BARD1 ISOFORMS IN LUNG AND COLORECTAL CANCER AND USE THEREOF

Field of the Invention

The present invention relates to new BARD1 isoforms specific to lung cancer and colorectal cancer, a method for detecting thereof and a method for treating and/or preventing lung cancer and colorectal cancer.

Background of the Invention

Lung cancer is the leading cause of cancer death worldwide. Treatment methods other than surgery are not very efficient and lead to resistance. Thus, insights into the etiology of lung cancer and its progression are urgently needed. Colorectal cancer is another leading cause of cancer-related death and the fourth most common cancer worldwide. The survival and prognosis of colorectal cancer patients depends on the stage of the tumor at the time of diagnosis. Early stages of colorectal cancer can be curable. Unfortunately, over 57% have regional or distant spread of the disease at the time of diagnosis. Despite significant investment and advances in the management of cancer, the five-year survival is only 15% for advanced stage colorectal cancer patients.

Recently, many groups have addressed the mechanisms that drive lung cancer by comparing protein, RNA, and microRNA in tumours with healthy tissue. Besides *TP53*, the most frequently deleted or mutated gene in lung cancer, components of the p53-ARF pathway are also consistently deleted, mutated, or epigenetically modified. As to the colorectal cancer, the challenges are to understand the molecular basis, and to determine factors that initiate the development, and drive the progression. The molecular events involved in colorectal cancer onset and metastatic progression have only been partially clarified. Recent studies have revealed the potential use of molecular and biochemical markers in colorectal cancer to predict outcome and response to chemotherapy, like MLH1, MSH2, β-Catenin, and p53.

Molecular profiles are emerging as predictive and prognostic parameters in non-small-cell lung cancer (NSCLC), including genes involved in DNA damage repair, such as *ERCC1*, *RRM1*,

and *BRCA1*. The upregulated expression of the breast cancer predisposition gene, *BRCA1* was proposed as prognostic and predictive marker for response to treatment in NSCLC. Concerning colorectal cancer, the studies of the BRCA1 are mainly limited in colorectal cancer risk and BRCA1 mutations. Several studies attempted to correlate BRCA1 mutations and colorectal cancer risk, but without any clear conclusions. Based on the current limited available evidence, BRCA mutation carriers should be regarded as at high risk for colorectal cancer. However the specific role of BRCA1 expression in colorectal cancer is unclear.

BRCA1 is expressed in many proliferating tissues and acts as a tumour suppressor in DNA repair pathways and cell cycle control. BRCA1 protein stability and function depend on its interaction with BARD1 (BRCA1 associated RING domain protein 1). The BRCA1-BARD1 heterodimer has E3 ubiquitin ligase activity, thus controlling the stability of key target proteins through ubiquitination. BARD1 is also involved in p53-dependent apoptosis, which is deficient in most lung cancers. BARD1 stabilizes p53 and promotes its phosphorylation, and expression of BARD1 is required for proper p53 functioning in signalling towards apoptosis. Thus, BARD1 plays a dual role in tumour suppression, as a binding partner of both BRCA1 and p53. Several studies have shown that BARD1 is upregulated during mitosis, transcriptionally by E2F and posttranslationally by phosphorylation, and importantly, that it is essential for mitosis. According to other studies, both BRCA1 and BARD1 were shown to interact with hMSH2, a gene commonly associated with hereditary nonpolyposis colorectal cancer (HNPCC) and mutations of hMSH2 appear to account for approximately 30-40% of HNPCC. Defects in the BRCA1-hMSH2 signalling process lead to increased susceptibility to tumorigenesis.

WO 98/12327 (Board of Regents, the University of Texas System) discloses several genes, identified in screening assays based upon binding to the breast cancer protein, BRCA1. One of these genes is termed BARD1, a RING protein that interacts with BRCA1 and is envisioned for use in various cancer-related diagnostic and therapeutic methods, particularly those connected with breast, ovarian and uterine cancer.

WO 2008/119802 (Université de Genève) discloses that in gynecological cancers, deletion-bearing isoforms of BARD1 are overexpressed and aberrantly localized to the cytoplasm, and their expression correlated with poor prognosis in breast and ovarian cancer. Structural analysis of these isoforms showed that they lacked the regions that interact with BRCA1 or

induce apoptosis. These isoforms are specific to gynecological cancers and are termed as isoforms α, β, η, γ, ε, φ, δ and θ.

Due to the severity and incurability of lung and colorectal cancers, there is still a need to develop an effective detecting method which would allow the identification of these cancers and further allow development of effective methods and compositions for treatment or prevention thereof. The main problem is that to date, no efficient methods or strategies have been developed to overcome this problem.

Summary of the Invention

The present invention provides a method for detecting the presence of a BARD1 isoform specific to lung cancer and colorectal cancer in a biological sample obtained from a subject comprising the step of detecting in said sample at least one of the BARD1 isoforms specific to lung cancer and colorectal cancer selected from the group comprising

isoform π comprising SEQ ID NO: 1, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 1, and

isoform κ comprising SEQ ID NO:2, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:2,

wherein the presence of said BARD1 isoforms specific to lung cancer and colorectal cancer in a sample from said subject is an indication that said subject is afflicted with lung cancer and/or colorectal cancer, has an increased risk of lung cancer and/or colorectal cancer, and/or has a risk of recurrence after a treatment for lung cancer and/or colorectal cancer.

The present invention further provides an isolated and/or purified polypeptide comprising SEQ ID NO: 1, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 1 for use as a biomarker in the method of claims 1 to 6 and an isolated and/or purified polypeptide comprising SEQ ID NO:2, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 2 for use as a biomarker in the method of claims 1 to 6.

Another object of the present invention is a peptide selected from the group comprising SEQ ID NOs: 13 to 80 for use in a method for detecting the presence of BARD1 isoforms of the present invention.

A further object of the present invention is a kit for detecting the presence of BARD1 isoforms specific to lung cancer and colorectal cancer in a sample obtained from a subject, comprising

at least one polynucleotide primer or probe wherein said polynucleotide primer or probe is specific for a polynucleotide that encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, and/or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, and/or

combination of antibodies or fragments thereof that specifically binds to different epitopes of at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, and/or

at least one peptide selected from the group comprising SEQ ID NOs: 13 to 80.

