CLAIMS

1. A metagenomics sequencing process comprising:

degrading host nucleic acids in a body fluid sample by contacting the sample with magnetic particles coupled to enzymes to degrade the nucleic acids present in the sample, wherein the magnetic particles coupled to enzymes are capable of degrading both DNA and RNA followed by applying a magnetic field to remove the magnetic particles coupled to enzymes from the sample; and

creating a DNA and RNA library from the degraded sample in a one-pot process.

2. The metagenomics sequencing process of claim 1, wherein the enzyme is a nuclease.

3. The metagenomics sequencing process of claim 1, wherein the one-pot process uses a set of primers to prime single-stranded DNA and at the same time prime RNA.

4. The metagenomics sequencing process of claim 1, wherein the sample includes more than one type of nucleic acid including single-stranded and/or double-stranded DNA and/or RNA as a template of subsequent extensions and amplifications and the one-pot process includes preparing a first DNA strand from the sample including annealing one or more first DNA strand generation primers to any of the DNA and/or RNA template, and extending from the

annealed first DNA strand generation primer including employing a DNA polymerase that enables synthesis of the first DNA strand from either or both of DNA and/or RNA templates to obtain the first DNA strand.

5. The metagenomics sequencing process of claim 1, wherein the magnetic particles coupled to enzymes comprise magnetic particles coupled to both a DNAse and a RNAse, a magnetic particle coupled to an enzyme capable of degrading both DNA and RNA, a mixture comprising a magnetic particle coupled to a DNAse and a magnetic particle coupled to a RNAse, or combinations thereof.

6. The metagenomics sequencing process of claim 1 or claim 2, wherein the nucleic acids comprise cell-free nucleic acids.

7. The metagenomics sequencing process of any one of claims 1-5, wherein the degrading of the nucleic acids in the sample further comprises applying a lysing agent to the sample for selectively lysing biological complexes in the sample to free said nucleic acids for degradation by the enzymes, optionally wherein the lysing agent is substantially incapable of lysing viruses and intact cells selected from bacteria, protozoa, fungi and parasites.

8. The metagenomics sequencing process of claim 7, wherein the lysing agent comprise a mild detergent.

9. The metagenomics sequencing process of claim 1, wherein the enzyme is a nuclease.

10. A method of detecting non-host species in a host sample, the method comprising:

contacting the host sample with magnetic particles coupled to enzymes to degrade cell-free host nucleic acids present in the host sample, wherein the magnetic particles coupled to enzymes are capable of degrading both DNA and RNA;

applying a magnetic field to remove the magnetic particles coupled to enzymes from the host sample;

creating a DNA and RNA library from the degraded sample in a one-pot process; and

detecting the presence of non-host nucleic acids from the DNA and RNA library.

11. The method of claim 10, wherein the one-pot process uses a set of primers to prime single-stranded DNA and at the same time prime RNA.

12. The method of claim 10, wherein the sample includes more than one type of nucleic acid including single-stranded and/or double-stranded DNA and/or RNA as a template of subsequent extensions and amplifications and the one-pot process includes preparing a first DNA strand from the sample including annealing one or more first DNA strand generation primers to any of the DNA and/or RNA template, and extending from the annealed first DNA strand

generation primer including employing a DNA polymerase that enables synthesis of the first DNA strand from either or both of DNA and/or RNA templates to obtain the first DNA strand.

13. The method of claim 10, further comprising removing host cells from the host sample prior to contacting the host sample with magnetic particles coupled to enzymes.

14. The method of claim 10, further comprising applying a first lysing agent to the host sample for selectively lysing biological complexes to free host nucleic acids contained therein prior to the contacting step, optionally wherein the first lysing agent is substantially incapable of lysing non-host species to free the nucleic acids contained therein for degradation by the enzymes.

15. The method of claim 14, wherein the lysing agent comprise a mild detergent.

16. The method of claim 10, wherein the step of detecting the presence of non-host nucleic acids in the sample comprises:

applying a second lysing agent to the host sample for lysing non-host species to free the nucleic acids contained therein.

17. The method of claim 10, wherein the second lysing agent comprises lysing particles that are capable of imparting a mechanical force to lyse the non-host species and free the nucleic acids contained therein.

18. The method of claim 10, wherein detecting the presence of non-host nucleic acids in the sample comprises sequencing the non-host nucleic acids.