What is claimed is:

1. An artificial intelligence-based system to detect changes in gene expression at base resolution, comprising:

an input generation logic that accesses a sequence database and generates an input base sequence, wherein the input base sequence includes a target base sequence, and wherein the target base sequence is flanked by a right base sequence with downstream context bases, and a left base sequence with upstream context bases;

a biological quantities model that processes the input base sequence and generates an alternative representation of the input base sequence; and

a biological quantities output generation logic that processes the alternative representation of the input base sequence and generates a plurality of biological quantities output sequences,

wherein a first biological quantities output sequence in the plurality of biological quantities output sequences includes a first respective per-base biological quantities outputs for the respective target bases in the target base sequence,

wherein the first respective per-base biological quantities outputs specify respective measurements of evolutionary conservation of the respective target bases across a plurality of species, and

wherein a second biological quantities output sequence in the plurality of biological quantities output sequences includes a second respective per-base biological quantities outputs for the respective target bases in the target base sequence,

wherein the second respective per-base biological quantities outputs specify respective measurements of transcription initiation of the respective target bases at respective positions in the target base sequence.

2. The artificial intelligence-based system of claim 1, wherein the respective measurements of evolutionary conservation are phylogenetic P-values (phyloP) scores that specify a deviation from a null model of neural substitution to detect a reduction in a rate of substitution of a given target base at a given position in the target base sequence as conservation, and to detect an increase in the rate of substitution of the given target base at the given position as acceleration.

3. The artificial intelligence-based system of claim 1, wherein the respective measurements of transcription initiation are cap analysis of gene expression (CAGE) scores that specify a transcription initiation frequency of the given target base at the given position.

4. The artificial intelligence-based system of claim 1, wherein a third biological quantities output sequence in the plurality of biological quantities output sequences includes a third respective per-base biological quantities outputs for the respective target bases in the target base sequence,

wherein the third respective per-base biological quantities outputs specify respective measurements of epigenetic signal levels of the respective target bases at respective positions in the target base sequence.

5. The artificial intelligence-based system of claim 1, further configured to comprise:

a gene expression model that processes the plurality of biological quantities output sequences and generates an alternative representation of the plurality of biological quantities output sequences; and

a gene expression output generation logic that processes the alternative representation of the plurality of biological quantities output sequences and generates a gene expression output sequence of respective per-base gene expression outputs for the respective target bases in the target base sequence,

wherein a given per-base gene expression output in the gene expression output sequence for the given target base at the given position specifies a measure of gene expression level of the given target base at the given position.

6. The artificial intelligence-based system of claim 1, further configured to comprise a variant classification logic.

7. The artificial intelligence-based system of claim 1, wherein the target base sequence is a coding region of a gene.

8. The artificial intelligence-based system of claim 1, wherein the target base sequence is a non-coding region of a gene.

9. The artificial intelligence-based system of claim 1, wherein the biological quantities model has a first set of weights,

wherein the biological quantities output generation logic has a second set of weights.

10. The artificial intelligence-based system of claim 1, wherein the gene expression model has a third set of weights,

wherein the gene expression output generation logic has a fourth set of weights.

11. The artificial intelligence-based system of claim 1, wherein, during training, the biological quantities model and the biological quantities output generation logic are first trained from scratch and end-to-end to translate analysis of input base sequences into base-wise evolutionary conservation chromatin sequences, and then retrained end-to-end to translate analysis of input base sequences into base-wise transcription initiation frequency chromatin sequences.

12. The artificial intelligence-based system of claim 1, wherein, during training, the biological quantities model and the biological quantities output generation logic are first trained from scratch and end-to-end to translate

analysis of input base sequences into base-wise epigenetic signal level chromatin sequences, and then retrained end-to-end to translate analysis of input base sequences into base-wise evolutionary conservation chromatin sequences.

13. The artificial intelligence-based system of claim 1, wherein, during training, the biological quantities model and the biological quantities output generation logic are first trained from scratch and end-to-end to translate analysis of input base sequences into base-wise epigenetic signal level chromatin sequences, and then retrained end-to-end to translate analysis of input base sequences into base-wise transcription initiation frequency chromatin sequences.

14. The artificial intelligence-based system of claim 1, wherein, during training, the biological quantities model and the biological quantities output generation logic are first trained from scratch and end-to-end to translate analysis of input base sequences into base-wise epigenetic signal level chromatin sequences, and then retrained end-to-end to translate analysis of input base sequences into base-wise evolutionary conservation chromatin sequences and base-wise transcription initiation frequency chromatin sequences.

15. The artificial intelligence-based system of claim 1, further configured to comprise a first training set of training input base sequences that include variants confounded by a plurality of epigenetic effects.

16. The artificial intelligence-based system of claim 1, wherein the input base sequences and the plurality of biological quantities output sequences span the plurality of tissue types.

17. The artificial intelligence-based system of claim 1, wherein the input base sequences and the plurality of biological quantities output sequences span the plurality of cell types.

18. The artificial intelligence-based system of claim 1, wherein the biological quantities model and the biological quantities output generation logic are first trained end-to-end on the first training set, and then retrained on the second training set.

19. The artificial intelligence-based system of claim 1, wherein a size of the target base sequence varies during training to account for varying offset locations of transcription start sites (TSSs).

20. An artificial intelligence-based system to detect changes in gene expression at base resolution, comprising:

an input generation logic that accesses a sequence database and generates an input base sequence, wherein the input base sequence includes a target base sequence, and wherein the target base sequence is flanked by a right base sequence with downstream context bases, and a left base sequence with upstream context bases;

a biological quantities model that processes the input base sequence and generates an alternative representation of the input base sequence; and

a biological quantities output generation logic that processes the alternative representation of the input base sequence and generates a plurality of biological quantities output sequences,

wherein each biological quantities output sequence in the plurality of biological quantities output sequences includes respective per-base biological quantities outputs for respective target bases in the target base sequence.