CLAIMS

1. A method of spectral pattern analysis of sequentially expressed nucleic acids and proteins in FTIR spectra from benign, premalignant and malignant skin tumourous tissues for characterization of multi-stage skin epidermal carcinogenesis on a biopsied tissue sample of a human, comprising of:

(i) recognizing the spectral pattern of sequentially expressed nucleic acids to DNA (965 cm^{-1}), DNA/RNA (1055 cm^{-1}), DNA/RNA triad (1071,1084/1085,1095 cm^{-1}) from determined precise order of expressed nucleic acid peaks in FTIR spectra corresponding to common expression of the nucleic acid with carcinogenesis of the tissue to be detected in benign skin tumourous tissues with reference to benign compound nevus (BCN), or premalignant skin tumourous tissues with reference to Bowen's disease (BD), or malignant skin tumourous tissues with reference to basal cell carcinoma (BCC), or malignant skin tumourous tissues with reference to squamous cell carcinoma (SCC), or malignant skin tumourous tissues with reference to malignant melanoma (MM);

(ii) recognizing the spectral pattern of sequentially expressed nucleic acids from detected expressed nucleic acids mean peaks values and their calculated intensities in FTIR spectra corresponding to specific expression of the nucleic acid with carcinogenesis of the tissue to be detected in benign, premalignant or malignant skin tumourous tissues with reference to BCN, BD, MM, SCC or BCC, wherein the spectral patterns of sequentially expressed nucleic acids for

benign skin tumourous tissues is

(965) < (1055) < (1071,1084/1085,1095),

premalignant skin tumourous tissues is

(965) < (1055) < (1071,1084/1085,1095),

or

(no peak expression) (no peak expression) (1071,1084/1085,1095),

malignant skin tumourous tissues is

(965) > (no peak expression) < (1071,1084/1085,1095), or

(965) > (1055) < (1071,1084/1085,1095), or

(965) = (1055) < (1071,1084/1085,1095), or

(965) < (1055) < (1071,1084/1085,1095), or

(965) < (1055) > (1071,1084/1085,1095);

(iii) calculating proportional ratio of mean sum of peak values in DNA/RNA triad to DNA/amide III peak value at 1245 cm^{-1},

wherein characteristic range for

benign skin tumourous tissues is [0.7:1] - [0.9:1],

premalignant skin tumourous tissues is [0.7:1] - [0.9:1],

malignant skin tumourous tissues is [0.7:1] - [1:1];

(iv) recognizing the spectral pattern of sequentially expressed proteins to amide III at 1245 cm^{-1}, to non-specific proteins at 1310 cm^{-1}, 1390 cm^{-1} and 1450 cm^{-1}, to amide II at 1540 cm^{-1} and to amide I at 1650 cm^{-1} from detected their expressed mean peaks values and calculated intensities in FTIR spectra corresponding to specific expression of the proteins with carcinogenesis of the tissue to be detected in benign skin tumourous tissues with reference to BCN, or premalignant skin tumourous tissues with reference to BD, or malignant skin tumourous tissues with reference to BCC, or malignant skin tumourous tissues with reference to SCC, or malignant skin tumourous tissues with reference to MM, wherein

the spectral patterns of sequentially expressed proteins for

benign skin tumourous tissues is

(1245) > (1310) < (1390) < (1450) < (1540) < (1650), or

(1245) = (1310) < (1390) = (1450) < (1540) < (1650),

premalignant skin tumourous tissues is

(1245) = (1310) < (1390) = (1450) < (1540) < (1650),

malignant skin tumourous tissues is

(1245) = (1310) = (1390) = (1450) < (1540) < (1650), or

(1245) > (1310) = (1390) = (1450) < (1540) < (1650), or

(1245) = (1310) < (1390) = (1450) < (1540) < (1650), or

(1245) > (1310) < (1390) = (1450) < (1540) < (1650);

(v) correlating said spectral patterns of sequential expression of nucleic acids and proteins in FTIR spectra with said proportional ratio to characterize the expression of nucleic acids and proteins with carcinogenesis of the tissue to be detected;

(vi) comparing the sequential expression of nucleic acids and proteins in recognized spectral patterns obtained on a biopsied tissue sample to identify differences corresponding to specific expression of nucleic acids and proteins with carcinogenesis of the tissue to be detected, wherein the spectral patterns of sequential expression of nucleic

acids and proteins in normal skin tissue are used as a baseline for the comparison; and

(vii) comparing the expression of nucleic acids and proteins in detected peaks values and their intensities obtained on a biopsied tissue sample to identify differences corresponding to specific expression of nucleic acids and proteins with carcinogenesis of the tissue to be detected in certain skin tumour types, wherein normal skin tissue numerical ranges of mean peaks values and intensities for nucleic acids and proteins are used as references for the comparison.