The present invention also relates to a method for discriminating lung cancer and colorectal cancer from gynecological cancers, said method comprising the step of detecting in a biological sample obtained from a subject at least one of the BARD1 isoforms specific to lung cancer and colorectal cancer selected from the group comprising

isoform π comprising SEQ ID NO: 1, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 1, and

isoform κ comprising SEQ ID NO:2, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 2.

wherein the presence of said BARD1 isoforms specific to lung cancer and colorectal cancer is an indication for lung cancer and/or colorectal cancer.

Additionally the present invention relates to antibody, recombinant siRNA and modulator of the biological activity of the BARD1 isoforms of the present invention for use in a method for treating and/or preventing lung cancer and colorectal cancer.

Brief description of the Figures

Figure 1 shows BARD1 expression in NSCLC. Immunohistochemistry was performed on 100 NSCLC cases with BARD1 antibodies N19, C20, PVC, WFS, and BRCA1. ***(A)*** Schematic presentation of BARD1 exons (1-11) with protein motifs indicated above as RING finger (RING), ankyrin repeats (ANK), and BRCT domains. Approximate positions of epitopes recognized by the various antibodies are designated (N19, PVC, WFS, C20). ***(B-D)*** Examples of immunohistochemical staining using BARD1 antibodies and BRCA1 antibody. BARD1 N19 and C20 showed cytoplasmic granular staining, and sometimes colocalized to the same cells or regions. BARD1 PVC and WFS staining was cytoplasmic or diffusely nuclear and cytoplasmic. BRCA1 staining colocalized with BARD1 N19 staining (B). Examples of no or little staining with PVC and WFS (C) and negligible staining with N-19 and C20 (D) are shown. Scale bar are indicated (upper panels = 200 μm; lower panels = 100 μm). ***(E)*** Observed staining of 73 of 100 NSCLC cases probed with all four N19, PVC, WFS, and C20. "+" indicates positive staining, "-" indicates negative staining. Positive staining with all four antibodies was the most frequent expression pattern. ***(F)*** Pairwise comparison of BARD1 N19, PVC, WFS, and C20 staining. BARD1 N19 and C20 and PVC and WFS were strongly correlated. Weak or no correlation was observed between N19 and PVC, N19 and WFS, C20 and PVC, C20 and WFS.

Figure 2 shows Comparison of BARD1 expression in tumour and peri-tumour tissues and correlation with clinical features. ***(A)*** Comparison of BARD1 N19, BARD1 C20, and BRCA1 staining in tumour and peri-tumour tissues of 20 (10 female and 10 male) NSCLC patients. Staining for all antibodies was increased in tumour tissues as compared to "normal" tissues. ***(B)*** BARD1 N19, BARD1 C20, and BRCA1 staining were tested in tumour tissues 10 female and 10 male NSCLC patients. Staining for all antibodies was increased in tumours from female as compared to male patients. ***(C)*** Comparison of BARD antibody staining and tumour types in 100 NSCLC cases. Positive staining was more frequent in non-adenocarcinoma (AC) (including squamous cell carcinoma and large cell carcinoma) than in AC. Increased PVC and WFS stainings were statistically significant. ***(D-E)*** Correlation of BARD1 expression with patient survival. ***(D)*** Kaplan-Meyer analysis of disease free survival (DFS) according to the combinations of 4 antibodies positive staining and less than 4 antibodies positive staining, as defined in Fig. 1E. ***(E)*** Kaplan-Meyer analysis of overall

survival (OS) according to the combinations of 4 antibodies positive staining and less than 4 antibodies positive staining, as defined in Fig. 1E.

Figure 3 shows time course of BARD1 isoform expression in experimental mouse model of induced lung cancer. ***(A)*** BARD1 expression in morphologically normal lung tissue (Normal) in urethane treated animals. BARD1 PVC and WFS epitopes were detected in some type II pneumocyte, but not in type I pneumocytes at 16 weeks (wk). All epitopes were expressed in type II and type I pneumocytes at 24 weeks and 32 weeks, and expression was upregulated from 24 weeks to 32 weeks. C20 staining was inversed to the others: strong staining at 16 weeks, week staining at 24 weeks, and almost negative at 32 weeks. ***(B)*** BARD1 expression in tumours. In tumour regions, BARD1 PVC and specifically WFS expression were upregulated from 16 to 32 weeks, while C20 expression was downregulated from 16 to 32 weeks. ***(C-D)*** Expression pattern of BARD1 epitopes in normal (C) and tumour (D) tissues of three mice is summarized. The staining scores, percentage of positive cells, are indicated (0 indicates negative staining, 1 to 4 indicate increasing intensities and numbers of cells with positive staining).

Figure 4 shows expression and structure of BARD1 transcripts in human lung tumour and peri-tumour tissues. ***(A-D)*** RT-PCR was performed with primers amplifying the entire BARD1 coding region or regions comprising exons 1- 4, or 1- 6. GAPDH was amplified as control RT-PCR. Molecular size markers (M) are shown on the left. Presumed FL BARD1 and differentially spliced isoforms are indicated on the right. ***(A)*** BARD1 RNA expression in normal lung tissue. RT-PCR performed on lung biopsies of individuals with benign lung diseases (see Methods section) shows absence of BARD1 expression in most samples and amplification of individual isoforms (γ, δ, η) in 5 cases of 8. ***(B)*** Amplification of FL BARD1 and/or truncated isoforms using forward primer in exon 1, and reverse primer in exon 11 or exon 4. Examples of pairs of normal peri-tumour (N) and tumour (T) tissue are shown for tissues from male and female patients. Presumed FL BARD1 and differentially spliced isoforms are indicated on the right. Normal and tumour tissues express the same pattern of isoforms. ***(C)*** Amplification of exons 1 to 6 was performed to distinguish FL BARD1, β, and novel isoforms κ and π. Isoform π is specifically expressed in tumours, but not or weakly in normal tissues. ***(D)*** Expression of Estrogen Receptor α, determined by RT-PCR, was found in most cases. Similar expression levels were found in normal and tumour, in male and female samples. ***(E)*** Structure of known BARD1 isoforms and lung cancer specific novel forms isoform κ and π. Schematic exon (1 to 11) structure of FL BARD1 and protein features (RING, ANK,

BRCT) and nuclear localization signals (NLS) and positions of primers are indicated. Schematic presumed protein structures of isoforms are shown below in grey, noncoding exons in white, and alternative open reading frames (β, γ and η) in light grey dots (points). Novel isoform κ is shown with deletion of exon 3 and presumed translation start (ATG) within exon 4. Novel isoform π is designed with deletion within exon 4, and known BARD1 mutations and polymorphisms that map within this region are indicated. Designated names of isoforms are shown on the left, size (amino acids) and molecular weights (MW) on the right side.

