WHAT IS CLAIMED IS:

1. A method of comparing genetic identity, comprising:

providing a target gene group;

providing a test specimen comprising a first test specimen, a second test specimen and a third test specimen;

comparing an identity between human leukocyte antigen genes of the first test specimen and human leukocyte antigen genes of the target gene group to obtain a comparison result of human leukocyte antigen genes;

comparing an identity between short tandem repeats of the second test specimen and short tandem repeats of the target gene group to obtain a comparison result of short tandem repeats;

comparing an identity between killer-cell immunoglobulin-like receptor genes of the third test specimen and killer-cell immunoglobulin-like receptor genes of the target gene group to obtain a comparison result of killer-cell immunoglobulin-like receptor genes;

wherein when the comparison result of human leukocyte antigen genes, the comparison result of short tandem repeats and the comparison result of killer-cell immunoglobulin-like receptor genes are all identical, the target gene group is determined to be identical to a test gene group of the test specimen.

2. The method of claim 1, wherein the first test specimen comprises blood.

3. The method of claim 1, wherein the step of comparing the identity between the human leukocyte antigen genes of the first test specimen and the human leukocyte antigen genes of the target gene group comprises:

extracting and amplifying the human leukocyte antigen genes of the first test specimen; and

analyzing and comparing the identity between the human leukocyte antigen genes of the first test specimen and the human leukocyte antigen genes of the target gene group by using next generation sequencing.

4. The method of claim 1, wherein the step of comparing the identity between the human leukocyte antigen genes of the first test specimen and the human leukocyte antigen genes of the target gene group comprises: comparing genetic identity of HLA-A, HLA-B, HLA-C, HLA-DRB1, HLA-DQB1, or a combination thereof.

5. The method of claim 1, wherein the step of comparing the identity between the human leukocyte antigen genes of the first test specimen and the human leukocyte antigen genes of the target gene group comprises:

comparing an identity between a coding region of the human leukocyte antigen genes of the first test specimen and a coding region of the human leukocyte antigen genes of the target gene group; and

comparing an identity between a non-coding region of the human leukocyte antigen genes of the first test specimen and a non-coding region of the human leukocyte antigen genes of the target gene group.

6. The method of claim 1, wherein the second test specimen comprises human tissue cells.

7. The method of claim 1, wherein the step of comparing the identity between the short tandem repeats of the second test specimen and the short tandem repeats of the target gene group comprises:

extracting the short tandem repeats of the second test specimen; and

analyzing and comparing the identity between the short tandem repeats of the second test specimen and the short tandem repeats of the target gene group by using sequencing-based typing.

8. The method of claim 1, wherein the step of comparing the identity between the short tandem repeats of the second test specimen and the short tandem repeats of the target gene group comprises: comparing genetic identity of gene locus D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, Amelogenin, D5S818, FGA, or a combination thereof.

9. The method of claim 1, wherein the third test specimen comprises blood.

10. The method of claim 1, wherein the step of comparing the identity between the killer-cell immunoglobulin-like receptor genes of the third test

specimen and the killer-cell immunoglobulin-like receptor genes of the target gene group comprises:

extracting the killer-cell immunoglobulin-like receptor genes of the third test specimen; and

analyzing and comparing the identity between the killer-cell immunoglobulin-like receptor genes of the third test specimen and the killer-cell immunoglobulin-like receptor genes of the target gene group by using polymerase chain reaction-sequence-specific oligonucleotides probes, polymerase chain reaction-sequence-specific primers, sequencing-based typing, or a combination thereof.

11. The method of claim 1, wherein the step of comparing the identity between the killer-cell immunoglobulin-like receptor genes of the third test specimen and the killer-cell immunoglobulin-like receptor genes of the target gene group comprises: comparing genetic identity of 2DL1, 2DL2, 2DL3, 2DL4, 2DL5, 2DS1, 2DS2, 2DS3, 2DS4, 2DS5, 3DL1, 3DL2, 3DL3, 3DS1, 2DP1, 3DP1, or a combination thereof.

