WHAT IS CLAIMED IS:

1. A method for identifying a tumor antigen candidate in a tumor cell sample, wherein said method comprises:

(a) isolating and sequencing MAPs in a tumor cell sample;

(b) performing whole transcriptome sequencing on said tumor cell sample, thereby obtaining tumor RNA-sequences;

(c) generating a tumor-specific proteome database by:

(i) extracting a set of subsequences comprising at least 33 nucleotides from said tumor RNA-sequences;

(ii) comparing the set of tumor subsequences of (i) to a set of corresponding control subsequences comprising at least 33 nucleotides extracted from RNA-sequences from normal cells, wherein said normal cells comprise medullary thymic epithelial cells (mTEC);

(iii) extracting the tumor subsequences that are absent, or underexpressed by at least 4-fold, in the corresponding control subsequences, thereby obtaining tumor-specific subsequences; and

(iv) *in silico* translating the tumor-specific subsequences, thereby obtaining the tumor-specific proteome database;

(d) generating a personalized tumor proteome database by:

(i) comparing the tumor RNA-sequences to a reference genome sequence to identify single-base mutations in said tumor RNA-sequences, wherein the reference genome is a human genome assembly;

(ii) inserting the single-base mutations identified in (i) in the reference genome sequence, thereby creating a personalized tumor genome sequence;

(iii) *in silico* translating the expressed protein-coding transcripts from said personalized tumor genome sequence, thereby obtaining the personalized tumor proteome database;

(e) generating a personalized normal proteome database by:

(i) comparing RNA-sequences from normal cells to the reference genome sequence to identify single-base mutations in said normal RNA-sequences;

(ii) inserting the single-base mutations identified in (i) in the reference genome sequence, thereby creating a personalized normal genome sequence;

(iii) *in silico* translating the expressed protein-coding transcripts from said personalized normal genome sequence, thereby obtaining the personalized normal proteome database;

(f) generating a normal and a tumor k-mer database by (i) extracting a set of subsequences comprising at least 24 nucleotides from said RNA-sequences from normal cells and said tumor RNA-sequences;

(g) comparing the sequences of the MAPs obtained in (a) with the sequences of the tumor-specific proteome database of (c) and the personalized tumor proteome database of (d) to identify tumor-associated MAPs, wherein the tumor-associated MAPs are MAPs whose sequences is present in the tumor-specific proteome database and/or personalized tumor proteome database; and

(h) identifying a tumor antigen candidate among the tumor-associated MAPs identified in (g), wherein a tumor antigen candidate corresponds to a MAP (1) whose sequence is not present in the personalized normal proteome database; and (2) (i) whose sequence is present in the personalized tumor proteome database; and/or (ii) whose encoding nucleotide sequence is overexpressed or overrepresented in said tumor k-mer database relative to said normal k-mer database.

2. The method of claim 1, wherein said isolating MAPs comprises (i) releasing said MAPs from said tumor cell sample by mild acid treatment; and (ii) subjecting the released MAPs to chromatography.

3. The method of claim 2, wherein said method further comprises filtering the released MAPs with a size exclusion column prior to said chromatography.

4. The method of any one of claims 1 to 3, wherein said tumor subsequences, control subsequences and tumor-specific subsequences comprise from 33 to 54 base pairs.

5. The method of any one of claims 1 to 4, further comprising assembling overlapping tumor-specific subsequences into longer tumor subsequences (contigs).

6. The method of any one of claims 1 to 5, wherein said sequencing of MAPs comprises subjecting the isolated MAPs to mass spectrometry (MS) sequencing analysis.

7. The method of any one of claims 1 to 6, wherein the MAP encoding nucleotide sequence is overexpressed or overrepresented by at least 10-fold in said tumor k-mer database relative to said normal k-mer database.

8. The method of any one of claims 1 to 7, wherein the MAP encoding nucleotide sequence is absent from said normal k-mer database.

9. The method of any one of claims 1 to 8, wherein said method further comprises selecting MAPs having a length of 8 to 11 amino acids.

10. The method of any one of claims 1 to 9, further comprising comparing the coding sequence of said tumor antigen candidate to sequences from normal tissues.

11. The method of any one of claims 1 to 10, further comprising assessing the binding of the tumor antigen candidate to an MHC molecule *in vitro* and/or *in silico*.

12. The method of claim 11, wherein said binding is assessed using an MHC binding prediction algorithm.

13. The method of any one of claims 1 to 12, further comprising assessing the frequency of T cells recognizing the tumor antigen candidate in a cell population *in vitro*.

14. The method of claim 13, wherein the frequency of T cells recognizing the tumor antigen candidate is assessed using multimeric MHC class I molecules comprising said tumor antigen candidate in their peptide binding groove.

15. The method of any one of claims 1 to 14, further comprising assessing the ability of the tumor antigen candidate to induce T cell activation *in vitro*.

16. The method of claim 15, wherein the ability of the tumor antigen candidate to induce T cell activation is assessed by measuring cytokine production by T cells contacted with cells having said tumor antigen candidate bound to MHC class I molecules at their cell surface.

17. The method of claim 16, wherein said cytokine production comprises interferon-gamma (IFN-γ) production.

18. The method of any one of claims 1 to 17, further comprising assessing the ability of said tumor antigen candidate to induce T-cell-mediated tumor cell killing and/or to inhibit tumor growth *in vitro*.