

Claims

1. A method for predicting the prognosis of breast cancer, the method comprising:

(a) isolating mRNA from a sample of a tissue containing cancer cells of a breast cancer patient;

(b) measuring the mRNA expression level ~~of at least one gene selected from the group consisting~~ of TRBC1 (T cell receptor beta constant 1), ~~BTN3A2 (butyrophilin, subfamily 3, member A2), and HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)~~;

(c) normalizing the measured mRNA expression level of the TRBC1 gene; and

(d) determining the overexpression of the TRBC1 gene as indicating good prognosis.

2. The method of claim 1, wherein the measuring of the expression level is conducted through PCR amplification of a target gene.

3. The method of claim 1, wherein the sample is a formalin-fixed paraffin-embedded (FFPE) sample of a tissue containing cancer cells of a patient.

4. The method of claim 1, wherein the normalizing is conducted by calculating the ratio of the mean expression level compared with at least one standard gene selected from the group consisting of CTBP1 (C-terminal-binding protein 1), TBP (TATA-binding protein), HMBS (hydroxymethylbilane synthase), CUL1 (cullin 1), and UBQLN1 (ubiquilin-1).

~~5. A composition for predicting or diagnosing the prognosis of breast cancer, the composition comprising a primer pair as an active ingredient, wherein the primer pair is for at least one gene selected from the group consisting of TRBC1 (T cell receptor beta constant 1), BTN3A2 (butyrophilin,~~

~~subfamily 3, member A2), and HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1), and wherein the primer pair is capable of amplifying a target gene through PCR amplification.~~

~~6. A kit for predicting or diagnosing the prognosis of breast cancer, the kit comprising the composition of claim 5.~~

~~7.5.~~ A method for calculating a predictive value of the prognosis of breast cancer to provide information necessary for predicting or diagnosing the prognosis of a breast cancer patient, the method comprising:

(a) isolating mRNA from a sample of a tissue containing cancer cells of a ~~the~~ breast cancer patient;

(b) measuring the mRNA expression level of ~~at least one gene selected from the group consisting of~~ TRBC1 (T cell receptor beta constant 1), ~~BTN3A2 (butyrophilin, subfamily 3, member A2), and HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1);~~

(c) normalizing the measured mRNA expression level of the TRBC1 gene;

(d) inserting the normalized value into a pre-determined calculation formula to calculate a predictive ~~numerical~~ value; and

(e) determining the prognosis of breast cancer as being good or poor depending on the predictive ~~numerical~~ value.

~~8.6.~~ The method of claim ~~7~~5, wherein the measuring of the expression level is conducted through PCR amplification of a target gene.

~~9.7.~~ The method of claim ~~7~~5, wherein the sample is a formalin-fixed paraffin-embedded (FFPE) sample of a tissue containing cancer cells of a patient.

~~10.8.~~ The method of claim ~~7~~5, wherein the normalizing is

conducted by calculating the ratio of the mean expression level compared with at least one standard gene selected from the group consisting of CTBP1 (C-terminal-binding protein 1), TBP (TATA-binding protein), HMBS (hydroxymethylbilane synthase), CUL1 (cullin 1), and UBQLN1 (ubiquilin-1).

~~11.9.~~ A method for predicting or diagnosing the prognosis of breast cancer, the method comprising a step of using a primer pair to measuring a mRNA expression level of a selected gene from a sample of a breast cancer patient, wherein the primer pair is for ~~at least one gene selected from the group consisting of~~ TRBC1 (T cell receptor beta constant 1), ~~BTN3A2 (butyrophilin, subfamily 3, member A2), and HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1),~~ and wherein the primer pair is capable of amplifying a target gene through PCR amplification.

~~12.~~ A primer pair for ~~at least one gene selected from the group consisting of~~ TRBC1 (T cell receptor beta constant 1), ~~BTN3A2 (butyrophilin, subfamily 3, member A2), and HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1),~~ wherein the primer pair is capable of amplifying a target gene through PCR amplification.

~~13.10.~~ Use of a composition comprising a primer pair for preparing an agent as an active agent in the manufacture of a medicament for predicting the prognosis of breast cancer, wherein the primer pair is ~~for at least one gene selected from the group consisting of~~ TRBC1 (T cell receptor beta constant 1), ~~BTN3A2 (butyrophilin, subfamily 3, member A2), and HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1),~~ and wherein the primer pair is capable of amplifying a target gene through PCR amplification.

11. A kit for predicting the prognosis of breast cancer, the kit comprising the composition of claim 10.

~~14.12.~~ A method for calculating a predictive value of the prognosis of breast cancer to provide information necessary for predicting or diagnosing the prognosis of a breast cancer patient, the method comprising:

(a) isolating mRNA from a sample of a tissue containing cancer cells of a the breast cancer patient;

(b) measuring the mRNA expression level of ~~at least one gene selected from the i-gene group consisting of~~ TRBC1 (T cell receptor beta constant 1), ~~BTN3A2 (butyrophilin, subfamily 3, member A2), and HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1),~~ and the mRNA expression level of at least one gene selected from the p-gene group consisting of AURKA (Aurora Kinase A), CCNB2 (Cyclin B2), FOXM1 (Forkhead box protein M1), MMP11 (Matrix Metalloproteinase 11), PTTG1 (Pituitary Tumor-Transforming 1), RACGAP1 (Rac GTPase Activating Protein 1), RRM2 (Ribonucleotide Reductase M2), TOP2A (Topoisomerase II Alpha) and UBE2C (Ubiquitin-Conjugating Enzyme E2C);

(c) normalizing the measured mRNA expression levels of the TRBC1 gene and the at least one p-gene; and

~~(d) calculating a predictive value of the prognosis of breast cancer by combining the numerical value of the gene~~

(d) inserting the normalized values of the TRBC1 gene and the at least one p-gene into a pre-determined calculation formula to calculate a predictive value of the prognosis of breast cancer; and

(e) determining the prognosis of breast cancer as being good or poor depending on the predictive value.