Figure 5 shows comparison of BARD1, BRCA1 and Aurora B expression morphologically normal peri-tumour (left) and in tumour tissues (right) of female and male NSCLC patients. BARD1 (N19 and C20) and C-terminal-specific antibody p8, BRCA1, and Aurora B antibody staining was used for immunohistochemistry. Denotation n = nuclear staining.

Figure 6 shows alternative splicing and/or transcription initiation within exon 4. **(A)** Diagram of various fragments of BARD1 amplified with forward primers within exon (Ex) 4, exon 5, and exon 6 (on the left), and reverse primer in exon 11 (on the right). Position of primers and expected size of amplified band is marked in parentheses (bp). **(B)** Amplification of BARD1 transcripts in human lung tumour tissues (T) and adjacent normal peri-tumour tissues (N) of male (left panel) and female (right panel) NSCLC patients with primers indicated in A are shown. Note that amplification with primers within exon 4 is variable in different samples, but all samples can be amplified with primers in exon 5 or exon 6. Variations in BARD1 mRNA and protein expression might be due to alternatively spliced or differential initiation of transcription in this region.

Figure 7 shows comparison and correlation of BARD1 mRNA isoform expression in tumour (Tumour) and peri-tumour (Normal) tissues of female and male patients. FL BARD1 and BARD1 isoforms of 20 pairs of tumour/morphologically normal tissue samples, including 10 males and 10 females, were scored and are presented. Expression was quantified with ImageJ software (see Methods section). The results are shown in the figures as means ± SE (standard error) of values. **(A)** Comparison of FL BARD1 and isoforms in peri-tumour and tumour tissues. All forms are upregulated in tumours with statistical significance, with exception of isoform β and κ. **(B-C)** FL BARD1 and BARD1 isoforms are more abundant in tumour than in peri-tumour tissues, in both males (B) and females (C). **(D/E)** Comparison of BARD1 expression between male and female in tumour tissues (D) and in normal tissues (E). BARD1 isoform β and κ are more expressed in tissues from males than females in tumour and

peri-tumour tissues. This is statistically significant. FL BARD1 and BARD1 isoforms γ, ε, and η may be more expressed in tissues from females than from males, in tumour and peri-tumour tissues, but this is not statistically significant. ***(F)*** Comparison of FL BARD1 and isoforms in young (< 60 years) and old (> 60 years) patients groups. FL BARD1 and isoform γ are up regulated in young (< 60 years) patients. This is statistically significant.

Figure 8 shows examples of immunohistochemistry of BARD1 and BRCA1 expression in colorectal cancer. Immunohistochemistry was performed on samples of 148 colorectal cancer cases with BARD1 antibodies N19, C20, PVC, WFS, and BRCA1. All samples were presented as tissue microarray with tetramerous for each of the cases. One hundred and forty-five samples were eligible for analysis after immunohistochemistry assay.

(A) Frequency of positive staining cases with antibodies for BARD1 and BRCA1. Positive staining rates for each of the four antibodies were variable. BARD1 N19 and C20 stainings were less frequent, as well as BRCA1 staining. BARD1 PVC and WFS positive stainings were observed in most of the colorectal cancer cases. ***(B)*** BARD1 expression pattern in colorectal cancer. Expression patterns were obtained with four BARD1 antibodies based on positive (+) and negative (-) staining for each of the cases. PVC and WFS positive, but N19 and C20 negative staining was the most frequent expression pattern, "all four antibodies positive" staining was the second, N19 negative while PVC, WFS and C20 positive staining was the third most frequently observed expression pattern. ***(C-F)*** Examples of immunohistostaining using BARD1 antibodies and BRCA1 antibody. BARD1 N19 and C20 showed cytoplasmic granular staining, and co localized to the same cells or regions. BARD1 PVC and WFS staining was diffusely cytoplasmic. BRCA1 staining was granular in both cytoplasm and nucleus. Examples of positive staining with BARD1 antibodies and BRCA1 antibody (C), negligible staining with N-19 and C20 (D), positive staining with all four BARD1 antibodies (E) and negative staining with N19 (F) are shown. Scale bars are shown (upper panels = 200 μm; lower panels = 50 μm).

Figure 9 shows correlation between distinct antibody staining for BARD1 and BRCA1 in colorectal cancer. ***(A)*** Correlation of BARD1 N19, PVC, WFS, and C20 staining. BARD1 N19 and C20 staining was strongly correlated, PVC and WFS, PVC and C20, and WFS and C20 staining was weakly correlated. No correlation was observed between N19 and PVC, and N19 and WFS. ***(B)*** Correlation of antibody staining of BRCA1 and BARD1. BRCA1 staining was not correlated with any staining of the four BARD1 antibodies.

Figure 10 shows correlation of distinct epitopes of BARD1 and BRCA1 expression with clinical variables in colorectal cancer. BARD1 N19 positive staining was more frequent in female gender ($P = 0.014$) (A). No correlation were found between different antibodies of BARD1 and BRCA1 staining and tumour histopathological grade (Grade) (B), tumour size or nearby tissue invasion (Tumour) (C), lymph node involvement (Node) (D), distant metastases (Metastasis) (E) and tumour stage (Stage) (F). The *P* value is obtained by the $\chi 2$ test.

Figure 11 shows expression and structure of *BARD1* transcripts in colorectal cancer tissue (T) and normal peri-tumour tissue (N). ***(A)*** Amplification of FL BARD1 and/or truncated isoforms using forward primer in exon 1, and reverse primer in exon 11 (Ex 1-11) or exon 4 (Ex 1- 4). As examples, pairs of peri-tumour and tumour tissues of 5 male and 5 female patients are shown. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) expression is shown for the same samples as standard. Molecular marker is shown on the left (M). Presumed FL BARD1 and truncated isoforms are indicated on the right. Peri-tumour and tumour tissues expressed different patterns of isoforms: less frequent expression in peri-tumour tissues than tumour tissues. Two novel isoforms, κ and π, also identified in NSCLC, were expressed in colorectal cancer. ***(B)*** Amplification of estrogen receptor α (ERα) in same samples, MCF-7 was used as positive control (right). No ERα expression was observed in colorectal tissues, neither in peri-tumour nor in tumour samples of males and females.

