Claims:

1. A method for identifying target multiple myeloma associated surface antigens, said method comprising:

identifying a plurality of genes that express cell-surface proteins in a first multiple myeloma sample and a second multiple myeloma sample;

selecting nucleic acids from said first multiple myeloma sample that have expression levels higher than a control gene unrelated to hematopoietic cells, and identifying the proteins corresponding to the detected elevated expressed nucleic acids to designate a first pool of selected proteins;

conducting mass spec analysis on proteins isolated from said second myeloma sample to identify proteins that are present in higher concentration in said second multiple myeloma relative to normal tissues, wherein such proteins represent a second pool of selected proteins;

excluding proteins with high expression in brain, spinal cord, gut, liver and kidney from said first and second pools to produce a modified first and second pool of proteins; and

identifying proteins common to said first and second modified pool of proteins as target multiple myeloma associated surface antigens.

2. The method of claim 1 wherein said first multiple myeloma sample and said second multiple myeloma sample are taken from the same tissue source.

3. The method of claim 1 wherein said first multiple myeloma sample is a nucleic acid pool of expressed genes from MM patients and said second multiple myeloma sample represents proteins expressed in MM cell lines.

4. The method of claim 1, wherein the target multiple myeloma associated surface antigen has an expression level in a normal tissue sample that is more than one standard deviation below the normal peak of the protein expression level distribution of the normal tissue sample.

5. The method of claim 1, wherein mRNA is measured to determine the expression level of the nucleic acids used to identify proteins for the first pool of selected proteins.