

What is claimed:

1. A method for detecting ploidy in an embryo, comprising:
  - receiving an embryo sequence data;
  - 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 sequence data by comparing the received sequence data to the aligned reference genome;
  - determining a ploidy score comprising counting the number of observed SNPs in the region of interest;
  - comparing the ploidy score to a predetermined threshold; and
  - identifying the embryo as polyploid if the ploidy score is below the predetermined threshold.
2. The method of Claim 1, further comprising identifying the embryo as euploid if the ploidy score is above the predetermined threshold.
3. The method of Claim 1, wherein the polyploid is a balanced polyploid.
4. The method of Claim 1, wherein the embryo sequence data is acquired by low-coverage sequencing.
5. The method of Claim 4, wherein the low-coverage sequencing is between about 0.001 and 10x.
6. The method of Claim 4, wherein the low-coverage sequencing is between about 0.01 and 0.5x.
7. The method of Claim 4, wherein the low-coverage sequencing is between about 0.25 and 0.2x.
8. The method of Claim 1, wherein the region of interest is genome wide.
9. The method of Claim 1, further comprising filtering the embryo sequencing data to remove sequencing artifacts.
10. The method of Claim 9, wherein the filtering comprises excluding SNPs that are not included in a reference database of known SNPs.

11. The method of Claim 10, wherein the reference database includes about 1000 known genomes.
12. A non-transitory computer-readable medium storing computer instructions for detecting ploidy in an embryo, comprising:
  - receiving an embryo sequence data;
  - 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 sequence data by comparing the received sequence data to the aligned reference genome;
  - determining a ploidy score comprising counting the number of observed SNPs in the region of interest;
  - comparing the ploidy score to a predetermined threshold; and
  - identifying the embryo as polyploid if the ploidy score is below the predetermined threshold.
13. The method of Claim 12, further comprising identifying the embryo as euploid if the ploidy score is above the predetermined threshold.
14. The method of Claim 13, wherein the polyploid is a balanced polyploid.
15. The method of Claim 12, wherein the embryo sequence data is acquired by low-coverage sequencing.
16. The method of Claim 15, wherein the low-coverage sequencing is between about 0.001 and 10x.
17. The method of Claim 15, wherein the low-coverage sequencing is between about 0.01 and 0.5x.
18. The method of Claim 15, wherein the low-coverage sequencing is between about 0.25 and 0.2x.
19. The method of Claim 12, wherein the region of interest is genome wide.
20. The method of Claim 12, further comprising filtering the embryo sequencing data to remove sequencing artifacts.

21. The method of Claim 20, wherein the filtering comprises excluding SNPs that are not included in a reference database of known SNPs.
22. The method of Claim 21, wherein the reference database includes about 1000 known genomes.
23. A system for detecting ploidy in an embryo, comprising:
- a data store for receiving an embryo sequence data;
  - a computing device communicatively connected to the data store, the computing device comprising
    - an 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 sequence data by comparing the received sequence data to the aligned reference genome; and
    - a scoring engine configured to determine a polyploid score comprising counting the number of observed SNPs in the region of interest, compare the polyploid score to a predetermined threshold, and identifying the embryo as polyploid if the polyploid score is below the predetermined threshold;
  - and
  - a display communicatively connected to the computing device and configured to display a report containing the polyploid classification of the embryo.
24. The system of Claim 23, wherein the scoring engine is further configured to identify the embryo as euploid if the polyploid score is above the predetermined threshold.
25. The system of Claim 24, wherein the display is further configured to display a report containing the euploid classification of the embryo.
26. The system of Claim 23, wherein the polyploid is a balanced polyploid.
27. The system of Claim 23, wherein the embryo sequence data is acquired by low-coverage sequencing.
28. The system of Claim 27, wherein the low-coverage sequencing is between about 0.001 and 10x.

- 29. The system of Claim 27, wherein the low-coverage sequencing is between about 0.01 and 0.5x.
- 30. The system of Claim 27, wherein the low-coverage sequencing is between about 0.25 and 0.2x.
- 31. The system of Claim 23, wherein the region of interest is genome wide.
- 32. The system of Claim 23, wherein the SNP identification engine is further configured to filter the embryo sequencing data to remove sequencing artifacts.
- 33. The system of Claim 32, wherein the filtering comprises excluding SNPs that are not included in a reference database of known SNPs.
- 34. The system of Claim 33, wherein the reference database includes about 1000 known genomes.