Figure 12 shows comparison of BARD1 mRNA isoform expression in tumour (Tumour) and peri-tumour (Normal) tissues of male and female patients with colorectal cancer. FL BARD1 and BARD1 isoforms of 20 pairs of tumor/peri-tumor tissue samples of colorectal cancer, including 10 males and 10 females, were scored and are presented. Expression was quantified based on presence or absence of expression in each of the peri-tumour or tumour samples (A), and for each of the isoforms (B, C, D). ***(A)*** Comparison of BARD1 expression in peri-tumour and tumour tissues, including in males, females and in combined samples, based on absence or presence of any of the forms of BARD1. BARD1 expression was more abundant and more frequent in tissues from tumours than peri-tumours ($P = 0.0003$), both in females ($P = 0.0010$) and in males ($P = 0.0679$). ***(B)*** Comparison of FL BARD1 and isoform expression in peri-tumour and tumour tissues. All forms were upregulated in tumours with statistical significance ($P < 0.05$ for all). ***(C/D)*** Comparison of FL BARD1 and isoform expression in colorectal tissues from males and females. The expression of FL BARD1 and isoforms was similar in tissues from males and females, both in peri-tumour (C) and in tumour (D) tissues ($P > 0.05$ for all). The *P* value is obtained by the $\chi 2$ test.

Figure 13 shows correlation of FL BARD1 and isoforms mRNA expression with clinicopathological variables in colorectal cancer. ***(A)*** Comparison of FL BARD1 and isoform expression in younger (≤ 60 years) and older (> 60 years) patients. FL BARD1 and all isoforms, except isoform β, were more up regulated in older than in younger patients. Specially, expression of isoforms φ, δ, and π were significantly associated with older patients ($P < 0.01$). ***(B-E)*** Comparison of FL BARD1 and isoforms expression with primary tumor and lymph node status, and tumor stage and grade. BARD1 isoform κ expression was significantly associated with large tumor size or nearby tissue invasion (B), lymph node involvement (C), and advanced stage (stage III and IV) (D). No correlation was found between BARD1 isoforms expression and tumor histopathological grade (E). The *P* value is obtained by the $\chi 2$ test. Comparison for $P > 0.05$ was not shown.

Figure 14 shows an example of ELISA test for BARD1 isoform-specific antibodies detection in blood or serum.

Figure 15 shows amplification of isoform π with primers at ATG and deletion junction in π. A second isoform, π', derived from additional deletion of exon 2 is identified.

Figure 16 shows Western blot with anti-Bard1 antibodies on HeLa, MCF7, RPE1 and NLF cells. **Ab** Bethyl BL518 (BL) recognizes epitopes encoded in mid exon 4. **Ab** PGP was generated against epitopes encoded by β-specific alternative ORF in exon 1. Recognizes BARD1 isoform β and BARD1 isoform β-d-5 (β') and BARD1 isoform η.

Figure 17 shows siRNA repression of BARD1 isoforms. A) Location of siRNA target sequence. Two siRNAs in exon 4 were used, K401 and K423. K401, located within the deletion of isoform pi, K423 is upstream of deletion. B-C) K401 had less effect on growth than K423. B) siRNA expression is coupled to GFP expression. Many positive cells are growing in K401 expressing cells, few are growing in K423 expressing cells. C) Growth curves confirm that K423 represses cell growth as efficiently as previously reported K78, which targets all forms of BARD1.

Figure 18 shows microRNAs affect BARD1 and BARD1 isoform expression. RT-PCR shows that all forms of BARD1 are slightly repressed by miR-203. Western blot shows strong repression of FL, β and π by miR-203 overexpression.

Detailed description of the Invention

Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. The publications and applications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. In addition, the materials, methods, and examples are illustrative only and are not intended to be limiting.

In the case of conflict, the present specification, including definitions, will control. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in art to which the subject matter herein belongs. As used herein, the following definitions are supplied in order to facilitate the understanding of the present invention.

The term “comprise” is generally used in the sense of include, that is to say permitting the presence of one or more features or components.

As used in the specification and claims, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example a BARD1 isoform means at least one BARD1 isoform.

As used herein the term “isoform” is any of several different forms of the same protein, such as BARD1 protein in the present invention. Different forms of a protein, such as BARD1, may be produced from related genes, or may arise from the same gene by alternative splicing. A large number of isoforms are caused by single-nucleotide polymorphisms or SNPs, small genetic differences between alleles of the same gene. These occur at specific individual nucleotide positions within a gene.

As used herein the terms "subject" or "patient" are well-recognized in the art, and, are used herein to refer to a mammal, and most preferably a human. In some embodiments, the subject is a subject in need of treatment or a subject with lung and/or colorectal cancer. However, in other embodiments, the subject can be a normal subject who has not developed lung and/or colorectal cancer symptoms or the subject who has already undergone a treatment against lung and/or colorectal cancer. The term does not denote a particular age or sex. Thus, adult and newborn subjects, whether male or female, are intended to be covered.

As used herein, the terms "peptide", "protein", "polypeptide", "polypeptidic" and "peptidic" are used interchangeably to designate a series of amino acid residues connected to the other by peptide bonds between the alpha-amino and carboxy groups of adjacent residues.

Contrary to what was expected, the Applicants have surprisingly identified in each sample from a 100 non-small cell lung cancer (NSCLC) and a 165 colorectal cancer patient cohort two new additional BARD1 isoforms besides already known isoforms α, β, η, γ, ε, φ, δ and θ. Another surprising feature is that isoform α was absent in each sample from a 100 NSCLC and a 165 colorectal cancer patient cohort. These new isoforms were denoted κ and π. Indeed BARD1 isoforms expressed similar pattern in tumour tissues of NSCLC and colorectal cancer, they all expressed two new isoforms κ and π, which differ from BARD1 isoforms identified in gynaecological cancers (WO 2008/119802). This finding indicated that abnormal expression of BARD1 might be different in female hormone dependent and non-female hormone dependent tumour tissues.

New isoform κ carries a deletion of exon 3, Translation of exon 2 into exon 4 is not in-frame, but translation may be initiated within exon 4. The resulting protein product would be similar in antibody reactivity to isoform β.