2. The method of Claim 1, further comprising the analysis of a systemic progression of the grade of activity of expressed nucleic acids and proteins contributing to carcinogenesis from benign to malignant skin tumourous tissue.

3. The method of any of Claims 1-2, wherein the spectral patterns of sequentially expressed nucleic acids and proteins in FTIR spectra for benign skin tumourous tissues with reference to BCN, is further characterized by the following features:

1 BCN spectral pattern of sequential expression of nucleic acids, based on mean peaks values and intensities

as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.7:1], or [0.8:1], or [0.9:1],

wherein

BCN spectral pattern of nucleic acids as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is characterized by

mean DNA peak values at 965 cm^{-1} within 0.12-0.18,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.17-0.24,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.19-0.27,

mean DNA peak intensities at 965 cm^{-1} within 0.47-0.56,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.59-0.75,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.72-0.84; and

1 among 3 BCN spectral patterns of sequential expression of proteins, based on mean peaks values and intensities

as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.7:1], or

as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.7:1], or [0.8:1], or

as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) < (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.9:1],

wherein

BCN spectral pattern of proteins as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) < (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within (0.3) > (0.2) < (0.3) < (0.4) < (0.7) < (1.0),

BCN spectral pattern of proteins as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within (0.3) > (0.2) < (0.3) = (0.3) < (0.7) < (1.0),

BCN spectral pattern of proteins as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within (0.3) = (0.3) < (0.4) = (0.4) < (0.8) < (1.0).

4. The method of any of Claims 1-2, wherein the spectral patterns of sequentially expressed nucleic acids and proteins in FTIR spectra for premalignant skin tumourous tissues with reference to BD, is further characterized by the following features:

1 among 2 BD spectral patterns of sequential expression of nucleic acids, based on mean peaks values and intensities

as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.8:1], or [0.9:1], or

as *(no peak expression) (no peak expression) (1071, 1084/1085, 1095 cm^{-1})* versus [0.7:1],

wherein

BD spectral pattern of nucleic acids as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is characterized by

mean DNA peak values at 965 cm^{-1} within 0.09-0.23,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.15-0.26,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.18-0.29,

mean DNA peak intensities at 965 cm^{-1} within 0.41-0.70,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.68-0.79,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.82-0.88,

BD spectral pattern of nucleic acids as *(no peak expression) (no peak expression) (1071, 1084/1085, 1095 cm^{-1})* is characterized by

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.07,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.64; and

1 BD spectral pattern of sequential expression of proteins, based on mean peaks values and intensities

as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.7:1], or [0.8:1], or [0.9:1],

wherein

BD spectral pattern of proteins as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within

(0.3) = (0.3) < (0.4) = (0.4) < (0.8) < (1.0), or

(0.2) = (0.2) < (0.3) = (0.3) < (0.7) < (1.0), or

(0.1) = (0.1) < (0.2) = (0.2) < (0.6) < (1.0).

5. The method of any of Claims 1-2, wherein the spectral patterns of sequentially expressed nucleic acids and proteins in FTIR spectra for malignant skin tumourous tissues with reference to MM, is further characterized by the following features:

1 among 3 MM spectral patterns of sequentially expressed nucleic acids, based on mean peaks values and intensities

as (*965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.8:1], or

as *(965 cm^{-1}) > (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.8:1], or

as *(965 cm^{-1}) > (no peak expression) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.7:1],

wherein

MM spectral pattern of nucleic acids as (*965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is characterized by

mean DNA peak values at 965 cm^{-1} within 0.23,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.26,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.30,

mean DNA peak intensities at 965 cm^{-1} within 0.61,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.69,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095

cm^{-1} within 0.79,

MM spectral pattern as *(965 cm^{-1}) > (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is charactrized by

mean DNA peak values at 965 cm^{-1} within 0.19,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.14,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.27,

mean DNA peak intensities at 965 cm^{-1} within 0.63,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.47,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.90,

MM spectral pattern as *(965 cm^{-1}) > (no peak expression) < (1071, 1084/1085, 1095 cm^{-1})* is charactrized by

mean DNA peak values at 965 cm^{-1} within 0.25,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.35,

mean DNA peak intensities at 965 cm^{-1} within 0.52,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.73; and

1 among 2 MM spectral patterns of sequentially expressed proteins, based on mean peaks values and intensities

as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.8:1], or

as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.7:1],

wherein

MM spectral pattern of proteins as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within

(0.3) = (0.3) < (0.4) = (0.4) < (0.8) < (1.0), or

(0.4) = (0.4) < (0.5) = (0.5) < (0.8) < (1.0),

MM spectral pattern of proteins as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within (0.5) > (0.4) < (0.5) = (0.5) < (0.8) < (1.0).