12. A method of determining identity of a plurility of source subjects of a plurility of specimens, comprising:

providing a test specimen and a target specimen;

comparing an identity between human leukocyte antigen genes of the test specimen and human leukocyte antigen genes of the target specimen to obtain a comparison result of human leukocyte antigen genes;

comparing an identity between short tandem repeats of the test specimen and short tandem repeats of the target specimen to obtain a comparison result of short tandem repeats;

comparing an identity between killer-cell immunoglobulin-like receptor genes of the test specimen and killer-cell immunoglobulin-like receptor genes of the target specimen to obtain a comparison result of killer-cell immunoglobulin-like receptor genes; and

wherein when the comparison result of human leukocyte antigen genes, the comparison result of short tandem repeats and the comparison result of killer-cell immunoglobulin-like receptor genes are all identical, a source subject of the test specimen is determined to be identical to a source subject of the target specimen.

13. The method of claim 12, wherein the test specimen and the target specimen comprise blood.

14. The method of claim 12, wherein the step of comparing the identity between the human leukocyte antigen genes of the test specimen and the human leukocyte antigen genes of the target specimen comprises:

extracting and amplifying the human leukocyte antigen genes of the test specimen and the human leukocyte antigen genes of the target specimen; and

analyzing and comparing the identity between the human leukocyte antigen genes of the test specimen and the human leukocyte antigen genes of the target specimen by using next generation sequencing.

15. The method of claim 12, wherein the step of comparing the identity between the human leukocyte antigen genes of the test specimen and the human leukocyte antigen genes of the target specimen comprises: comparing genetic identity of HLA-A, HLA-B, HLA-C, HLA-DRB1, HLA-DQB1, or a combination thereof.

16. The method of claim 12, wherein the step of comparing the identity between the human leukocyte antigen genes of the test specimen and the human leukocyte antigen genes of the target specimen comprises:

comparing an identity between a coding region of the human leukocyte antigen genes of the test specimen and a coding region of the human leukocyte antigen genes of the target specimen; and

comparing an identity between a non-coding region of the human leukocyte antigen genes of the test specimen and a non-coding region of the human leukocyte antigen genes of the target specimen.

17. The method of claim 12, wherein the step of comparing the identity between the short tandem repeats of the test specimen and the short tandem repeats of the target specimen comprises:

extracting the short tandem repeats of the test specimen and the short tandem repeats of the target specimen; and

analyzing and comparing the identity between the short tandem repeats of the test specimen and the short tandem repeats of the target specimen by using

sequencing-based typing.

18. The method of claim 12, wherein the step of comparing the identity between the short tandem repeats of the test specimen and the short tandem repeats of the target specimen comprises: comparing genetic identity of gene locus D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, Amelogenin, D5S818, FGA, or a combination thereof.

19. The method of claim 12, wherein the step of comparing the identity between the killer-cell immunoglobulin-like receptor genes of the test specimen and the killer-cell immunoglobulin-like receptor genes of the target specimen, comprising:

extracting the killer-cell immunoglobulin-like receptor genes of the test specimen and the killer-cell immunoglobulin-like receptor genes of the target specimen; and

analyzing and comparing the identity between the killer-cell immunoglobulin-like receptor genes of the test specimen and the killer-cell immunoglobulin-like receptor genes of the target specimen by using polymerase chain reaction-sequence-specific oligonucleotides probes, polymerase chain reaction-sequence-specific primers, sequencing-based typing, or a combination thereof.

20. The method of claim 12, wherein the step of comparing the identity

between the killer-cell immunoglobulin-like receptor genes of the test specimen and the killer-cell immunoglobulin-like receptor genes of the target specimen comprises comparing genetic identity of 2DL1, 2DL2, 2DL3, 2DL4, 2DL5, 2DS1, 2DS2, 2DS3, 2DS4, 2DS5, 3DL1, 3DL2, 3DL3, 3DS1, 2DP1, 3DP1, or a combination thereof.