New isoform π carries a deletion of 408 bp, encoding amino acids 301 to 436 within exon 4. Translation of isoform π would result in a protein reacting with antibodies PVC and WFS, but lacking important NLSs (Fig. 4C, E and Fig. 6). Isoform π is derived from a novel splicing mechanism that generates a partial deletion of exon 4, but retains the exons 1- 3 and the beginning of exon 4, thus maintaining the BRCA1 binding RING finger domain. Isoform π retains the exons 1 to 3 and the beginning of exon 4, thus the epitopes recognized by PVC and

WFS, a combination of epitopes not found in any other isoform. Isoform π can be detected with antibodies PVC and WFS; these antibodies show increased staining in advanced mouse lung tumours. Thus, isoform π may be an oncogenic driver of tumour progression in NSCLC. The partial deletion of exon 4 in isoform π might be an important region, as it harbors several cancer-associated mutations and NLS (Fig. 4E), which might explain the cytoplasmic localization of PVC and WFS staining. Aberrant intracellular localization could affect protein modifications, e.g. phosphorylation and protein-protein interactions.

Isoform π seems particularly important for lung cancer as it is the only isoform that is significantly up regulated in tumour tissue and is absent or only weakly expressed in peri-tumour tissue, while all other BARD1 isoforms were expressed in tumour and peri-tumour tissue alike (Fig. 4B; Fig. 7). The partial deletion of exon 4 leads to loss of an important NLS on BARD1 that might explain the cytoplasmic localization.

An additional isoform π', derived from deletion of exon 2, was co-expressed with isoform π in lung cancer and colorectal cancer.

The Applicants showed that FL BARD1 (Full Length BARD1) and spliced isoforms are expressed in tumour and normal peri-tumour tissue and might contribute to tumour initiation and progression. However, isoform π is specifically expressed in tumours and might be involved in oncogenic progression. FL BARD1 is expressed on the mRNA level, but there is no protein translation of FL BARD1. Thus on the protein level, BARD1 isoforms, but not FL BARD1, are expressed in each sample from a 100 NSCLC and a 165 colorectal cancer patient cohort. Isoform expression and localization is not correlated with BRCA1, indicating that the E3 ubiquitin ligase functions of the BRCA1-BARD1 heterodimer are jeopardized in both types of cancer. BRCA1 protein stability and localization largely depend on BARD1. Absence of FL BARD1, causing absence of the tumour suppressor functions of BRCA1-BARD1, leads to genomic instability and resistance to apoptosis. Besides this effect of loss of FL BARD1, the over expressed differentially spliced BARD1 isoforms may be drivers of tumorigenesis.

Alternative splicing is a frequently observed phenomenon in lung cancer, and has been demonstrated for a number of regulatory proteins. Splicing isoforms can be translated into aberrant protein isoforms with antagonistic functions. This has been demonstrated for two

BARD1 splice variants, BARD1β and BARD1δ, which act antagonistically to FL BARD1 functions by stabilizing Aurora B and on ERα, respectively. Thus, BARD1 isoform expression in NSCLC might not merely be a bystander, but may be a driver of tumorigenesis. Indeed, the expression of epitopes mapping to exons 3 and 4, recognized by antibodies PVC and WFS, respectively, is increased in aggressive stages of lung tumours in mouse model of induced lung cancer (Fig. 3).

All lung tumour and peri-tumour tissue samples express also isoforms found in gynaecological cancers; specifically isoform δ. BARD1 isoform δ binds and stabilizes ERα, opposing the function of the BRCA1-BARD1 heterodimer. Since ERα is also expressed in all samples, BARD1 isoforms might be upregulated by estrogen and involved in estrogen signaling in lung cancer. Thus, several BARD1 isoforms seem to be associated with carcinogenesis.

As cancer cells need BARD1 or BARD1 isoforms to proliferate, BARD1 isoform expression in NSCLC and colorectal cancer is not merely a bystander, but may be a driver of tumorigenesis. Especially isoforms that express epitopes mapping to exons 3 and 4 seem to be correlated with short survival in both NSCLC and colorectal cancer. These epitopes were up regulated in invasive tumours in the mouse lung cancer model. The BARD1 isoforms expressed in NSCLC and colorectal cancer are derived from alternative splicing. For example the splicing isoforms can be translated into aberrant protein isoforms with antagonistic functions.

All lung tumour samples and peri-tumour tissue samples express ERα and isoform δ. However, there was no ERα mRNA expression in the series of colorectal cancer cases, and no differences were found between BARD1 isoforms expression and gender.

Interestingly, however, high frequency of N19 positive staining was significantly associated with female sex in colorectal cancer ($P = 0.014$), and this finding is in line with expression of BARD1 N-terminal epitope correlated with female sex in NSCLC (the statistical significant was marginal, $P = 0.051$). In NSCLC, high mRNA level expression of BARD1 isoforms γ, ε, and η were observed in female, while isoforms β and κ were over expressed in males. Isoforms γ and ε expression could be detected by BARD1 N19, while isoforms β, κ and η could not. Thus, protein level and mRNA level of BARD1 isoforms expression were compatible, suggesting that gender-specific BARD1 isoforms are expressed in these cancers.

BARD1 isoforms showed a different pattern of expression in tumour tissues versus peri-tumour tissues in NSCLC and colorectal cancer. In NSCLC, all isoforms, with the exception of isoform π, were expressed in peri-tumour tissue and only slightly increased in the tumour tissues, but less or no expression of any form of BARD1 was observed in control tissues obtained from benign lung disease. On the contrary, in colorectal cancer, BARD1 isoforms were more frequently expressed in tumour tissues, but not or less expressed in peri-tumour tissues. This result might be explained by diverse modulation of alternative splicing according to different cell type, in response to external stimuli or certain pathological conditions and/or the difference of ERα expression between lung and colorectal tissues.

The positive staining obtained with either PVC antibody or WFS antibody or with both of them is correlated with reduced survival of NSCLC patients. However, four antibodies positive staining pattern was significantly associated with longer survival in colorectal cancer, as well as the case for N19 positive staining; while PVC and WFS positive staining pattern was strongly correlated with shorter survival but not their positive staining individual. In fact, different expression patterns not only reflect expression of different BARD1 isoforms but also isoforms combination. According to the correlation of different epitopes of BARD1 expression, several BARD1 isoforms seem to be observed: N-terminally and C-terminally truncated form and internally deleted forms in both NSCLC and colorectal cancer, as well as additional form of loss of N- terminus in colorectal cancer. The expression pattern for four antibodies positive staining does not indicate expression of isoform π, but might reflect simultaneous expression of different isoforms of BARD1.

