wherein each cell within a single clonal population comprises the same single, unique barcode.~~

~~8. The method of claim 7, wherein the relative abundance of cells in each clonal population is approximately equal to the number of cells in each other clonal population in step (a).~~

~~9. The method of claim 7, wherein the relative abundance of cells in each clonal population is determined relative to the number of cells comprising each barcode as determined in the first sequencing step.~~

~~10. The method of any one of claims 1 to 9, wherein a level of two or more barcodes sequenced in the first sequencing, second sequencing, and/or third sequencing are determined.~~

~~11. The method of any one of claims 1 to 10, further comprising identifying a barcode(s) that is enriched in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells.~~

~~12. The method of claim 11, wherein the barcode(s) is enriched compared to one or more other barcodes in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells.~~

~~13. The method of claim 11, wherein the barcode(s) is enriched compared to the amount of the barcode(s) in the plurality of barcoded cells.~~

~~14. The method of any one of claims 11 to 13, further comprising identifying one or more genes having higher levels of expression in cells comprising the enriched barcode(s).~~

~~15. The method of claim 14, wherein the identifying the one or more genes comprises determining that the level of expression of at least one gene is higher in the first sequencing, second sequencing, and/or the third sequencing and/or one or more subsequent sequencings in the cells comprising the enriched barcode(s) compared to cells comprising a different barcode(s) that had a different level of enrichment or no enrichment.~~

~~16. The method of claim 14 or 15, wherein the identifying comprises identifying an adaptive trait based upon higher expression of the at least one gene.~~

~~17. The method of claim 14 or 15, wherein the identifying comprises identifying that the gene is involved in adaptation of the cell to the selection pressure or therapeutic agent based upon higher expression of the at least one gene.~~

~~18. The method of any one of claims 11 to 17, further comprising identifying one or more genes having lower levels of expression in cells comprising the enriched barcode(s) compared to cells comprising a different barcode(s) that had a different level of enrichment.~~

~~19. The method of claim 18, wherein the identifying one or more genes having lower levels of expression comprises determining the level of expression of at least one gene is lower in the first sequencing, second sequencing, and/or the third sequencing and/or one or more subsequent sequencings in the cells comprising the enriched barcode(s) compared to cells comprising a different barcode(s) that had a different level of enrichment or no enrichment.~~

20. The method of claim 18 or 19, wherein the identifying comprises identifying an adaptive trait based upon lower expression of the at least one gene.

21. The method of claim 18 or 19, wherein the identifying comprises determining that the gene is involved in adaptation of the cell to the selection pressure or therapeutic agent based upon lower expression of the at least one gene.

22. The method of any one of claims 1 to 21, further comprising:

(h) identifying a barcode(s) that is enriched in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells;

(i) identifying from the first sequencing a first gene having a higher level of expression in cells comprising the enriched barcode(s) than in cells comprising a barcode(s) that is not enriched in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells, such that the higher expression of the first gene indicates that the first gene is a candidate pre-existing trait for resistance or sensitivity to the selective pressure or therapeutic agent.

23. The method of any one of claims 1 to 22, further comprising:

(j) identifying a barcode(s) that is enriched in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells;

(k) identifying from the first sequencing a second gene having a lower level of expression in cells comprising the enriched barcode(s) than in cells comprising a barcode(s) that is not enriched in the first plurality of cells and/or the second plurality of cells and or one or more subsequent pluralities of cells, such that the lower expression of the second gene indicates that the second gene is a candidate pre-existing trait for resistance or sensitivity to the selective pressure or therapeutic agent.

24. The method of any one of claims 1 to 23, further comprising:

(l) identifying a barcode that is enriched in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells;

(m) identifying from the second sequencing a third gene having a higher level of expression in cells comprising the enriched barcode(s) than in cells comprising a barcode that is not enriched in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells, such that the higher expression of the third gene

~~indicates that the third gene is a candidate adaptive trait for resistance or sensitivity to the selective pressure or therapeutic agent.~~

~~25. The method of claim 24, wherein the expression of the third gene is not higher in cells comprising a barcode(s) that is not enriched in the first plurality of cells and/or the second plurality of cells and/or one more subsequent pluralities of cells.~~

~~26. The method of any one of claims 1 to 25, further comprising:~~
~~(n) identifying a barcode(s) that is enriched in the first plurality of cells and/or the second plurality of cells and/or one more subsequent pluralities of cells;~~
~~(o) identifying from the second sequencing and/or the third sequencing a fourth gene having a lower level of expression in cells comprising the enriched barcode(s) than in cells comprising a barcode(s) that is not enriched in the first plurality of cells and/or the second plurality of cells and/or one or more subsequent pluralities of cells, such that the lower expression of the fourth gene indicates that the first gene is a candidate adaptive trait for resistance or sensitivity to the selective pressure or therapeutic agent.~~

~~27. The method of claim 26, wherein the expression of the fourth gene is not lower in cells comprising a barcode(s) that is not enriched in the first plurality of cells and/or the second plurality of cells.~~

~~28. The method of any one of the above claims, wherein the one or more genes comprises a gene set.~~

~~29. The method of any one of the above claims, wherein the unique barcode is integrated into the genome of the barcoded cell.~~

~~30. The method of any one of the above claims, wherein the unique barcode is not integrated into the genome of the barcoded cell.~~

~~31. The method of any one of the above claims, wherein the unique barcode is a unique combination of barcodes.~~

~~32. The method of any one of the above claims, wherein the first sequencing, second sequencing, and/or the third sequencing and/or one or more subsequent sequencings is performed using RNA-seq.~~

~~33. The method of claim 32, wherein the RNA-seq is single cell RNA-seq.~~

~~34. The method of any one of the above claims, wherein the first sequencing, second sequencing, and/or the third sequencing and/or one or more subsequent sequencings is DNA sequencing.~~

