CLAIMS

1. A method for searching and identifying a genetic condition prodromal of the onset of solid tumors, with the exception of brain tumors, in a healthy subject, characterized by including an evaluation cycle for the evaluation of genetic stability or instability condition and a series of repetition cycles of such evaluation, said repetition cycles being periodically performed on the subject, with each cycle comprising the steps of:
   - taking a sample of a liquid biopsy of the subject, isolating DNA from the biological material, amplifying and sequencing the isolated DNA;
   - verifying the presence of mutations selected in a predetermined set of genes of the sample under consideration, said set of genes and said mutations being associated with the onset of solid tumors;
   - the predetermined set of genes and selected mutations are defined in view of the subject's anamnesis;
   - the predetermined set of genes including either a subset of the set of genes or hotspots connected to one or more solid tumors, or the entire set of genes connected to solid tumors;
   - verifying the frequency of mutations detected for each gene and for each evaluation cycle, the mutations being chosen from the aforementioned selected mutations;
   - recording the mutations detected for each gene or group of genes and their frequency;
   - defining or updating a genetic instability index of the subject, the genetic instability index is either an overall (I_T,) or for a single gene (I_G) for each repetition cycle, wherein the genetic instability index is defined as the increase in mutation frequency over a previous evaluation cycle; and

- evaluating, in each repetition cycle, the subject's entry into a genetic condition prodromal of the onset of one or more solid tumors or groups of solid tumors on the basis of a threshold value (I_{TS},I_{GS}) of said genetic instability index (I_T,I_G), defined for each single gene or group of genes, being exceeded,

wherein, when the threshold value is exceeded, the method further comprising verifying the presence of circulating tumor DNA (ctDNA) in the DNA sample, the presence of ctDNA and said exceeded threshold value indicate an increased likelihood for the individual to develop a solid tumor.

2. The method of claim 1, wherein said overall genetic instability index (I_T) is defined as the summation of the relationships between a value (ΔF_k) responsive to the increase in the observed mutations for each gene and the number of genes evaluated in consideration of the whole group of monitored genes.
3. The method of claim 1, wherein said index of genetic instability for single gene (I_G) is defined as the summation of the relationships between a value (ΔF_j) responsive to the increase in the observed mutations for each hotspot and the number of hotspots evaluated, in consideration of the whole group of monitored hotspots.
4. The method of claim 1, wherein the phase of verification of the presence of mutations in the predetermined set of genes is performed on a DNA sample isolated from said liquid biopsy and subsequently amplified and sequenced.
5. The method of claim 4, wherein the liquid biopsy is peripheral blood.
6. The method of claim 4, wherein the liquid biopsy is urine or spinal fluid.
7. A method according to one of the claims 4 to 6, wherein circulating tumor DNA (ctDNA) isolated from the liquid biopsy is also sought in the DNA sample being analyzed.
8. The method of claim 7, wherein, following the identification of ctDNA in said DNA sample being analyzed, the presence of CTC ("*Circulating Tumor Cells*") is sought in said liquid biopsy.
9. The method of claim 1, wherein the predetermined set of genes and selected

mutations are defined in view of their connection to particular types of tumor.

10. A method of claim 1, wherein the repetition period is recalculated after each repetition cycle according to a value of said instability index (I_T,I_G) calculated in the current cycle and a value of the same as calculated in one or more previous cycles.
11. A method of claim 1, wherein a greater analysis sensitivity related to the monitored gene or panel of genes is set in each repetition cycle, following an increase in the calculated value for said instability index (I_T,I_G) with respect to the value of the same index (I_T,I_G) calculated in one or more previous cycles.
12. The method of claim 1, wherein, in each of said evaluation and repetition cycles, germ DNA is also isolated and sequenced, and only the mutations present in the isolated DNA and not present in said germ DNA are considered for the subsequent calculation of the instability index.
13. A system for searching and identifying a genetic condition prodromal of the onset of solid tumors in a healthy subject, comprising a set of instructions of computer program aimed at carrying out an evaluation cycle of a genetic stability or instability condition and at least one repetition cycle of said evaluation defined according to claim 1.