In fact, BARD1 isoform π expression is consistent with the epitopes recognized by PVC and WFS, a combination of epitopes not found in any other isoform. Indeed, PVC and WFS staining is cytoplasmic. Expression of PVC and WFS is clearly linked with poor prognosis in both NSCLC and colorectal cancer, PVC and WFS staining also correlated with cancer progression in the mouse lung cancer model.

Strong expression of PVC and WFS reactive epitopes, coupled with weak expression of N-terminal and C-terminal epitopes might indicate that these epitopes are blocked by steric configuration and/or protein-protein interactions. Posttranscriptional regulation or differential

protein stability of FL BARD1 versus BARD1 isoforms might also account explain the absence of FL BARD1 on the protein level, while it is present on the mRNA level.

The Applicants demonstrated that BARD1 isoforms expression was common in NSCLC and colorectal cancer. Expression of these isoforms were significant associated with prognosis in NSCLC and colorectal cancer, either poor or better prognosis, and strongly suggest that BARD1 isoforms are involved in tumorigenesis, progression, and lethality. Therefore, BARD1 and isoforms thereof could be a promising diagnostic and prognostic markers, not only to identify individuals with poor prognostic potential for more aggressive treatment, but also point to a new direction for searching effective molecular targeted therapies. For example BARD1 isoforms, such as κ and π, could be targets for new strategies for lung and colorectal cancer treatment.

Detecting specific isoforms κ and π is helpful for identification of subjects with the highest risk of dying of NSCLC and colorectal cancer before and/or after potentially curative surgical treatment, since it is a critical step in selecting subjects for subsequent treatment with adjuvant chemotherapy.

The present invention provides a method for detecting the presence of a BARD1 isoform specific to lung cancer and colorectal cancer in a biological sample obtained from a subject comprising the step of detecting in said sample at least one of the BARD1 isoforms specific to lung cancer and colorectal cancer selected from the group comprising

isoform π comprising SEQ ID NO: 1, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 1, and

isoform κ comprising SEQ ID NO:2, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:2,

wherein the presence of said BARD1 isoforms specific to lung cancer and colorectal cancer in a sample from said subject is an indication that said subject is afflicted with lung cancer and/or colorectal cancer, has an increased risk of lung cancer and/or colorectal cancer, and/or has a risk of recurrence after a treatment for lung cancer and/or colorectal cancer.

Preferably the step of detecting comprises detecting both BARD1 isoform π comprising SEQ ID NO: 1, a biologically active fragment thereof, or a sequence having at least 95% homology

to SEQ ID NO: 1, and BARD1 isoform κ comprising SEQ ID NO:2, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:2,

Also preferably the method of the invention comprises the step of detecting in said biological sample BARD1 isoform π consisting of SEQ ID NO: 1 and BARD1 isoform κ consisting of SEQ ID NO:2.

The method of the invention further comprises detecting in said biological sample at least one of the BARD1 isoforms selected from the group comprising

isoform π' comprising SEQ ID NO:105, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:105,

isoform β comprising SEQ ID NO:5, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:5,

isoform δ comprising SEQ ID NO:6, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:6, and

isoform γ comprising SEQ ID NO:7, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:7,

isoform β' comprising SEQ ID NO:106, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:106,

Preferably the method of the invention further comprises detecting in said biological sample at least one of the BARD1 isoforms selected from the group comprising

isoform π' comprising SEQ ID NO:105, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:105,

isoform β comprising SEQ ID NO:5, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:5,

isoform β' comprising SEQ ID NO:106, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO:106,

Also preferably the method of the invention comprises the step of detecting in said biological sample BARD1 isoform π consisting of SEQ ID NO: 1, BARD1 isoform κ consisting of SEQ ID NO:2 and BARD1 isoform β consisting of SEQ ID NO:5.

In the context of the present invention "biologically active fragment" refers to regions of the BARD1 isoforms of the invention, which are necessary for normal function, for example, antagonistic functions of BARD1 isoforms. Biologically active fragments include polypeptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of SEQ ID NOs: 1 to 7, 105 to 106, which include fewer amino acids than the full-length BARD1 isoforms, and exhibit at least one antagonistic activity. Typically, biologically active fragments comprise a domain or motif with at least one antagonistic activity. A biologically active fragment of BARD1 isoforms of the invention can be a polypeptide that is, for example, 10, 25, 50, 100 or more amino acid residues in length. Moreover, other biologically active fragments, in which other regions are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native BARD1 isoforms of the invention.

For example one biological active fragment of isoform π can consist in SEQ ID NO:3, one biological active fragment of isoform κ can consist in SEQ ID NO:4 and one biological active fragment of isoform β can consist in SEQ ID NO:4.

In a further embodiment, BARD1 isoforms of the invention is a polypeptide that comprises an amino acid sequence having at least 70%, 80%, 90%, 95% or 99%, preferably 95% homology to the amino acid sequence comprising SEQ ID NOs: 1 to 7, 105 to 106 and retains the activity of BARD1 isoforms comprising SEQ ID NOs: 1 to 7, 105 to 106.

To determine the percent of homology of two amino acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid for optimal alignment with a second amino acid sequence). The amino acid residues at corresponding amino acid positions are then compared. When a position in the first sequence is occupied by the same amino acid residue as the corresponding position in the second sequence, then the molecules are homologous at that position. The alignment and the percent homology can be determined using any suitable software program known in the art, for example those described in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (F. M. Ausubel et al. (eds) 1987, Supplement 30, section 7.7.18). Preferred programs include the GCG Pileup program, FASTA (Pearson et al. (1988) Proc. Natl, Acad. Sci USA 85:2444-2448), and BLAST (BLAST Manual, Altschul et al., Natl. Cent. Biotechnol. Inf., Natl Lib. Med. (NCIB

NLM NIH), Bethesda, Md., and Altschul et al., (1997) NAR 25:3389-3402). Another preferred alignment program is ALIGN Plus (Scientific and Educational Software, PA), preferably using default parameters. Another sequence software program that finds use is the TFASTA Data Searching Program available in the Sequence Software Package Version 6.0 (Genetics Computer Group, University of Wisconsin, Madison, Wis.).