6. The method of any of Claims 1-2, wherein the spectral patterns of sequentially expressed nucleic acids and proteins in FTIR spectra for malignant skin tumourous tissues with reference to SCC, is further characterized by the following features:

1 among 4 SCC spectral patterns of sequentially expressed nucleic acids, based on mean peaks values and intensities

as *(965 cm^{-1}) > (no peak expression) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.7:1], or

as *(965 cm^{-1}) > (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.7:1], or

as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.9:1], or

as *(965 cm^{-1}) < (1055 cm^{-1}) > (1071, 1084/1085, 1095 cm^{-1})* versus [1:1],

wherein

SCC spectral pattern of nucleic acids as *(965 cm^{-1}) > (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is charactrized by

mean DNA peak values at 965 cm^{-1} within 0.19,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.13,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.16,

SCC spectral pattern of nucleic acids as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is charactrized by

mean DNA peak values at 965 cm^{-1} within 0.26,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.30,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.35,

mean DNA peak intensities at 965 cm^{-1} within 0.70,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.81,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.88,

SCC spectral pattern of nucleic acids as *(965 cm^{-1}) < (1055 cm^{-1}) > (1071, 1084/1085, 1095 cm^{-1})* is characterized by

mean DNA peak values at 965 cm^{-1} within 0.60,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.66,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.65,

mean DNA peak intensities at 965 cm^{-1} within 0.41, or 0.91,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.77, or 1.00,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.71, or 0.99,

SCC spectral pattern of nucleic acids *(965 cm^{-1}) > (no peak expression) < (1071, 1084/1085, 1095 cm^{-1})* is charactrized by

mean DNA peak values at 965 cm^{-1} within 0.07,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.12,

mean DNA peak intensities at 965 cm^{-1} within 0.91,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.76; and

1 among 3 SCC spectral patterns of sequentially expressed proteins, based on mean peaks values and intensities

as *(1245 cm^{-1}) = (1310 cm^{-1}) = (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.7:1], or [0.9:1], or

as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [1:1], or

as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.7:1],

wherein

SCC spectral pattern of proteins as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within

(0.2) = (0.2) = (0.2) = (0.2) < (0.6) < (1.0), or

(0.4) = (0.4) = (0.4) = (0.4) < (0.7) < (1.0),

SCC spectral pattern of proteins as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within

(0.2) = (0.2) < (0.3) = (0.3) < (0.6) < (1.0),

SCC spectral pattern of proteins as *(1245 cm^{-1}) > (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean proteins peaks values and intensities within

(0.7) = (0.6) < (0.7) = (0.7) < (0.9) < (1.0).

7. The method of any of Claims 1-2, wherein the spectral patterns of sequentially expressed nucleic acids and proteins in FTIR spectra for malignant skin tumourous tissues associated with BCC, is further characterized by the following features:

1 among 3 BCC spectral patterns of sequentially expressed nucleic acids, based on mean peaks values and intensities

as *(965 cm^{-1}) = (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.8:1], or

as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.8:1], or [1:1], or

as *(965 cm^{-1}) < (1055 cm^{-1}) > (1071, 1084/1085, 1095 cm^{-1})* versus [0.8:1], or [1:1], wherein

BCC spectral pattern of nucleic acids as *(965 cm^{-1}) = (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is characterized by

mean DNA peak values at 965 cm^{-1} within 0.09,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.09,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.23,

mean DNA peak intensities at 965 cm^{-1} within 0.45,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.45,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 1.15,

BCC spectral pattern of nucleic acids as *(965 cm^{-1}) < (1055 cm^{-1}) < (1071, 1084/1085, 1095 cm^{-1})* is characterized by

mean DNA peak values at 965 cm^{-1} within 0.08, or 0.31, or 0.35,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.14, or 0.43, or 0.44,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.16, or 0.45, or 0.48,

mean DNA peak intensities at 965 cm^{-1} within 0.38, or 0.71,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.67, or 0.98,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.76, or 1.09,

BCC spectral pattern of nucleic acids as *(965 cm^{-1}) < (1055 cm^{-1}) > (1071, 1084/1085, 1095 cm^{-1})* is charactrized by

mean DNA peak values at 965 cm^{-1} within 0.11, or 0.35,

mean DNA/RNA peak values at 1055 cm^{-1} within 0.19, or 0.42,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.18, or 0.40,

mean DNA peak intensities at 965 cm^{-1} within 0.50, or 0.88,

mean DNA/RNA peak intensities at 1055 cm^{-1} within 0.87, or 1.05,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.82, or 1.00; and

