CLAIMS

We Claim:

1. A method for improved single molecule sequencing, the method comprising:

preparing a set of unique molecular identifier (UMI)-based molecules associated with a set of target nucleic acid sequences;

facilitating generation a set of tagged nucleic acid molecules based on the set of UMI-based molecules and a set of nucleic acid molecules corresponding to the set of target nucleic acid sequences, wherein each tagged nucleic acid molecule of the set of tagged nucleic acid molecules comprises:

a UMI region comprising a set of random "N" bases, wherein each random “N” base is selected from any one of an "A" base, a "G" base, a "T" base, and a "C" base; and

a target region corresponding to a target nucleic acid sequence of the set of target nucleic acid sequences; and

facilitating single molecule sequencing with the set of tagged nucleic acid molecules, wherein performing the single molecule sequencing comprises:

determining a comparison between a first set of sequence regions and a second set of sequence regions, wherein the first set of sequence regions comprises a first UMI region and a first target region of a sequenced tagged nucleic acid molecule of the set of tagged nucleic acid molecules, and wherein the second set of sequence regions comprises a second UMI region and a second target region of a tagged nucleic acid molecule of the set of tagged nucleic acid molecules; and

stopping sequencing of the tagged nucleic acid molecule based on the comparison between the first set of sequence regions and the second set of sequence regions.

2. The method of Claim 1, wherein stopping sequencing of the tagged nucleic acid molecule based on the comparison comprises stopping the sequencing of the tagged nucleic acid molecule in response to the first UMI region and the first target region matching the second UMI region and the second target region.

3. The method of Claim 2 wherein facilitating the single molecule sequencing comprises determining the first set of sequence regions of the sequenced tagged nucleic acid molecule; and storing the first set of sequence regions, wherein determining the comparison between the first set of sequence regions and the second set of sequence regions comprises retrieving the first set of sequence regions for the comparison to the second set of sequence regions.

4. The method of Claim 3, wherein determining the first set of sequence regions, storing the first set of sequence regions, determining the comparison between the first set of sequence regions and the second set of sequence regions, and stopping the sequencing of the tagged nucleic acid molecule are each performed in at least substantially real-time during a single sequencing run of the single molecule sequencing.

5. The method of Claim 1, wherein stopping the sequencing of the tagged nucleic acid molecule comprises stopping the sequencing based on the comparison and a defined limit for the sequencing of tagged nucleic acid molecules associated with the first set of sequence regions, wherein the set of tagged nucleic acid molecules comprises the tagged nucleic acid molecules associated with the first set of sequence regions, wherein preparing the set of UMI-based molecules comprises determining a number of different UMI regions for facilitating the generation of the set of tagged nucleic acid molecules, based on the set of target nucleic acid sequences and the defined limit for the sequencing of the tagged nucleic acid molecules.

6. The method of Claim 1, further comprising determining absolute molecule counts associated with microorganisms from a sample comprising the set of nucleic acid molecules, based on the single molecule sequencing of the UMI regions of the set of tagged nucleic acid molecules, wherein facilitating the single molecule sequencing with the set of tagged nucleic acid molecules comprises facilitating the single molecule sequencing for improving detection and absolute counting of underrepresented nucleic acid molecules from the set of nucleic acid molecules.

7. The method of Claim 1, wherein the set of target nucleic acid sequences comprises at least one of a first set of targets and a second set of targets, wherein the first set of targets comprises a 16S rRNA target and a 18S rRNA target, and wherein the second set of targets comprises a 16S rRNA target and an HPV-associated target.

8. The method of Claim 1, wherein facilitating the single molecule sequencing with the set of tagged nucleic acid molecules comprises facilitating the single molecule sequencing with read until-based technology.

9. A method for improved single molecule sequencing, the method comprising:

facilitating generation of a set of tagged nucleic acid molecules based on a set of unique molecular identifier (UMI)-based molecules and a set of nucleic acid molecules corresponding to a set of target nucleic acid sequences; and

facilitating single molecule sequencing with the set of tagged nucleic acid molecules, wherein facilitating the single molecule sequencing comprises:

determining a comparison between a first UMI region and a second UMI region, wherein the first UMI region is of a sequenced tagged nucleic acid molecule of the set of tagged nucleic acid molecules, and wherein the second UMI region is of a tagged nucleic acid molecule of the set of tagged nucleic acid molecules; set of sequence regions and a second set of sequence regions, wherein the first set of sequence regions comprises a first UMI region of a sequenced tagged nucleic acid molecule of the set of tagged nucleic acid molecules, and wherein the second set of sequence regions comprises a second UMI region and a second target region of a tagged nucleic acid molecule of the set of tagged nucleic acid molecules; and

stopping sequencing of the tagged nucleic acid molecule based on the comparison between the first UMI region and the second UMI region.

10. The method of Claim 9, wherein determining the comparison comprises determining the comparison between the first UMI region, a first target region of

the sequenced tagged nucleic acid molecule, the second UMI region, and a second target region of the tagged nucleic acid molecule, wherein the first and the second target regions are associated with a target nucleic acid sequence of the set of target nucleic acid sequences, and wherein stopping the sequencing of the tagged nucleic molecule comprises stopping the sequencing based on the comparison between the first UMI region, the first target region, the second UMI region, and the second target region.

11. The method of Claim 10, wherein stopping the sequencing of the tagged nucleic acid molecule comprises stopping the sequencing based on the comparison and a defined limit for the sequencing of tagged nucleic acid molecules associated with the target nucleic acid sequence, wherein the set of tagged nucleic acid molecules comprises the tagged nucleic acid molecules associated with the target nucleic acid sequence.

12. The method of Claim 11, further comprising determining an absolute molecule count associated with the target nucleic acid sequence based on the defined limit for the sequencing of tagged nucleic acid molecules associated with the target nucleic acid sequence.

13. The method of Claim 9, wherein stopping sequencing of the tagged nucleic acid molecule based on the comparison comprises stopping the sequencing of the tagged nucleic acid molecule based on the first UMI region matching the second UMI region.

14. The method of Claim 9, wherein facilitating the generation of the set of tagged nucleic acid molecules comprises: performing at least one amplification process based on the set of UMI-based molecules and the set of nucleic acid molecules for balancing a set of amplicons associated with underrepresented nucleic acid molecules and overrepresented nucleic acid molecules of the set of nucleic acid molecules; or generating a PCR-amplified subset of nucleic acid molecules based on performing a PCR amplification process with a first subset of nucleic acid

molecules of the set of nucleic acid molecules; and generating the set of tagged nucleic acid molecules based on the PCR-amplified subset of nucleic acid molecules and a PCR-independent subset of nucleic acid molecules of the set of nucleic acid molecules.

15. The method of Claim 9, wherein the set of target nucleic acid sequences comprises target nucleic acid sequences associated with at least one of antibiotic resistance and a viral capsid gene.