Fragments are sequences sharing at least 40% amino acids in length with the respective sequence of the BARD1 isoforms of the present invention. These sequences can be used as long as they exhibit the same biological properties as the native sequence from which they derive, for example antagonistic activity. Preferably these sequences share more than 70%, preferably more than 80%, in particular more than 90% and the most preferably 95% amino acids in length with the respective sequence from which it derives. These fragments can be prepared by a variety of methods and techniques known in the art such as for example chemical synthesis.

The present invention also encompasses variants of BARD1 isoforms. A variant is a peptide or a polypeptide having an amino acid sequence that differs to some extent from a native sequence peptide or polypeptide, which is an amino acid sequence that varies from the native sequence by conservative amino acid substitutions, whereby one or more amino acids are substituted by another with same characteristics and conformational roles. The amino acid sequence variants possess substitutions, deletions, side-chain modifications and/or insertions at certain positions within the amino acid sequence of the native amino acid sequence. Conservative amino acid substitutions are herein defined as exchanges within one of the following five groups:

I. Small aliphatic, nonpolar or slightly polar residues: Ala, Ser, Thr, Pro, Gly
II. Polar, positively charged residues: His, Arg, Lys
III. Polar, negatively charged residues: and their amides: Asp, Asn, Glu, Gln
IV. Large, aromatic residues: Phe, Tyr, Trp
V. Large, aliphatic, nonpolar residues: Met, Leu, Ile, Val, Cys.

It is to be understood that some non-conventional amino acids may also be suitable replacements for the naturally occurring amino acids. For example Lys residues may be

substituted by ornithine, homoarginine, nor-Lys, N-methyl-Lys, N, N-dimethyl-Lys and N, N, N- trimethyl-Lys. Lys residues can also be replaced with synthetic basic amino acids including, but not limited to, N-1- (2-pyrazolinyl)-Arg, 2- (4-piperinyl)-Gly, 2- (4- piperinyl)-Ala, 2- [3- (2S) pyrrolininyl]-Gly and2- [3- (2S) pyrolininyl]-Ala. Tyr residues may be substituted with 4-
5 methoxy tyrosine (MeY), meta-Tyr,ortho-Tyr, nor-Tyr,1251-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr, and nitro-Tyr.

Tyr residues may also be substituted with the 3-hydroxyl or 2-hydroxyl isomers (meta-Tyr or ortho-Tyr, respectively) and corresponding O-sulpho-and O-phospho derivatives. Tyr residues
10 can also be replaced with synthetic hydroxyl containing amino acids including, but not limited to4-hydroxymethyl-Phe, 4-hydroxyphenyl- Gly, 2, 6-dimethyl-Tyr and 5-amino-Tyr. Aliphatic amino acids may be substituted by synthetic derivatives bearing non-natural aliphatic branched or linear side chains CnH2n+2 where n is a number from 1 up to and including 8. Examples of suitable conservative substitutions by non-conventional amino acids are given in WO
15 02/064740.

Insertions encompass the addition of one or more naturally occurring or non conventional amino acid residues. Deletion encompasses the deletion of one or more amino acid residues.

20 Furthermore, since an inherent problem with native peptides (in L-form) is the degradation by natural proteases, the physiological active protein of the invention may be prepared in order to include D-forms and/or "retro-inverso isomers" of the peptide. Preferably, retro-inverso isomers of short parts, variants or combinations of the physiological active protein of the invention are prepared. Retro-inverso peptides are prepared for peptides of known sequence as
25 described for example in Sela and Zisman, in a review published in FASEB J. 1997 May;11(6):449-56. By "retro-inverso isomer" is meant an isomer of a linear peptide in which the direction of the sequence is reversed and the chirality of each amino acid residue is inverted; thus, there can be no end-group complementarity.

30 The invention also includes analogs in which one or more peptide bonds have been replaced with an alternative type of covalent bond (a "peptide mimetic") which is not susceptible to cleavage by peptidases. Where proteolytic degradation of the peptides following injection into the subject is a problem, replacement of a particularly sensitive peptide bond with a

noncleavable peptide mimetic will make the resulting peptide more stable and thus more useful as an active substance. Such mimetics, and methods of incorporating them into peptides, are well known in the art.

Preferably the biological sample is selected from the group comprising a biopsy sample, a histology sample, lung liquids, frozen tissue sample, tumor tissue sample, feces sample, cerebrospinal fluid (CSF), circulating tumour cells (CTC) and blood sample; and preferably the subject is a human. The most preferably the biological sample is serum derived from blood sample obtained from a subject.

Detecting the presence of BARD1 isoforms of the present invention can be carried out by conventional methods such as protein immunostaining, protein immunoprecipitation, immunoelectrophoresis, immunoblotting, BCA protein assay, Western blot, spectrophotometry. The presence of BARD1 isoforms can be also detected via the presence of their corresponding mRNA by conventional methods such as Northern blot, nuclease protection assays (NPA), in situ hybridization, and reverse transcription-polymerase chain reaction (RT-PCR). Preferably the expression of BARD1 isoform-specific RNA is detected in circulating tumour cells (CTC).

In an embodiment of the present invention, the presence of BARD1 isoforms is detected by using antibodies specific to BARD1 isoforms of the invention. Preferably said antibodies are polyclonal or monoclonal antibodies or fragments thereof that specifically bind to at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106. Also preferably said antibodies are a combination of antibodies or fragments thereof that specifically bind to different epitopes of at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106. Preferably said epitopes are exons 3 and 4.

Preferably said polyclonal or monoclonal antibodies or said combination of antibodies specifically bind to at least one of the BARD1 isoforms comprising amino acid sequences

selected from the group comprising SEQ ID NOs: 1 and 2, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-2.

