

What is claimed:

1. A method for verifying a genomic variant region in an embryo, comprising:
receiving, by one or more processors, embryo sequencing data;
aligning, by the one or more processors, the received embryo sequencing data to a reference genome;
identifying, by the one or more processors, a genomic variant region in the aligned embryo sequencing data;
counting, by the one or more processors, a number of single nucleotide variants (SNVs) in the identified genomic variant region;
normalizing, by the one or more processors, the counted number of SNVs in the identified genomic variant region against a baseline count of SNVs for a reference region corresponding to the identified genomic variant region to generate a normalized SNV density for the genomic variant region; and
verifying, by the one or more processors, the identified genomic variant region, if the normalized SNV density in the identified genomic variant region satisfies a tolerance criterion.
2. The method of claim 1, wherein the genomic variant region is a copy number variation region.
3. The method of claim 1, wherein the genomic variant region is an aneuploidy region.
4. The method of claim 1, wherein the genomic variant region is a polyploidy region.
5. The method of claim 1, wherein the reference region is an exact length of the identified genomic variant region.
6. The method of claim 1, wherein the reference region is derived from an euploid sample.
7. The method of claim 1, wherein the tolerance criterion is an expected SNV density for a reference region derived from an euploid embryo.

8. The method of claim 7, wherein the identified genomic variant region is verified if the normalized SNV density of the identified genomic variant region is greater or lesser than a pre-set confidence interval of the expected SNV density for the reference region.
9. The method of claim 8, wherein the lower pre-set confidence interval is 95%.
10. The method of claim 1, wherein the tolerance criterion is an expected SNV density for a reference region derived from a mosaic embryo.
11. The method of claim 10, wherein the identified genomic variant region is verified if the normalized SNV density of the identified genomic variant region is above a pre-set confidence interval of the expected SNV density for the reference region.
12. The method of claim 11, wherein the pre-set confidence interval 95%.
13. The method of claim 1, wherein the tolerance criterion is a preset variance number of SNVs over or under a baseline count of SNVs for the reference region.
14. A non-transitory computer-readable medium storing computer instruction for verifying a genomic variant region in an embryo, comprising:
 - receiving, by one or more processors, embryo sequencing data;
 - aligning, by the one or more processors, the received embryo sequencing data to a reference genome;
 - identifying, by the one or more processors, a genomic variant region in the aligned embryo sequencing data;
 - counting, by the one or more processors, a number of single nucleotide variants (SNVs) in the identified genomic variant region;
 - normalizing, by the one or more processors, the counted number of SNVs in the identified genomic variant region against a baseline count of SNVs for a reference region corresponding to the identified genomic variant region to generate a normalized SNV density for the genomic variant region; and
 - verifying, by the one or more processors, the identified genomic variant region, if the normalized SNV density in the identified genomic variant region satisfies a tolerance criterion.

15. A system for verifying a genomic variant region in an embryo, comprising:
 - a data store for storing embryo sequencing data;
 - a computing device communicatively connected to the data store, comprising,
 - an alignment engine configured to receive and align the embryo sequencing data against a reference genome,
 - a genomic variant caller configured to identify a genomic variant region in the aligned embryo sequencing data, and
 - a verification engine configured to:
 - count a number of single nucleotide variants (SNVs) in the identified genomic variant region and normalize the SNVs count in the identified genomic variant region against a baseline count of SNVs for a reference region corresponding to the identified genomic variant region to generate a normalized SNV density for the identified genomic variant region, and
 - verify the identified genomic variant region if the normalized SNV density in the identified genomic variant region satisfies a tolerance criterion; and
 - a display communicatively connected to the computing device and configured to display a report containing genomic variant region results from the verification engine.
16. The system of claim 15, wherein the genomic variant region is a copy number variation region.
17. The system of claim 15, wherein the genomic variant region is an aneuploidy region.
18. The system of claim 15, wherein the genomic variant region is a polyploidy region.
19. The system of claim 15, wherein the reference region is an exact length of the identified genomic variant region.
20. The system of claim 15, wherein the reference region is derived from an euploid sample.
21. The system of claim 15, wherein the tolerance criterion is an expected SNV density for a reference region derived from an euploid embryo.

22. The system of claim 21, wherein the identified genomic variant region is verified if the normalized SNV density of the identified genomic variant region is greater or lesser than a pre-set confidence interval of the expected SNV density for the reference region.
23. The system of claim 22, wherein the lower pre-set confidence interval is 95%.
24. The system of claim 15, wherein the tolerance criterion is an expected SNV density for a reference region derived from a mosaic embryo.
25. The system of claim 24, wherein the identified genomic variant region is verified if the normalized SNV density of the identified genomic variant region is above a pre-set confidence interval of the expected SNV density for the reference region.
26. The system of claim 25, wherein the pre-set confidence interval 95%.
27. The system of claim 15, wherein the tolerance criterion is a preset variance number of SNVs over or under a baseline count of SNVs for the reference region.