~~35. The method of any one of the above claims, wherein the first sequencing, second sequencing, and/or the third sequencing and/or one or more subsequent sequencings is epigenetic sequencing.~~

~~36. The method of any one of the above claims, wherein the first sequencing, second sequencing, and/or one or more subsequent sequencings is protein sequencing.~~

~~37. The method of any one of claims 1 to 30, wherein the first sequencing, second sequencing, and/or the third sequencing and/or one or more subsequent sequencings is not one or more of RNA-seq, DNA sequencing, epigenetic sequencing, or protein sequencing.~~

~~38. The method of claim 37, wherein the first sequencing, second sequencing, and/or the third sequencing and/or one or more subsequent sequencings is not DNA sequencing.~~

~~39. The method of any one of the above claims, wherein the selective pressure is 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.~~

~~40. The method of any one of the above claims, wherein the first period of time is between about 30 minutes and about 1 month.~~

~~41. The method of any one of the above claims, wherein the second period of time is between about 12 hours and about 12 months.~~

~~42.~~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.

~~43. The method of claim 42, 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.~~

~~44.~~4. The method of claim ~~43~~ 3, wherein step (j) further comprises determining a level of one or more barcodes in the one or more subsequent sequencing steps.

~~45.~~5. The method of ~~any one of claims 42 to 44~~ 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.

~~46.~~6. The method of any one of claims ~~42 to 45~~ 3 to 5, wherein the single, unique barcode is a unique combination of barcodes.

~~47.~~7. The method of claim ~~45~~ 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).

~~48.~~8. The method of claim ~~47~~ 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).

~~49.~~9. The method of any one of claims ~~42 to 48~~ 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.

~~50.~~10. The method of claim ~~49~~ 9, further comprising identifying one or more genes having higher levels of expression in cells comprising the enriched barcode(s).

~~51.~~11. The method of any one of claims ~~42 to 50~~ 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.

~~52.~~12. The method of claim ~~51~~ 11, further comprising comparing the first level of expression of the gene to the second level of expression of the gene.

~~53.~~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.

~~54.~~14. The method of claim ~~53~~ 13, wherein step (b) or (c) is repeated for one or more iterations.

~~55. The method of claim 53, wherein step (c) is repeated for one or more iterations.~~

~~56.~~15. The method of claim ~~53~~ 13, wherein steps (b) and (c) are repeated for one or more iterations.

~~57.~~16. The method of any one of claims ~~53 to 56~~ 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.

~~58.~~17. The method of claim ~~57~~ 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.

~~59.~~18. The method of any one of claims ~~53 to 58~~ 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.

~~60.~~19. The method of any one of claims ~~53 to 59~~ 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.

~~61.~~20. The method of any one of claims ~~53 to 60~~ 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.

~~62. The method of any one of claims 53 to 61, further comprising comparing 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 to genetic, transcriptomic and/or proteomic information of a different clonal population of cells having a different unique barcode that was subjected to the selective pressure.~~

~~63. The method of any one of claims 53 to 62, further comprising comparing 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 from a clonal population of cells having a unique barcode, to genetic, transcriptomic and/or proteomic information from a different determination step for the clonal population of cells.~~

~~64. The method of claim 62 or 63, wherein the unique barcode is a unique combination of barcodes.~~

~~65.~~21. The method of any one of claims ~~53 to 63~~ 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.

~~66. The method of claim 65, wherein the RNA-seq is single cell RNA-seq.~~

~~67. The method of any one of claims 53 to 66, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises DNA sequencing.~~

~~68. The method of any one of claims 53 to 67, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises epigenetic sequencing.~~

~~69. The method of any one of claims 53 to 68, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises protein sequencing.~~

~~70. The method of any one of claims 53 to 70, wherein obtaining the genetic, transcriptomic, and/or proteomic information does not include one or more of RNA-seq, DNA sequencing, epigenetic sequencing, or protein sequencing.~~

~~71. The method of claim 70, wherein obtaining the genetic, transcriptomic, and/or proteomic information does not include DNA sequencing.~~

~~72.~~22. The method of any one of claims ~~53 to 69~~ 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.

~~73.~~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.

~~74. The method of claim 73, wherein approximately equal numbers of clones of cells containing each barcode are used to create the starting cell pool.~~

~~75.~~24. The method of claim ~~74~~ 23, wherein the numbers of clones of cells are normalized relative to the numbers of cells comprising each barcode as obtained in step (c).

~~76.~~25. The method of ~~any one of claims 73 to 75~~ 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.

~~77.~~26. The method of claim ~~76~~ 25, wherein step (h) further comprises quantifying a level of each barcode in the one or more additional intermediate cell pools.

~~78.~~27. The method of any one of claims ~~73 to 77~~ 23 to 26, wherein the single, unique barcode is a unique combination of barcodes.

~~79.~~28. The method of any one of claims ~~73 to 77~~ 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.

~~80.~~29. The method of any one of claims ~~73 to 79~~ 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.

~~81. The method of claim 80, wherein the RNA-seq is single cell RNA-seq.~~

~~82. The method of any one of claims 73 to 81, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises DNA sequencing.~~

~~83. The method of any one of claims 73 to 82, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises epigenetic sequencing.~~

~~84. The method of any one of claims 73 to 83, wherein obtaining the genetic, transcriptomic, and/or proteomic information comprises protein sequencing.~~

~~85. The method of any one of claims 73 to 79, wherein obtaining the genetic, transcriptomic, and/or proteomic information does not include one or more of RNA-seq, DNA sequencing, epigenetic sequencing, or protein sequencing.~~

~~86. The method of claim 85, wherein obtaining the genetic, transcriptomic, and/or proteomic information does not include DNA sequencing.~~