

What is claimed:

1. A method for determining the genetic relationship of a conceptus with a sperm provider and oocyte provider, comprising:
 - receiving conceptus, sperm provider, and oocyte provider sequence data;
 - aligning the received sequence data to a reference genome;
 - identifying single nucleotide polymorphisms (SNPs) in the sperm provider, oocyte provider, and conceptus sequence data;
 - imputing missing gaps in the sperm provider sequence data and the oocyte provider sequence data using an imputation reference;
 - calculating a paternal consistency score between the sperm provider and the conceptus, the score comprising (a) a count of SNPs that are common between the conceptus and sperm provider and (b) a count of SNPs found in the conceptus but not the sperm provider;
 - calculating a maternal consistency score between the oocyte provider and conceptus, the score comprising (a) a count of SNPs that are common between the conceptus and oocyte provider and (b) a count of SNPs found in the conceptus but not the 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, wherein the conceptus is a preimplantation conceptus.
3. 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.
4. The method of Claim 3, wherein the region of interest is genome wide.
5. The method of Claim 3, wherein the region of interest is a copy number variation.

6. 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.
7. The method of Claim 6, wherein the low-coverage sequencing is between about 0.001 and 10x.
8. The method of Claim 6, wherein the low-coverage sequencing is between about 0.01 and 0.5x.
9. The method of Claim 6, wherein the low-coverage sequencing is between about 0.25 and 0.2x.
10. The method of Claim 1, wherein the imputation reference comprises at least 1000 genomes.
11. The method of Claim 1, further comprising filtering at least one of the conceptus, sperm provider, and oocyte provider sequencing data to remove sequencing artifacts.
12. The method of Claim 11, wherein the filtering includes excluding SNPs that are not included in a reference list of known SNPs.
13. The method of Claim 12, wherein the reference list includes about 1000 known genomes.
14. The method of Claim 11, wherein the filtering comprises excluding SNPs that are inconsistent with Mendelian inheritance.
15. The method of Claim 11, wherein the filtering comprises excluding sequences of sites with any missing alleles between the conceptus, sperm and oocyte.
16. The method of Claim 11, wherein the filtering comprises excluding sequences of sites with constant alleles across between the conceptus, sperm and oocyte.
17. The method of Claim 11, wherein the filtering comprises excluding sequences of sites with a novel allele within one of the conceptus, sperm and oocyte.
18. The method of Claim 1, further comprising:
 - identifying a region of interest in the aligned conceptus sequence data,
 - counting the number of SNPs that are common between the conceptus and the oocyte in the identified region of interest for the conceptus sequence data and a

corresponding region on the oocyte provider sequence data to determine a maternal contribution value;

counting the number of SNPs that are common between the conceptus and the sperm in the identified region of interest for the conceptus sequence data and a corresponding region on the sperm provider sequence data to determine a paternal contribution value; and

classifying a pattern of inheritance for the conceptus as maternal or paternal based on the relative contribution values between oocyte and sperm.

19. The method of Claim 18, wherein the region of interest is the entire genome, the method further comprising counting SNPs across the entire genome to determine the maternal and paternal contribution values and determine if the conceptus is polyploid.
20. The method of Claim 19, wherein for a conceptus that is polyploid, the method further comprising classifying a pattern of inheritance for the polyploid as maternal or paternal based on the relative contribution values between oocyte and sperm.
21. A non-transitory computer-readable medium storing computer instructions for determining the genetic relationship of a conceptus with a sperm provider and oocyte provider, comprising:

receiving conceptus, sperm provider, 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;

calculating a paternal consistency score between the sperm provider and the conceptus, the score comprising (a) a count of SNPs that are common between the conceptus and sperm provider and (b) a count of SNPs found in the conceptus but not the sperm provider;

calculating a maternal consistency score between the oocyte provider and conceptus, the score comprising (a) a count of SNPs that are common between the conceptus and oocyte provider and (b) a count of SNPs found in the conceptus but not the 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.

22. The method of Claim 21, wherein the conceptus is a preimplantation conceptus.
23. The method of Claim 21, 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.
24. The method of Claim 23, wherein the region of interest is genome wide.
25. The method of Claim 23, wherein the region of interest is a copy number variation.
26. The method of Claim 21, wherein at least one of the conceptus, sperm provider, and oocyte provider sequence data is acquired by low-coverage sequencing.
27. The method of Claim 26, wherein the low-coverage sequencing is between about 0.001 and 10x.
28. The method of Claim 26, wherein the low-coverage sequencing is between about 0.01 and 0.5x.
29. The method of Claim 26, wherein the low-coverage sequencing is between about 0.25 and 0.2x.
30. The method of Claim 21, wherein the imputation reference comprises at least 1000 genomes.
31. The method of Claim 21, further comprising filtering at least one of the conceptus, sperm provider, and oocyte provider sequencing data to remove sequencing artifacts.
32. The method of Claim 31, wherein the filtering includes excluding SNPs that are not included in a reference list of known SNPs.

