What is claimed:

1. A method for determining pattern of inheritance in an embryo for a region of interest, comprising:

receiving low-coverage embryo, maternal and paternal sequence data, wherein the maternal sequence data is from a mother of the embryo and the paternal sequence data is from a father of the embryo, and wherein the embryo, maternal and paternal sequence data are between 0.001x and 10x;

aligning the received sequence data to a reference genome;

identifying a region of interest in the aligned embryo sequence data;

identifying single nucleotide polymorphisms (SNPs) in the maternal sequence data, paternal sequence data, and the identified region of interest in the embryo sequence data;

imputing missing gaps in the maternal sequence data and the paternal sequence data using an imputation reference;

filtering at least one of the embryo, maternal and paternal 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 embryo, father and mother;

(iii) excluding sequences of sites with constant alleles across the embryo, father and mother; and

(iv) excluding sequences of sites with a novel allele within one of the embryo, father and mother;

counting the number of SNPs that are common between the embryo and the mother in the identified region of interest for the embryo sequence data and a

corresponding region on the maternal sequence data to determine a maternal contribution value, designated *OvM*, based on the count;

counting the number of SNPs that are common between the embryo and the father in the identified region of interest for the embryo sequence data and a corresponding region on the paternal sequence data to determine a paternal contribution value, designated *OvP*, based on the count;

calculating a statistic describing a relative contribution value between mother and father according to the following formula: $log2\left(\frac{(OvM)+s}{(OvP)+s}\right)$, wherein s is a smoothing parameter; and

classifying a pattern of inheritance for the region of interest as maternal or paternal based on the statistic.

2. The method of Claim 1, wherein the low-coverage sequencing data is between 0.01 and 0.5x.

3. The method of Claim 1, wherein the region of interest is genome wide.

4. The method of Claim 1, wherein the region of interest is a copy number variation.

5. The method of Claim 1, wherein the imputation reference comprises at least 1000 genomes.

6. A non-transitory computer-readable medium storing computer instructions for determining pattern of inheritance in an embryo for a region of interest, comprising:

receiving low-coverage embryo, maternal and paternal sequence data, wherein the maternal sequence data is from a mother of the embryo and the paternal sequence data is from a father of the embryo, and wherein the embryo, maternal and paternal sequence data are between 0.001x and 10x;

aligning the received sequence data to a reference genome;

identifying a region of interest in the aligned embryo sequence data;

identifying single nucleotide polymorphisms (SNPs) in the maternal sequence data, paternal sequence data, and the identified region of interest in the embryo sequence data;

imputing missing gaps in the maternal sequence data and the paternal sequence data using an imputation reference;

filtering at least one of the embryo, maternal and paternal 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 embryo, father and mother;

(iii) excluding sequences of sites with constant alleles across the embryo, father and mother; and

(iv) excluding sequences of sites with a novel allele within one of the embryo, father and mother;

counting the number of SNPs that are common between the embryo and the mother in the identified region of interest for the embryo sequence data and a corresponding region on the maternal sequence data to determine a maternal contribution value, designated *OvM*, based on the count;

counting the number of SNPs that are common between the embryo and the father in the identified region of interest for the embryo sequence data and a corresponding region on the paternal sequence data to determine a paternal contribution value, designated *OvP*, based on the count;

calculating a statistic describing a relative contribution value between mother and father according to the following formula: $log2\left(\frac{(OvM)+s}{(OvP)+s}\right)$, wherein s is a smoothing parameter; and

classifying a pattern of inheritance for the region of interest as maternal or paternal based on the statistic.

7. The non-transitory computer-readable medium of Claim 6, wherein the low-coverage sequencing data is between 0.01x and 0.5x.

8. The non-transitory computer-readable medium of Claim 6, wherein the region of interest is genome wide.

9. The non-transitory computer-readable medium of Claim 6, wherein the region of interest is a copy number variation.

10. The non-transitory computer-readable medium of Claim 6, wherein the imputation reference comprises at least 1000 genomes.

11. A system for determining pattern of inheritance in an embryo for a region of interest, comprising:

a data store for receiving low-coverage embryo, maternal and paternal sequence data, wherein the maternal sequence data is from a mother of the embryo and the paternal sequence data is from a father of the embryo, and wherein the embryo, maternal and paternal sequence data are between 0.001x and 10x;

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

a region of interest (ROI) engine configured to align the received sequence data to a reference genome, and identify a region of interest in the aligned embryo sequence data;

a SNP identification engine configured to identify single nucleotide polymorphisms (SNPs) in the maternal sequence data, paternal sequence data, and the identified region of interest in the embryo sequence data;

an imputation engine configured to impute missing gaps in the maternal sequence data and the paternal sequence data using an imputation reference and filter at least one of the embryo, maternal and paternal

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 embryo, father and mother;

(iii) excluding sequences of sites with constant alleles across between the embryo, father and mother; and

(iv) excluding sequences of sites with a novel allele within one of the embryo, father and mother; and

a pattern of inheritance (POI) engine configured to:

count the number of SNPs that are common between the embryo and the mother in the identified region of interest for the embryo sequence data and a corresponding region on the maternal sequence data to determine a maternal contribution value, designated *OvM*, based on the count;

count the number of SNPs that are common between the embryo and the father in the identified region of interest for the embryo sequence data and a corresponding region on the paternal sequence data to determine a paternal contribution value, designated *OvP*, based on the count;

calculate a statistic describing a relative contribution values between mother and father according to the following formula: $log2\left(\frac{(OvM)+s}{(OvP)+s}\right)$, wherein s is a smoothing parameter; and

classify a pattern of inheritance for the region of interest as maternal or paternal based on the statistic;

and

a display communicatively connected to the computing device and configured to display a report containing the classified pattern of inheritance for the region of interest.

12. The system of Claim 11, wherein the low-coverage sequencing data is between 0.01x and 0.5x.

13. The system of Claim 11, wherein the region of interest is genome wide.

14. The system of Claim 11, wherein the region of interest is a copy number variation.

15. The system of Claim 11, wherein the imputation reference comprises at least 1000 genomes.