WHAT IS CLAIMED IS:

1. A method, comprising

making copies of two or more populations of polynucleotides, wherein the two or more populations of polynucleotides each comprise an identifier sequence unique to each population of polynucleotide, and wherein the making comprises forming clusters of copies covalently attached to a substrate and the copies comprise the identifier sequences and their complements,

after the making copies of the two or more populations of polynucleotides,

hybridizing two or more populations of identifier sequence oligonucleotide probes to the identifier sequences,

wherein the identifier sequence oligonucleotide probes of each population comprise sequences complementary to only one of the unique identifier sequences or complements thereto,

washing away identifier sequence oligonucleotide probes that are not hybridized to the identifier sequences, and

comparing amounts of identifier sequence oligonucleotide probes hybridized to the copies of the two or more populations of polynucleotides, wherein

at least one feature differs between the forming clusters of copies of each of the two or more populations of polynucleotides attached to the substrate.

2. The method of claim 1 wherein the identifier sequence oligonucleotide probes comprise a fluorophore.

3. The method of claim 1 or claim 2, further comprising detecting a difference between the amounts of identifier sequence oligonucleotide probes hybridized to the copies of the two or more populations of polynucleotides attached to the substrate, wherein the difference is at least about 10%.

4. The method of claim 3, wherein the difference is at least about 20%.

5. The method of claim 3, wherein the difference is at least about 30%.

6. The method of claim 1, wherein

the at least one feature comprises at least one of a difference in a guanine-cytosine content between at least two of the two or more populations of polynucleotides, a difference in a length between at least two of the two or more populations of polynucleotides, and/or a difference in a preparation method between at least two of the two or more populations of polynucleotides.

7. The method of claim 6, further comprising detecting a difference between amounts of identifier sequence oligonucleotide probes hybridized to the copies of the two or more populations of polynucleotides attached to the substrate, wherein the difference is at least about 10%.

8. The method of claim 7, wherein the difference is at least about 20%.

9. The method of claim 7, wherein the difference is at least about 30%.

10. A method, comprising

making copies of two or more populations of polynucleotides, wherein the two or more populations of polynucleotides each comprise a unique identifier sequence, and wherein the making comprises forming clusters of copies covalently attached to a substrate and the copies comprise the identifier sequences and their complements,

after the making copies of the two or more populations of polynucleotides,

hybridizing two or more populations of identifier sequence oligonucleotide probes comprising a fluorophore to the identifier sequences, wherein the identifier sequence oligonucleotide probes of each population comprise sequences complementary to only one of the unique identifier sequences or complements thereto,

washing away identifier sequence oligonucleotide probes that are not hybridized to the identifier sequences, and

detecting amounts of identifier sequence oligonucleotide probes hybridized to the copies of the two or more populations of polynucleotides attached to the substrate, wherein

at least one feature differs between the forming clusters of copies of each of the two or more populations of polynucleotides attached to the substrate.

11. The method of claim 10, further comprising detecting a difference between the amounts of identifier sequence oligonucleotide probes hybridized to copies of the two or more populations of polynucleotides, wherein the difference is at least about 10%.

12. The method of claim 11, wherein the difference is at least about 20%.

13. The method of claim 11, wherein the difference is at least about 30%.

14. The method of claim 10, wherein the two or more populations of polynucleotides comprise three or more populations of polynucleotides.

15. The method of claim 10, wherein the at least one feature comprises at least one of a difference in a guanine-cytosine content between at least two of the two or more populations of polynucleotides, a difference in a length between at least two of the two

or more populations of polynucleotides, and/or a difference in a preparation method between at least two of the two or more populations of polynucleotides.

16. The method of claim 15, wherein the two or more populations of polynucleotides comprise three or more populations of polynucleotides.

17. The method of claim 6, wherein the at least one feature comprises at least one of a polymerase used for the making of the copies, a polymerization reagent used for the making of the copies, a reagent used for rehybridizing copies during the forming clusters, a reagent used linearizing copies during the forming clusters, a polymer by which copies are attached to a substrate, or any combination of two or more of the foregoing.

18. The method of claim 10, wherein the at least one feature comprises at least one of a polymerase used for the making of the copies, a polymerization reagent used for the making of the copies, a reagent used for rehybridizing copies during the forming clusters, a reagent used linearizing copies during the forming clusters, a polymer by which copies are attached to a substrate, or any combination of two or more of the foregoing.

19. The method of claim 2, wherein the identifier sequence oligonucleotide probes of each population of identifier sequence oligonucleotide probes comprises a fluorophore unique to each population of identifier sequence oligonucleotide probes.

20. The method of claim 10 wherein each population of identifier sequence oligonucleotide probes comprises a fluorophore unique to each population of identifier sequence oligonucleotide probes.

21. The method of claim 1, wherein one of the two or more populations of identifier sequence oligonucleotide probes are hybridized to identifier sequences concurrently.