Claims

1. A method of reducing an adverse effect of a cancer therapy in a patient having a tumor, comprising:

using allele fraction information to reconstruct a haplotype of first and second loci from transcriptomic data obtained from the patient, the transcriptomic data comprising allele fraction information of first and second loci of an RNA molecule transcribed from a gene, wherein the first and second loci have first and second single nucleotide variations, respectively; and

generating or updating the patient's record with the reconstructed haplotype in relation to an expected effectiveness of the cancer therapy.

2. The method of claim 1, wherein the allele fraction information of the first and second loci is derived from the tumor of the patient and/or the haplotype is reconstructed to have the first and second nucleotide variations in an allele of the gene when the allele fractions of the first and second loci having the first and second nucleotide variations differs more than 10%.

3. The method of any preceding claim, wherein the transcriptomics data comprises a copy number of the first and second loci, and further comprising:

determining amplification of at least one of first and second loci; and

generating or updating the patient's record with amplification information of the gene in relation to the expected effectiveness of a cancer therapy.

4. The method of any preceding claim, further comprising adjusting recommended dose and schedule of the cancer therapy based on the expected effectiveness.

5. The method of any one of claims 2-4, wherein the transcriptomics data further comprises allele fraction information of the first and second loci derived from a healthy tissue of the patient.

6. The method of claim 5, further comprising:

using the allele fraction information derived from the healthy tissue to reconstruct a healthy tissue haplotype;

comparing the allele fraction information derived from the tumor tissue with the allele fraction information derived from the healthy tissue to obtain tumor-specific allele fraction information; and

generating or updating the patient's record with the allele fraction information and the tumor-specific allele fraction information.

7. A method of determining the recommended dose and schedule of cancer therapy in a patient having a tumor, comprising:

using allele fraction information to reconstruct a haplotype of the first and second RNA loci from transcriptomics data obtained from the patient, the transcriptomics data comprising allele fraction information of first and second RNA loci of an RNA molecule transcribed from a gene, wherein the first and second loci have first and second nucleotide variations, respectively;

inferring an expected effectiveness of a cancer therapy from the haplotype; and

determining the recommended dose and schedule of the cancer therapy based on the expected effectiveness.

8. The method of claim 7, wherein the haplotype is reconstructed to have the first and second nucleotide variations in an allele of the gene when the allele fractions of the first and second loci having the first and second nucleotide variations differ less than 10%, and/or further comprising generating or updating the patient's record with the reconstructed haplotype in relation to an expected effectiveness of the cancer therapy.

9. The method of either claim 7 or claim 8, wherein the transcriptomics data further comprises allele fraction information of the first and second RNA loci derived from a healthy tissue of the patient.

10. The method of claim 9, further comprising:

using the allele fraction information derived from the healthy tissue to reconstruct a healthy tissue haplotype;

comparing the allele fraction information derived from the tumor tissue with the allele fraction information derived from the healthy tissue to obtain tumor-specific allele fraction information; and

determining the recommended dose and schedule of the cancer therapy using the allele fraction information and the tumor-specific allele fraction information.

11. The method of any preceding claim, wherein :

i) the cancer therapy is identified by a pathway analysis using at least two of genomics, transcriptomics, and proteomics data of the patient;

ii) the first and second loci are at least 300 bp apart; and/or

iii) the gene is at least one of CYP3A5, CYP2D6, TPMT, F5, DPYD, G6PD, and NUDT15.

12. The method of any preceding claim, wherein:

i) the gene is CYP2D6, and the expected effectiveness of a cancer therapy comprises a reduced effectiveness of the cancer therapy by a fast metabolism of the cancer therapy; or

ii) the gene is CYP2D6 and the expected effectiveness comprises an increased toxicity of the cancer therapy by a slow metabolism of the cancer therapy.

13. The method of any preceding claim, further comprising adjusting recommended dose and schedule of the cancer therapy based on a comparison of the reconstructed healthy tissue's haplotype and the tumor-specific haplotype.

14. The method of any preceding claim, wherein:

i) the transcriptomics data comprises a copy number of the first and second RNA loci, and further comprising:

determining amplification of at least one of first and second RNA loci; and

generating or updating the patient's record with amplification information of the gene in relation to the expected effectiveness of a cancer therapy;

ii) the transcriptomics data further comprises allele fraction information of the first and second RNA loci derived from a healthy tissue of the patient; and/or

iii) the allele fraction information of the first and second loci is derived from the tumor of the patient.

15. The method of claim 8, further comprising generating or updating the patient's record with the allele fraction information and the tumor-specific allele fraction information.