CLAIMS

WHAT IS CLAIMED IS:

1. A polynucleotide library, the polynucleotide library with controlled stoichiometry comprising at least 5000 polynucleotides, wherein each of the at least 5000 polynucleotides is present in an amount such that, following hybridization with genomic fragments and sequencing of the hybridized genomic fragments, the polynucleotide library provides for at least 30 fold read depth of at least 90 percent of the bases of the genomic fragments under conditions for up to a 55 fold theoretical read depth for the bases of the genomic fragments.
2. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least 30 fold read depth of at least 95 percent of the bases of the genomic fragments under conditions for up to a 55 fold theoretical read depth for the bases of the genomic fragments.
3. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least 30 fold read depth of at least 98 percent of the bases of the genomic fragments under conditions for up to a 55 fold theoretical read depth for the bases of the genomic fragments.
4. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least 90 percent unique reads for the bases of the genomic fragments.
5. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least 95 percent unique reads for the bases of the genomic fragments.
6. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least 90 percent of the bases of the genomic fragments having a read depth within about 1.5 times the mean read depth.
7. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least 95 percent of the bases of the genomic fragments having a read depth within about 1.5 times the mean read depth.
8. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least 90 percent of the genomic fragments having a GC percentage from 10 percent to 30

percent or 70 percent to 90 percent having a read depth within about 1.5x of the mean read depth.

9. The polynucleotide library of claim 1, wherein the polynucleotide library provides for at least about 80 percent of the genomic fragments having a repeating or secondary structure sequence percentage from 10 percent to 30 percent or 70 percent to 90 percent having a read depth within about 1.5x of the mean read depth.

10. The polynucleotide library of claim 1, wherein each of the genomic fragments are about 100 bases to about 500 bases in length.

11. The polynucleotide library of claim 1, wherein at least about 80 percent of the at least 5000 polynucleotides are represented in an amount within at least about 1.5 times the mean representation for the polynucleotide library.

12. The polynucleotide library of claim 1, wherein at least 30 percent of the least 5000 polynucleotides comprise polynucleotides having a GC percentage from 10 percent to 30 percent or 70 percent to 90 percent.

13. The polynucleotide library of claim 1, wherein at least about 15 percent of the at least 5000 polynucleotides comprise polynucleotides having a repeating or secondary structure sequence percentage from 10 percent to 30 percent or 70 percent to 90 percent.

14. The polynucleotide library of claim 1, wherein the at least 5000 polynucleotides encode for at least 1000 genes.

15. The polynucleotide library of claim 1, wherein the polynucleotide library comprises at least 100,000 polynucleotides.

16. The polynucleotide library of claim 1, wherein the polynucleotide library comprises at least 700,000 polynucleotides.

17. The polynucleotide library of claim 1, wherein the at least 5000 polynucleotides comprise at least one exon sequence.

18. The polynucleotide library of claim 16, wherein the at least 700,000 polynucleotides comprise at least one set of polynucleotides collectively comprising a single exon sequence.

19. The polynucleotide library of claim 18, wherein the at least 700,000 polynucleotides comprises at least 150,000 sets.

20. A polynucleotide library, the polynucleotide library comprising at least 5000 polynucleotides, wherein each of the polynucleotides is about 20 to 200 bases in length,

wherein the plurality of polynucleotides encode sequences from each exon for at least 1000 preselected genes, wherein each polynucleotide comprises a molecular tag, wherein each of the at least 5000 polynucleotides are present in an amount such that, following hybridization with genomic fragments and sequencing of the hybridized genomic fragments, the polynucleotide library provides for at least 30 fold read depth of at least 90 percent of the bases of the genomic fragments under conditions for up to a 55 fold theoretical read depth for the bases of the genomic fragments.

21. The polynucleotide library of claim 20, wherein the polynucleotide library provides for at least 30 fold read depth of at least 95 percent of the bases of the genomic fragments under conditions for up to a 55 fold theoretical read depth for the bases of the genomic fragments.

22. The polynucleotide library of claim 20, wherein the polynucleotide library provides for at least 30 fold read depth of at least 98 percent of the bases of the genomic fragments under conditions for up to a 55 fold theoretical read depth for the bases of the genomic fragments.

23. The polynucleotide library of claim 20, wherein the polynucleotide library provides for at least 90 percent unique reads for the bases of the genomic fragments.

24. The polynucleotide library of claim 1, wherein the fragments are sequenced by a method comprising sequencing by synthesis.

25. The polynucleotide library of claim 24, wherein the fragments are sequenced on an Illumina Miseq sequencing instrument.

26. The polynucleotide library of claim 1, wherein the total number of sequencing reads is at least 30 million.

27. The polynucleotide library of claim 1, wherein the polynucleotides are configured to hybridize to genomic fragments comprising at least 30 million bases.

28. The polynucleotide library of claim 1, wherein the at least 5000 polynucleotides comprise sequences encoding for multiple exons.