CLAIMS

What is claimed is:

1. A method for sequencing a T cell receptor (TCR), comprising:
   a) sequencing short reads of less than 100 base pairs of RNA obtained from a T cell;
   b) aligning the short reads with a reference sequence, wherein the reference sequence does not contain a TCR gene sequence, thereby generating a read set comprising mapped short reads and unmapped short reads;
   c) discarding mapped short reads from the read set;
   d) assembling the unmapped short reads remaining in the read set into one or more long reads;
   e) translating the one or more long reads into corresponding amino acid sequences;
   f) fractioning TCR V region and TCR J region amino acid reference sequences into k-strings of six amino acids, aligning the k-strings with the corresponding amino acid sequences from step (e), detecting one or more conserved TCR CDR3 residues in the k-strings that map to the corresponding amino acid sequences, scoring the level of conservation detected, and selecting corresponding amino acid sequences with a conservation score above a threshold conservation score, and detecting a candidate CDR3 region amino acid sequence in the selected corresponding amino acid sequences;
   g) identifying the nucleic acid sequence of the candidate CDR3 region amino acid sequences in the one or more long reads;
   h) aligning the nucleic acid sequence of the one or more long reads upstream of the candidate CDR3 region nucleic acid sequence with one or more TCR V gene reference sequences, scoring the degree of alignment, and identifying long reads above a threshold alignment score as comprising a candidate TCR V gene sequence; and
   i) aligning the nucleic acid sequence of the one or more long reads downstream of the candidate CDR3 region nucleic acid sequence with one or more TCR J gene reference sequences, scoring the degree of alignment, and identifying long reads above a threshold alignment score as comprising a candidate TCR J gene sequence, thereby generating a TCR sequence.

2. The method of claim 1, wherein the short reads are obtained from random-priming of RNA.

3. The method of claim 1, wherein the T cell is obtained from a human or mouse.

4. The method of claim 1, wherein the reference sequence comprises a human genome, a mouse genome, a human transcriptome, or a mouse transcriptome.

5. The method of claim 1, wherein discarding mapped short reads from the read set further comprises discarding unmapped short reads from the read set that are less than 35 base pairs.

6. The method of claim 1, wherein assembling the unmapped short reads remaining in the read set into one or more long reads comprises:
   aligning the one or more unmapped short reads to one or more TCR sequences from a reference database of TCR sequences; and
   assembling, based on the alignment, the one or more unmapped short reads into long reads.

7. The method of claim 1 further comprising appending a TCR C region nucleic acid sequence to the TCR sequence.

8. The method of claim 1, wherein prior to sequencing the short reads of less than 100 base pairs of RNA obtained from the T cell, an immunotherapy has been administered to a subject from which the T cell is obtained.

9. The method of claim 8, wherein the immunotherapy comprises a monotherapy or a combination therapy.

10. The method of claim 9, wherein the combination therapy comprises a costimulatory agonist and a coinhibitory antagonist.

11. The method of claim 1, further comprising:

repeating steps a-i for a first plurality of T cells of a subject, wherein the T cells are collected prior to administration of a treatment;

determining a number of occurrences of unique TCR sequences present in the first plurality of T cells;

repeating steps a-i for a second plurality of T cells of the subject, wherein the T cells are collected after the administration of the treatment;

determining a number of occurrences of unique TCR sequences present in the second plurality of T cells; and

determining, based on the numbers of occurrences of unique TCR sequences present in the first plurality of T cells and the second plurality of T cell, one or more unique TCR sequences that experienced clonal expansion.

12. The method of claim 11, further comprising determining a T cell clonal expansion signature based on the one or more unique TCR sequences that experienced clonal expansion.

13. The method of claim 12, further comprising:

querying a database of T cell clonal expansion signatures and corresponding treatment responses using the T cell clonal expansion signature;

determining, based on the query, the subject's likelihood of responding to the treatment.

14. The method of claim 12, further comprising:

determining the subject's response to the treatment;

storing the T cell clonal expansion signature in a database; and

associating the subject's response to the treatment with the T cell clonal expansion signature in the database.