1 among 2 BCC spectral patterns of sequentially expressed proteins, based on mean peaks values and intensities

as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [0.8:1], or [1:1], or

as *(1245 cm^{-1}) > (1310 cm^{-1}) = (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* versus [1:1],

wherein

BCC spectral pattern of proteins as *(1245 cm^{-1}) = (1310 cm^{-1}) < (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within

(0.2) = (0.2) < (0.3) = (0.3) < (0.7) < (1.0), or

(0.2) = (0.2) < (0.3) = (0.3) < (0.8) < (1.0), or

(0.4) = (0.4) < (0.5) = (0.5) < (0.8) < (1.0),

BCC spectral pattern of proteins as *(1245 cm^{-1}) > (1310 cm^{-1}) = (1390 cm^{-1}) = (1450 cm^{-1}) < (1540 cm^{-1}) < (1650 cm^{-1})* is characterized by mean peaks values and intensities within (0.5) > (0.4) = (0.4) = (0.4) < (0.8) < (1.0).

8. The method of any of Claims 1-2, wherein the spectral patterns of sequentially expressed nucleic acids and proteins in FTIR spectra for normal skin tissue with reference to HS epidermis, is further characterized by the following features:

1 HS epidermis spectral pattern of sequentially expressed nucleic acids, based on

mean peaks values and intensities

as *(965 cm^{-1}) > (no peak expression) < (1071, 1084/1085, 1095 cm^{-1})* versus [0.5:1], or [0.7:1],

wherein

mean DNA peak values at 965 cm^{-1} within 0.15-0.24,

mean DNA/RNA triad max peak values at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.22-0.47,

mean DNA peak intensities at 965 cm^{-1} within 0.38-0.51,

mean DNA/RNA triad max peak intensities at 1071 cm^{-1}, 1084/1085 cm^{-1} or 1095 cm^{-1} within 0.49-1.00.

9. The method of any of Claims 1-2, further comprising one of the following:

comparing any received spectral patterns of sequentially expressed nucleic acids and proteins with referenced spectral patterns of sequentially expressed nucleic acids and proteins to be specific for benign, premalignant or malignant skin tumourous tissue with reference to BCC; SCC; MM; BD or BCN, in comparison to normal skin tissue; or

determining in any received spectral patterns of sequentially expressed nucleic acids and proteins which of the differences contribute to the carcinogenesis to be detected between normal and premalignant skin tissue cells, or between normal and malignant skin tissue cells, or between premalignant and malignant skin tissue cells; or

further analysing any received spectral patterns of sequentially expressed nucleic acids and proteins for a systemic progression of the grade of activity of nucleic acids and proteins between normal and benign skin tumourous tissues, characteristic for tumour progression towards benign skin tumourous tissue with reference to BCN; or

further analysing any received spectral patterns of sequentially expressed nucleic acids and proteins for a systemic progression of the grade of activity of nucleic acids and proteins between normal and premalignant skin tumourous tissues, characteristic for tumour progression towards premalignant skin tumourous tissue with reference to BD; or

further analysing any received spectral patterns of sequentially expressed nucleic acids and proteins for a systemic progression of the grade of activity of nucleic acids and proteins between normal and malignant skin tumourous tissues, characteristic for tumour progression towards malignant skin tumourous tissue with reference to MM, or with BCC, or with reference to SCC; or

further analysing received spectral patterns of sequentially expressed nucleic acids and proteins for a systemic progression of the grade of activity of nucleic acids and proteins within one type of tumour in association with MM to be characteristic for

malignant skin tumour progression in the same patient, wherein previously received spectral patterns of sequentially expressed nucleic acids and proteins were characteristic for benign skin tumourous tissue with reference to BCN, in comparison to normal skin tissue; or

further analysing received spectral patterns of sequentially expressed nucleic acids and proteins for a systemic progression of the grade of activity of nucleic acids and proteins within one type of tumour with reference to SCC to be characteristic for malignant skin tumour progression in the same patient, wherein previously received spectral patterns of sequentially expressed nucleic acids and proteins were characteristic for premalignant tumourous skin tissue with reference to BD, in comparison to normal skin tissue.

10. The method of Claims 1-9, wherein said expression levels of nucleic acids and proteins peaks are determined in normalized FTIR spectra to amide I at 1650 cm^{-1}.

11. The method of Claims 1-9, wherein DNA/RNA triad peak (1071, 1084/1085, 1095 cm^{-1}) is defined by the maximum peak in a triad.

12. The method of Claims 1-9, wherein the numerical values of peaks values of expressed proteins in FTIR spectra are numerically equalled to numercial values of calculated intensities of corresponding protein peaks in FTIR spectra normalized to amide I at 1650 cm^{-1}.