CLAIMS

1. A computer-implemented method comprising:

receiving, for one or more genomic coordinates of a genomic sample, a first genotype call corresponding to a first type of nucleotide reads shorter than a threshold number of nucleobases and a second genotype call corresponding to a second type of nucleotide reads satisfying the threshold number of nucleobases;

identifying a first set of sequencing metrics corresponding to the first genotype call and a second set of sequencing metrics corresponding to the second genotype call;

generating, utilizing a genotype-call-integration machine-learning model to process the first set of sequencing metrics and the second set of sequencing metrics, genotype probabilities of genotype calls for the one or more genomic coordinates; and

generating an output genotype call for the one or more genomic coordinates of the genomic sample based on the genotype probabilities.

2. The computer-implemented method of claim 1, wherein:

the first type of nucleotide reads comprise nucleotide reads synthesized from sample library fragments that are shorter than the threshold number of nucleobases; and

the second type of nucleotide reads comprises:

assembled nucleotide reads that have been assembled from shorter nucleotide reads to form a contiguous sequence satisfying the threshold number of nucleobases;

circular consensus sequencing (CCS) reads satisfying the threshold number of nucleobases; or

nanopore long reads satisfying the threshold number of nucleobases.

3. The computer-implemented method of claim 1 or 2,wherein:

generating the genotype probabilities comprises generating the genotype probabilities for one or more candidate single nucleotide polymorphisms (SNPs) utilizing the genotype-call-integration machine-learning model trained with SNP training data; and

generating the output genotype call comprises generating the output genotype call indicating a presence or absence of an SNP at the one or more genomic coordinates of the genomic sample.

4. The computer-implemented method of any one of claims 1-3, wherein generating the output genotype call comprises:

selecting the first genotype call or the second genotype call; or

generating a different genotype call differing from the first genotype call and the second genotype call.

5. The computer-implemented method of any one of claims 1-4, wherein generating the genotype probabilities comprises:

generating a first genotype probability of the genomic sample comprising a homozygous reference genotype at the one or more genomic coordinates;

generating a second genotype probability of the genomic sample comprising a heterozygous variant genotype at the one or more genomic coordinates; and

generating a third genotype probability of the genomic sample comprising a homozygous variant genotype at the one or more genomic coordinates.

6. The computer-implemented method of any one of claims 1-5, wherein the first genotype call comprises a first variant call or a first reference call, and the second genotype call comprises a second variant call or a second reference call.

7. The computer-implemented method of any one of claims 1-6, wherein the first genotype call or the second genotype call comprises a null-data indicator.

8. The computer-implemented method of any one of claims 1-7, further comprising

modifying a genotype metric, a base-call-quality metric, a genotype quality metric, a genotype probability metric, a genotype-likelihood metric, or a PHRED-scaled-genotype-likelihood metric based on the genotype probabilities; and

generating a variant call file that includes the modified genotype metric, the modified base-call-quality metric, the modified genotype quality metric, the modified genotype probability metric, the modified genotype-likelihood metric, or the modified PHRED-scaled-genotype-likelihood metric.

9. The computer-implemented method of any one of claims 1-8, wherein generating the output genotype call comprises selecting the first genotype call instead of the second genotype call by:

selecting a homozygous reference genotype call from the first genotype call instead of a heterozygous variant genotype call or a homozygous variant genotype call from the second genotype call;

selecting the heterozygous variant genotype call from the first genotype call instead of the homozygous reference genotype call or the homozygous variant genotype call from the second genotype call; or

selecting the homozygous variant genotype call from the first genotype call instead of the heterozygous variant genotype call or the homozygous reference genotype call from the second genotype call.

10. The computer-implemented method of any one of claims 1-9, wherein generating the output genotype call comprises selecting the second genotype call instead of the first genotype call by:

selecting a homozygous reference genotype call from the second genotype call instead of a heterozygous variant genotype call or a homozygous variant genotype call from the first genotype call;

selecting the heterozygous variant genotype call from the second genotype call instead of the homozygous reference genotype call or the homozygous variant genotype call from the first genotype call; or

selecting the homozygous variant genotype call from the second genotype call instead of the heterozygous variant genotype call or the homozygous reference genotype call from the first genotype call.

11. The computer-implemented method of any one of claims 1-10, wherein identifying the first set of sequencing metrics corresponding to the first genotype call and the second set of sequencing metrics corresponding to the second genotype call comprises identifying a shared set of sequencing metrics associated with both the first genotype call and the second genotype call.

12. The computer-implemented method of any one of claims 1-11, wherein identifying the first set of sequencing metrics corresponding to the first genotype call or the second set of sequencing metrics corresponding to the second genotype call comprises determining one or more of read-based sequencing metrics, call-model-generated sequencing metrics, externally sourced sequencing metrics, or second-read-type sequencing metrics associated with the second genotype call corresponding to the second type of nucleotide reads.

13. The computer-implemented method of any one of claims 1-12, wherein identifying the first set of sequencing metrics corresponding to the first genotype call or the second set of sequencing metrics corresponding to the second genotype call comprises identifying read-based sequencing metrics comprising one or more of:

an allele frequency corresponding to an allele for the first genotype call, an allele for the second genotype call, or a different allele for an alternative genotype call differing from the first and second genotype calls;

a coverage depth of the first type of nucleotide reads corresponding to the first genotype call or the second type of nucleotide reads corresponding to the second genotype call;

an average coverage depth of the first type of nucleotide reads corresponding to the first genotype call or the second type of nucleotide reads corresponding to the second genotype call;

a mapping-quality metric for the first type of nucleotide reads corresponding to the first genotype call or the second type of nucleotide reads corresponding to the second genotype call; or

a nucleobase composition of one or more nucleotide reads from the first type of nucleotide reads or the second type of nucleotide reads.

14. A system comprising at least one processor and a non-transitory computer readable medium comprising instructions that, when executed by the at least one processor, cause the system to perform a method according to any one of claims 1-13.

15. A non-transitory computer-readable medium storing instructions that, when executed by at least one processor, cause a computing device to perform a method according to any one of claims 1-13.