15. The method of claim 1, further comprising:

determining that the TCR sequence is present in a T cell clone that expands in response to a treatment;

producing one or more T cells containing the TCR sequence.

16. The method of claim 1, wherein sequencing short reads of less than 100 base pairs of RNA obtained from a T cell comprises bulk sequencing of short reads of less than 100 base pairs of RNA obtained from a plurality of T cells.

17. The method of claim 16, further comprising performing steps b-i for each of the plurality of T cells.

18. The method of claim 17, wherein performing steps b-i for each of the plurality of T cells comprising performing steps b-i comprises:
classifying at least a portion of one or more of steps b-i as a job; and
distributing a workload for each job across a plurality of processors in parallel.

19. An apparatus comprising:
one or more processors; and
a memory comprising processor executable instructions that, when executed by the one or more processors, cause the apparatus to:
a) receive sequence data comprising short reads of less than 100 base pairs of RNA obtained from a T cell;
b) align the short reads with a reference sequence, wherein the reference sequence does not contain a TCR gene sequence, thereby generating a read set comprising mapped short reads and unmapped short reads;
c) discard mapped short reads from the read set;
d) assemble the unmapped short reads remaining in the read set into one or more long reads;
e) translate the one or more long reads into corresponding amino acid sequences;
f) fraction TCR V region and TCR J region amino acid reference sequences into k-strings of six amino acids, aligning the k-strings with the corresponding amino acid sequences from step (e), detecting one or more conserved TCR CDR3 residues in the k-strings that map to the corresponding amino acid sequences, scoring the level of conservation detected, and selecting corresponding amino acid sequences with a conservation score above a threshold conservation score, and detecting a candidate CDR3 region amino acid sequence in the selected corresponding amino acid sequences;

g) identify the nucleic acid sequence of the candidate CDR3 region amino acid sequences in the one or more long reads;
h) align the nucleic acid sequence of the one or more long reads upstream of the candidate CDR3 region nucleic acid sequence with one or more TCR V gene reference sequences, scoring the degree of alignment, and identifying long reads above a threshold alignment score as comprising a candidate TCR V gene sequence; and
i) align the nucleic acid sequence of the one or more long reads downstream of the candidate CDR3 region nucleic acid sequence with one or more TCR J gene reference sequences, scoring the degree of alignment, and identifying long reads above a threshold alignment score as comprising a candidate TCR J gene sequence, thereby generating a TCR sequence.

20. A computer readable medium, having computer executable instructions embodied thereon, configured for performing a method comprising:
a) sequencing short reads of less than 100 base pairs of RNA obtained from a T cell;
b) aligning the short reads with a reference sequence, wherein the reference sequence does not contain a TCR gene sequence, thereby generating a read set comprising mapped short reads and unmapped short reads;
c) discarding mapped short reads from the read set;
d) assembling the unmapped short reads remaining in the read set into one or more long reads;
e) translating the one or more long reads into corresponding amino acid sequences;
f) fractioning TCR V region and TCR J region amino acid reference sequences into k-strings of six amino acids, aligning the k-strings with the corresponding amino acid sequences from step (e), detecting one or more conserved TCR CDR3 residues in the k-strings that map to the corresponding amino acid sequences, scoring the level of conservation detected, and selecting corresponding amino acid sequences with a conservation score above a threshold conservation score, and detecting a candidate CDR3 region amino acid sequence in the selected corresponding amino acid sequences;
g) identifying the nucleic acid sequence of the candidate CDR3 region amino acid sequences in the one or more long reads;

h) aligning the nucleic acid sequence of the one or more long reads upstream of the candidate CDR3 region nucleic acid sequence with one or more TCR V gene reference sequences, scoring the degree of alignment, and identifying long reads above a threshold alignment score as comprising a candidate TCR V gene sequence; and

i) aligning the nucleic acid sequence of the one or more long reads downstream of the candidate CDR3 region nucleic acid sequence with one or more TCR J gene reference sequences, scoring the degree of alignment, and identifying long reads above a threshold alignment score as comprising a candidate TCR J gene sequence, thereby generating a TCR sequence.