What is claimed:

1. A method for determining the genetic relationship of a preimplantation conceptus with a sperm provider and an oocyte provider, comprising:

receiving conceptus sequence data, sperm provider sequence data, and oocyte provider sequence data;

aligning the received sequence data to a reference genome;

identifying single nucleotide polymorphisms (SNPs) in the sperm provider sequence data, oocyte provider sequence data, and conceptus sequence data;

imputing missing gaps in the sperm provider sequence data and the oocyte provider sequence data using an imputation reference;

filtering at least one of the conceptus sequence data, sperm provider sequence data, and oocyte provider sequence data to remove sequencing artifacts, wherein the filtering comprises one or more of:

(i) excluding SNPs that are inconsistent with Mendelian inheritance;

(ii) excluding sequences of sites with any missing alleles between the conceptus, sperm and oocyte;

(iii) excluding sequences of sites with constant alleles across the conceptus, sperm and oocyte; and

(iv) excluding sequences of sites with a novel allele within one of the conceptus, sperm and oocyte;

calculating a paternal consistency score ($score_p$) between the sperm provider and the conceptus, wherein calculating the paternal consistency score includes using the following formula:

$score_p = (N_{Cp} \times N_n) / (N_{SNP} \times N_C)$ wherein N_{Cp} is the number of SNPs consistent between conceptus and sperm provider, N_n is the number of novel SNPs in conceptus, N_{SNP} is

the number of SNPs observed in the conceptus, sperm provider, and oocyte provider, and N_C is the number of SNPs consistent with either of the sperm provider and oocyte provider;

calculating a maternal consistency score ($score_m$) between the oocyte provider and conceptus wherein calculating the maternal consistency score includes using the following formula:

$score_m = (N_{Cm} \times N_n) / (N_{SNP} \times N_C)$ wherein N_{Cm} is the number of SNPs consistent between conceptus and oocyte provider, N_n is the number of novel SNPs in conceptus, N_{SNP} is the number of SNPs observed in the conceptus, sperm provider, and oocyte provider, and N_C is the number of SNPs consistent with either of the sperm provider and oocyte provider; and

classifying the sperm provider and/or the oocyte provider as related to the conceptus if the paternal consistency score and/or the maternal consistency score exceeds a predetermined threshold.

2. The method of Claim 1, further comprising identifying a region of interest in the aligned conceptus sequence data, and identifying SNPs in the sperm provider, oocyte provider, and the identified region of interest in the conceptus sequence data.

3. The method of Claim 2, wherein the region of interest is a copy number variation.

4. The method of Claim 1, wherein at least one of the conceptus, sperm provider, and oocyte provider sequence data is acquired by low-coverage sequencing.

5. The method of Claim 4, wherein the low-coverage sequencing is between 0.001 and 10x.

6. The method of Claim 4, wherein the low-coverage sequencing is between 0.01 and 0.5x.

7. A non-transitory computer-readable medium storing computer instructions for determining the genetic relationship of a preimplantation conceptus with a sperm provider and an oocyte provider, comprising:

receiving conceptus sequence data, sperm provider sequence data, and oocyte provider sequence data;

aligning the received sequence data to a reference genome;

identifying single nucleotide polymorphisms (SNPs) in the sperm provider sequence data, oocyte provider sequence data, and the conceptus sequence data;

imputing missing gaps in the sperm provider sequence data and the oocyte provider sequence data using an imputation reference;

filtering at least one of the conceptus, sperm provider, and oocyte provider sequencing data to remove sequencing artifacts, wherein the filtering comprises one or more of:

(i) excluding SNPs that are inconsistent with Mendelian inheritance;

(ii) excluding sequences of sites with any missing alleles between the conceptus, sperm and oocyte;

(iii) excluding sequences of sites with constant alleles across the conceptus, sperm and oocyte; and

(iv) excluding sequences of sites with a novel allele within one of the conceptus, sperm and oocyte;

calculating a paternal consistency score ($score_p$) between the sperm provider and the conceptus, wherein calculating the paternal consistency score includes using the following formula:

$score_p = (N_{Cp} \times N_n) / (N_{SNP} \times N_C)$ wherein N_{Cp} is the number of SNPs consistent between conceptus and sperm provider, N_n is the number of novel SNPs in conceptus, N_{SNP} is the number of SNPs observed in the conceptus, sperm provider, and oocyte provider, and N_C is the number of SNPs consistent with either of the sperm provider and oocyte provider;

calculating a maternal consistency score ($score_m$) between the oocyte provider and conceptus, wherein calculating the maternal consistency score includes using the following formula:

score$_m$ = (N_{Cm} x N_n) / (N_{SNP} x N_C) wherein N_{Cm} is the number of SNPs consistent between conceptus and oocyte provider, N_n is the number of novel SNPs in conceptus, N_{SNP} is the number of SNPs observed in the conceptus, sperm provider, and oocyte provider, and N_C is the number of SNPs consistent with either of the sperm provider and oocyte provider; and

classifying the sperm provider and/or the oocyte provider as related to the conceptus if the paternal consistency score and/or the maternal consistency score exceeds a predetermined threshold.

