CLAIMS

WHAT IS CLAIMED IS:

1. A method for processing a biological sample of a human subject, comprising:

(a) providing said biological sample from said human subject, wherein said biological sample of said human subject comprises (i) human nucleic acid molecules derived from said human subject, and (ii) non-human nucleic acid molecules derived from one or more non-human species, wherein said biological sample is derived from a tumor biopsy, whole blood, or blood plasma, wherein an amount of said human nucleic acid molecules derived from said human subject is 1,000 times or more greater than said non-human nucleic acid molecules derived from a non-human species;

(b) enriching said human nucleic acid molecules and said non-human nucleic acid molecules derived from said biological sample using a set of nucleic acid capture probes attached to a hybridization array or one or more beads, to yield an enriched set of nucleic acid molecules comprising (i) a subset of said human nucleic acids derived from said human subject and (ii) a subset of said non-human nucleic acids derived from one or more non-human species, wherein said set of nucleic acid capture probes comprises (i) a first plurality of nucleic acid probes configured to target elements of a human genome and (ii) a second plurality of nucleic acid probes configured to target elements of one or more non-human genome(s), wherein said first plurality of nucleic acid probes comprises probes configured to target junction sequences created by human V(D)J rearrangement or recombination, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target: human papilloma virus E6 gene, human papilloma virus E7 gene, or one or more elements of a bacterial 16S ribosomal RNA gene; and

(c) sequencing said enriched set of nucleic acid molecules to yield sequence information comprising sequences of said enriched set of nucleic acid molecules, where said sequences of said enriched set of nucleic acid molecules comprise sequences of (i) human nucleic acids from said biological sample from said human subject and (ii) non-human nucleic acids from said biological sample of said human subject.

2. The method of claim 1, wherein enriching said human nucleic acid molecules and said non-human nucleic acid molecules derived from said biological sample comprises conducting one or more hybridization reactions.

3. The method of claim 1, wherein a concentration of said second plurality of nucleic acid probes is greater than a concentration of said first plurality of nucleic acid probes in said set of nucleic acid capture probes.

4. The method of claim 1, wherein a concentration of said second plurality of nucleic acid probes in said set of nucleic acid capture probes is greater than a concentration of said first plurality of nucleic acid probes in said set of nucleic acid capture probes.

5. The method of claim 1, wherein said first plurality of nucleic acid probes comprises a human exome capture probe set.

6. The method of claim 1, wherein said sequencing comprises performing sequencing to generate paired-end read sequences of lengths from 130 bases to 280 bases.

7. The method of claim 1, wherein said enriching comprises differentially enriching said human nucleic acid molecules and said non-human nucleic acid molecules.

8. The method of claim 1, wherein said enriching comprises enriching said human nucleic acid molecules and said non-human nucleic acid molecules, concurrently.

9. The method of claim 1, wherein said enriching comprises enriching said human nucleic acid molecules and said non-human nucleic acid molecules in a same sample volume.

10. The method of claim 1, further comprising amplifying said enriched set of nucleic acid molecules of (b) prior to sequencing in (c) to yield said sequence information.

11. The method of claim 1, wherein said biological sample is derived from said tumor biopsy.

12. The method of claim 1, wherein said biological sample is derived from said whole blood.

13. The method of claim 1, wherein said biological sample is derived from said blood plasma.

14. The method of claim 1, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said human papilloma virus E6 gene.

15. The method of claim 1, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said human papilloma virus E7 gene.

16. The method of claim 1, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said one or more elements of said bacterial 16S ribosomal RNA gene.

17. The method of claim 1, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said human papilloma virus E6 gene and said human papilloma virus E7 gene.

18. The method of claim 1, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said human papilloma virus E6 gene, said human papilloma virus E7 gene and said one or more elements of said bacterial 16S ribosomal RNA gene.

19. The method of claim 1, wherein enriching of (b) is performed using said set of nucleic acid capture probes attached to said hybridization array.

20. The method of claim 1, wherein enriching of (b) is performed using said one or more beads.

21. The method of claim 11, and wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said human papilloma virus E6 gene or said human papilloma virus E7 gene.

22. The method of claim 11, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said one or more elements of said bacterial 16S ribosomal RNA gene.

23. The method of claim 12, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said human papilloma virus E6 gene or said human papilloma virus E7 gene.

24. The method of claim 12, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said one or more elements of said bacterial 16S ribosomal RNA gene.

25. The method of claim 13, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said human papilloma virus E6 gene or said human papilloma virus E7 gene.

26. The method of claim 13, wherein said second plurality of nucleic acid probes comprises one or more probes configured to target said one or more elements of said bacterial 16S ribosomal RNA gene.