What is claimed:

1. A method for detecting ploidy in an embryo, comprising:

receiving an embryo sequence data, wherein the sequence data is from low-coverage sequencing having a sequencing read depth of between 0.001x and 10x;

aligning the received sequence data to a reference genome;

identifying single nucleotide variants (SNVs) in the sequence data by comparing the received sequence data to the aligned reference genome;

filtering the embryo sequencing data to remove sequencing artifacts;

counting a number of alternate SNV-containing sequence reads (actual observed ALT SEQ);

calculating a number of alternate SNV-containing sequence reads expected to have been observed for a euploid embryo (predicted observed ALT SEQ);

determining a ploidy score comprising the deviation of the actual observed ALT SEQ from the predicted observed ALT SEQ;

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 low-coverage sequencing is between 0.01 and 0.5x.

5. The method of Claim 1, wherein the filtering comprises excluding SNVs that are not included in a reference database of known SNVs.

6. A non-transitory computer-readable medium storing computer instructions for detecting ploidy in an embryo, the instructions comprising:

receiving an embryo sequence data, wherein the sequence data is from low-coverage sequencing having a sequencing read depth of between 0.001x and 10x;

aligning the received sequence data to a reference genome;

identifying single nucleotide variants (SNVs) in the sequence data by comparing the received sequence data to the aligned reference genome;

filtering the embryo sequencing data to remove sequencing artifacts;

counting a number of alternate SNV-containing sequence reads (actual observed ALT SEQ);

calculating a number of alternate SNV-containing sequence reads expected to have been observed for a euploid embryo (predicted observed ALT SEQ);

determining a ploidy score comprising the deviation of the actual observed ALT SEQ from the predicted observed ALT SEQ;

comparing the ploidy score to a predetermined threshold; and

identifying the embryo as polyploid if the ploidy score is below the predetermined threshold.

7. The non-transitory computer-readable medium of Claim 6, the instructions further comprising identifying the embryo as euploid if the ploidy score is above the predetermined threshold.

8. The non-transitory computer-readable medium of Claim 6, wherein the polyploid is a balanced polyploid.

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

10. The non-transitory computer-readable medium of Claim 6, wherein the filtering comprises excluding SNVs that are not included in a reference database of known SNVs.

11. A system for detecting ploidy in an embryo, comprising:

a data store for receiving an embryo sequence data, wherein the sequence data is from low-coverage sequencing having a sequencing read depth of 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;

a SNV identification engine configured to identify single nucleotide variants (SNVs) in the sequence data by comparing the received sequence data to the aligned reference genome and filter the embryo sequencing data to remove sequencing artifacts; and

a scoring engine configured to count a number of alternate SNV-containing sequence reads (actual observed ALT SEQ), calculate a number of alternate SNV-containing sequence reads expected to have been observed for a euploid embryo (predicted observed ALT SEQ), determine a polyploid score comprising the deviation of the actual observed ALT SEQ from the predicted observed ALT SEQ, compare the polyploid score to a predetermined threshold, and identify 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.

12. The system of Claim 11, wherein the scoring engine is further configured to identify the embryo as euploid if the polyploid score is above the predetermined threshold.

13. The system of Claim 11, wherein the display is further configured to display a report containing the euploid classification of the embryo.

14. The system of Claim 11, wherein the polyploid is a balanced polyploid.

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

16. The system of Claim 11, wherein the filtering comprises excluding SNVs that are not included in a reference database of known SNVs.