8. The non-transitory computer-readable medium of Claim 7, further comprising identifying a region of interest in the aligned conceptus sequence data, and identifying SNPs in the sperm provider, oocyte provider, and the identified region of interest in the conceptus sequence data.

9. The non-transitory computer-readable medium of Claim 8, wherein the region of interest is a copy number variation.

10. The non-transitory computer-readable medium of Claim 7, wherein at least one of the conceptus, sperm provider, and oocyte provider sequence data is acquired by low-coverage sequencing.

11. The non-transitory computer-readable medium of Claim 10, wherein the low-coverage sequencing is between 0.001 and 10x.

12. The non-transitory computer-readable medium of Claim 10, wherein the low-coverage sequencing is between 0.01 and 0.5x.

13. A system for determining the genetic relationship of a preimplantation conceptus with a sperm provider and an oocyte provider, comprising:

a data store for receiving conceptus sequence data, sperm provider sequence data, and oocyte provider sequence data;

a computing device communicatively connected to the data store, the computing device comprising

an alignment engine configured to align the received sequence data to a reference genome;

a SNP identification engine configured to identify single nucleotide polymorphisms (SNPs) in the sperm provider sequence data, oocyte provider sequence data, and the conceptus sequence data;

an imputation engine configured to impute missing gaps in the sperm provider sequence data and the oocyte provider sequence data using an imputation reference and filter at least one of the conceptus, sperm provider, and oocyte provider sequencing data to remove sequencing artifacts, wherein the filtering comprises one or more of:

(i) excluding SNPs that are inconsistent with Mendelian inheritance;

(ii) excluding sequences of sites with any missing alleles between the conceptus, sperm and oocyte;

(iii) excluding sequences of sites with constant alleles across the conceptus, sperm and oocyte; and

(iv) excluding sequences of sites with a novel allele within one of the conceptus, sperm and oocyte; and

a relatedness engine configured to:

calculate a paternal consistency score ($score_p$) between the sperm provider and the conceptus, wherein calculating the paternal consistency score includes using the following formula:

$score_p = (N_{Cp} \times N_n) / (N_{SNP} \times N_C)$ wherein N_{Cp} is the number of SNPs consistent between conceptus and sperm provider, N_n is the number of novel SNPs in conceptus, N_{SNP} is the number of SNPs observed in the conceptus, sperm provider, and oocyte provider, and N_C is the number of SNPs consistent with either of the sperm provider and oocyte provider;

calculate a maternal consistency score ($score_m$) between the oocyte provider and conceptus, wherein calculating the maternal consistency score includes using the following formula:

$score_m = (N_{Cm} \times N_n) / (N_{SNP} \times N_C)$ wherein N_{Cm} is the number of SNPs consistent between conceptus and oocyte provider, N_n is the number of novel SNPs in conceptus, N_{SNP} is the number of SNPs observed in the conceptus, sperm provider, and oocyte provider, and N_C is the number of SNPs consistent with either of the sperm provider and oocyte provider; and

classify the sperm provider and/or the oocyte provider as related to the conceptus if the paternal consistency score and/or the maternal consistency score exceeds a predetermined threshold;

and

a display communicatively connected to the computing device and configured to display a report containing the classified relatedness to the conceptus.

14. The system of Claim 13, the alignment engine further configured to identify a region of interest in the aligned conceptus sequence data, and identify SNPs in the sperm provider, oocyte provider, and the identified region of interest in the conceptus sequence data.

15. The system of Claim 14, wherein the region of interest is a copy number variation.

16. The system of Claim 13, wherein at least one of the conceptus, sperm provider, and oocyte provider sequence data is acquired by low-coverage sequencing.

17. The system of Claim 16, wherein the low-coverage sequencing is between 0.001 and 10x.

18. The system of Claim 16, wherein the low-coverage sequencing is between 0.01 and 0.5x.