CLAIMS

1. A method of quantifying RNA-induced silencing complex (RISC) activity in a tumor tissue of a patient, comprising:

    obtaining omics data from a tumor tissue of the patient, wherein the tumor tissue is subtype luminal A breast cancer tissue;

    quantifying the RISC activity from the omics data using a probabilistic graphical pathway model having a plurality of pathway elements;

    wherein each of the pathway elements in the probabilistic graphical pathway model is represented by respective factor graphs; and

    wherein at least one of the factor graphs models the RISC and comprises at least one of AGO1, AGO2, AGO3, and AGO4.

2. The method of claim 1, wherein the omics data comprise copy number data, transcription level data, and miRNA data.

3. The method of claim 1, wherein the probabilistic graphical pathway model uses *a priori* known miRNA and respective miRNA targets, and/or wherein the factor graph that models the RISC comprises AGO2.

4. The method of claim 1, further comprising comparing the quantified RISC activity with a threshold level, optionally further comprising updating a patient record when the quantified RISC activity is above the threshold level or associating a clinical parameter with the quantified RISC activity.

5. A method of detecting RNA-induced silencing complex (RISC) activity in a tumor tissue of a patient, comprising:

    obtaining omics data from the tumor tissue of the patient;

    detecting the RISC activity in the patient by inputting the omics into a probabilistic graphical pathway model, wherein the probabilistic graphical pathway model uses *a priori* known miRNA and respective miRNA targets; and

    calculating from the omics data in the pathway model a RISC activity.

6. The method of claim 5, wherein the omics data comprise copy number data, transcription level data, and miRNA data.

7. The method of claim 5, wherein the probabilistic graphical pathway model uses a plurality of factor graphs, optionally wherein at least one of the plurality of factor graphs models RNA-induced silencing complex (RISC) comprising at least one of AGO1, AGO2, AGO3, and AGO4.

8. The method of claim 5, wherein the probabilistic graphical pathway is PARADIGM.

9. The method of claim 5, further comprising comparing the quantified RISC activity with a threshold level, optionally further comprising updating a patient record when the quantified RISC activity is above the threshold level or associating a clinical parameter with the quantified RISC activity.

10. A method of predicting overall survival of a patient having subtype luminal A breast cancer, comprising:

    obtaining omics data from a tumor tissue of the patient;

    quantifying the RISC activity from the omics data using a probabilistic graphical pathway model having a plurality of pathway elements;

    wherein each of the pathway elements in the probabilistic graphical pathway model is represented by respective factor graphs, and wherein at least one of the factor graphs models the RISC with AGO2; and

    diagnosing the patient as having a decreased overall survival when decreased RISC-AGO2 activity is detected.

11. The method of claim 10, wherein the omics data comprise copy number data, transcription level data, and miRNA data, and/or wherein the probabilistic graphical pathway model uses *a priori* known miRNA and respective miRNA targets, and/or wherein the probabilistic graphical pathway is PARADIGM.

12. A computer system for omics analysis, comprising:

    an omics database informationally coupled to an analysis engine;

    wherein the omics database stores omics data of a patient;

    wherein the analysis engine is programmed to:

    (a) receive the omics data from the omics database;

    (b) calculate, using the omics data and a probabilistic graphical pathway model a RISC activity;

(c) wherein the probabilistic graphical pathway model has a plurality of pathway elements, and wherein each of the pathway elements in the probabilistic graphical pathway model is represented by respective factor graphs; and

(d) wherein at least one of the factor graphs models the RISC and comprises at least one of AGO1, AGO2, AGO3, and AGO4.

13. The computer system of claim 12, wherein the omics data comprise copy number data, transcription level data, and miRNA data, and/or wherein the probabilistic graphical pathway model uses *a priori* known miRNA and respective miRNA targets, and/or wherein the probabilistic graphical pathway is PARADIGM.

14. The computer system of claim 12, wherein the factor graph that models the RISC comprises AGO2, and/or wherein the factor graph that models the RISC comprises at least one of AGO1, AGO3, and AGO4.

15. The computer system of claim 12, wherein the analysis engine is further programmed to compare the quantified RISC activity with a threshold level, optionally wherein the analysis engine is further programmed to update a patient record when the quantified RISC activity is above the threshold level or to associate a clinical parameter with the quantified RISC activity.