33. The method of Claim 32, wherein the reference list includes about 1000 known genomes.
34. The method of Claim 31, wherein the filtering comprises excluding SNPs that are inconsistent with Mendelian inheritance.
35. The method of Claim 31, wherein the filtering comprises excluding sequences of sites with any missing alleles between the conceptus, sperm and oocyte.
36. The method of Claim 31, wherein the filtering comprises excluding sequences of sites with constant alleles across between the conceptus, sperm and oocyte.
37. The method of Claim 31, wherein the filtering comprises excluding sequences of sites with a novel allele within one of the conceptus, sperm and oocyte.
38. The method of Claim 21, further comprising:
 - identifying a region of interest in the aligned conceptus sequence data,
 - counting the number of SNPs that are common between the conceptus and the oocyte in the identified region of interest for the conceptus sequence data and a corresponding region on the oocyte provider sequence data to determine a maternal contribution value;
 - counting the number of SNPs that are common between the conceptus and the sperm in the identified region of interest for the conceptus sequence data and a corresponding region on the sperm provider sequence data to determine a paternal contribution value; and
 - classifying a pattern of inheritance for the conceptus as maternal or paternal based on the relative contribution values between oocyte and sperm.
39. The method of Claim 38, wherein the region of interest is the entire genome, the method further comprising counting SNPs across the entire genome to determine the maternal and paternal contribution values and determine if the conceptus is polyploid.
40. The method of Claim 39, wherein for a conceptus that is polyploid, the method further comprising classifying a pattern of inheritance for the polyploid as maternal or paternal based on the relative contribution values between oocyte and sperm.

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

a data store for receiving conceptus, sperm provider, 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

a relatedness engine configured to:

calculate a paternal consistency score between the sperm provider and the conceptus, the score comprising (a) a count of SNPs that are common between the conceptus and sperm provider and (b) a count of SNPs found in the conceptus but not the sperm provider;

calculate a maternal consistency score between the oocyte provider and conceptus, the score comprising (a) a count of SNPs that are common between the conceptus and oocyte provider and (b) a count of SNPs found in the conceptus but not the 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.

42. The system of Claim 41, wherein the conceptus is a preimplantation conceptus.
43. The system of Claim 41, 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.
44. The system of Claim 43, wherein the region of interest is genome wide.
45. The system of Claim 43, wherein the region of interest is a copy number variation.
46. The system of Claim 41, wherein at least one of the conceptus, sperm provider, and oocyte provider sequence data is acquired by low-coverage sequencing.
47. The system of Claim 46, wherein the low-coverage sequencing is between about 0.001 and 10x.
48. The system of Claim 46, wherein the low-coverage sequencing is between about 0.01 and 0.5x.
49. The system of Claim 46, wherein the low-coverage sequencing is between about 0.25 and 0.2x.
50. The system of Claim 41, wherein the imputation reference comprises at least 1000 genomes.
51. The system of Claim 41, the imputation engine further configured to filter at least one of the conceptus, sperm provider, and oocyte provider sequencing data to remove sequencing artifacts.
52. The system of Claim 51, wherein the filtering includes excluding SNPs that are not included in a reference list of known SNPs.
53. The system of Claim 52, wherein the reference list includes about 1000 known genomes.
54. The system of Claim 51, wherein the filtering comprises excluding SNPs that are inconsistent with Mendelian inheritance.
55. The system of Claim 51, wherein the filtering comprises excluding sequences of sites with any missing alleles between the conceptus, sperm and oocyte.

56. The system of Claim 51, wherein the filtering comprises excluding sequences of sites with constant alleles across between the conceptus, sperm and oocyte.
57. The system of Claim 51, wherein the filtering comprises excluding sequences of sites with a novel allele within one of the conceptus, sperm and oocyte.
58. The system of Claim 41,
the alignment engine further configured to identify a region of interest in the aligned conceptus sequence data, and
the relatedness engine further configured to
count the number of SNPs that are common between the conceptus and the oocyte in the identified region of interest for the conceptus sequence data and a corresponding region on the oocyte provider sequence data to determine a maternal contribution value;
count the number of SNPs that are common between the conceptus and the sperm in the identified region of interest for the conceptus sequence data and a corresponding region on the sperm provider sequence data to determine a paternal contribution value; and
classify a pattern of inheritance for the conceptus as maternal or paternal based on the relative contribution values between oocyte and sperm.
59. The system of Claim 58, wherein the region of interest is the entire genome, the relatedness engine configured to count SNPs across the entire genome to determine the maternal and paternal contribution values and determine if the conceptus is polyploid.
60. The system of Claim 59, wherein for a conceptus that is polyploid, the relatedness engine configured to classify a pattern of inheritance for the polyploid as maternal or paternal based on the relative contribution values between oocyte and sperm.