For example, antibodies which allow detection of BARD1 isoforms of the invention are the following:

- N19, C20 and H300 (Santa Cruz Biotechnology, Santa Cruz, CA),
- PVC and WSF (begin of exon 4) were generated and applied as described previously (Irminger-Finger I et al., Mol Cell 8:1255-66, 2001 ; Feki A et al., Oncogene 24:3726-36, 2005 ; Hayami R et al., Cancer Res 65:6-10, 2005 ; Li L et al., Int J Biochem Cell Biol 39:1659-72, 2007 ; Redente EF et al., Anticancer Res 29:5095-101, 2009 ; Fabbro M et al., J Biol Chem 277:21315-24, 2002),
- BL (Bethy Laboratories),
- JH2 and JH3 (Gautier et al. Cancer Rsearch, 2000),
- PGP (Ryser et al., Cancer Research, 2000),
- ELS and KPD generated by Applicants
- MIQ (Irminger-Finger et al., JCB 1998)

The detection can be carried out by immunohistochemistry and is summarized in Table 1:

- BARD1 isoform π should be positive for either N19 (or PVC, or MIQ) plus either BL (or WFS) and negative for JH2. In order to distinguish isoform π from π' (*pi-d-2)*, this can only be done by size on Western blots.
- BARD1 isoform κ should be positive for BL (or WFS) and negative for N19 (or PVC, or MIQ).
- BARD1 isoform β should be positive for PGP, and either WFS or BL. In order to distinguish isoform β from β' (*beta-d-5)*, isoform β is positive for ELS.
- BARD1 isoform δ should be positive for N19 and negative for either PVC (or MIQ) and negative for BL (or WFS).
- BARD1 isoform γ should be positive for N19 and either PVC (or MIQ), but negative for C20 (or KPD).

Ab Isoform	MW(kD)	H300	PGP	N19	PVC	MIQ	WFS	BL	JH2	ELS	JH3	KPD	C20
Exon(s)		1-3, 4half	1alt	1	3	3	4start	4mid	4end	5	7	11mid	11end
FL BARD1	95	H300		N19	PVC	MIQ	WFS	BL	JH2	ELS	JH3	KPD	C20
alpha	85	H300		N19	PVC	MIQ	WFS	BL	JH2	ELS	JH3	KPD	C20
beta	75	H300	PGP	-	-	-	WFS	BL	JH2	ELS	JH3	KPD	C20
beta-D-5	72	H300	PGP	-	-	-	WFS	BL	JH2	-	JH3	KPD	C20
kappa	70	H300		-	-	-	WFS	BL	JH2	ELS	JH3	KPD	C20
pi	65	H300		N19	PVC	MIQ	WFS	BL	-	ELS	JH3	KPD	C20
pi-D-5	62	H300		N19	PVC	MIQ				ELS	JH3	KPD	C20
gama	39	-		N19	PVC	MIQ	-	-	-	-	-	-	-
omega	38	-		-	-	-	-	-	-	ELS	JH3	KPD	C20
phi	37	H300		N19	-	-	-	-	-	-	JH3	KPD	C20
delta	35	?H300		N19	-	-	-	-	-	-	JH3	KPD	C20
epsilon	30	H300		N19	PVC	MIQ	-	-	-	-	-	KPD	C20
eta	28	-	PGP	-	-	-	-	-	-	-	-	KPD	C20

Beta-D-5 is alternative name of isoform β' and pi-D-5 is alternative name for isoform π'

In another embodiment of the present invention, the presence of said BARD1 isoforms is detected by detecting the level (expression) of mRNA that encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106. Preferably said mRNA encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1 and 2, biologically active fragments thereof, or a sequence having at least 95% homology SEQ ID NOs: 1-2. The expression of said mRNA is preferably carried out in vitro in circulating tumour cells (CTC) obtained from a subject.

In a further embodiment of the present invention, the presence of said BARD1 isoforms is detected by detecting the presence of autoimmune antibodies specific to BARD1 isoforms of

the present invention in the blood sample obtained from the subject, preferably in serum. Preferably autoimmune antibodies are antibodies specific to BARD1 isoforms π and κ.

In the context of the present invention "autoimmune antibody" or "autoantibody" refers to a naturally occurring antibody directed to BARD1 isoforms of the invention, which the immune system of a subject recognizes as foreign proteins even though these BARD1 isoforms are actually originated in said subject. Thus these BARD1 isoforms elicit an immune response. Preferably said BARD1 isoforms are isoforms π and κ.

The autoimmune antibodies can be detected by conventional immunoassays well known in the art, for example different ELISA techniques, (either with antibody fixed on a plate surface or with the antigen fixed on the plate surface to capture the antibodies) radioimmunoassays and the like (see Immunoassay, E. Diamandis and T. Christopoulus, Academic Press, Inc., San Diego, CA, ; 1996) . Immunoassays for the detection of antibodies having a particular immunological specificity generally require the use of a reagent (antigen) that exhibits specific immunological reactivity with the antibody under test. Depending on the format of the assay this antigen may be immobilized on a solid support. A sample to be tested for the presence of the antibody (for example a blood sample) is brought into contact with the antigen and if antibodies of the required immunological, specificity are present in the sample they will immunologically react with the antigen, to form antibody-antigen complexes which may then be detected or quantitatively measured.

Thus according to an embodiment of the present invention, presence of BARD1 isoforms is detected by detecting the presence of autoimmune antibodies specific to said BARD1 isoforms in the blood sample obtained from the subject, wherein at least one antigen (peptide), preferably at least four antigens (peptides), selected from the group comprising SEQ ID NOs: 13 – 80 are used for detecting said autoimmune antibodies specific to said BARD1 isoforms. Said BARD1 isoforms are selected from the group comprising isoforms α, β, β', η, γ, ε, φ, δ, θ, π, π' and κ. Preferably said BARD1 isoforms are selected from the group comprising isoforms β, β' δ, γ, π, π' and κ. More preferably said BARD1 isoforms are selected from the group comprising isoforms β, π and κ. The most preferably said BARD1 isoforms are selected from the group comprising isoforms π and κ. The detection of autoimmune antibodies is preferably carried out in vitro on a blood sample obtained from a subject, preferably in serum.

More preferably, BARD1 isoforms are isoforms π and κ specific to lung cancer and colorectal cancer and the antigens are selected from the group comprising SEQ ID NOs: 16, 17, 18, 23, 59-67, 68, 69, 74, 75, 76-80. Most preferably the antigens are selected from the group comprising SEQ ID NOs: 16, 17, 18, 23, 68, 69, 74 and 75.

In an embodiment, the present invention provides peptide selected from the group comprising SEQ ID NOs: 13 to 80 for use in a method for detecting the presence of BARD1 isoforms of the invention.

Applicants have also discovered that the antigens selected from the group comprising SEQ ID NOs: 13 – 80 can also be used for detecting other cancers selected among breast cancer, ovarian cancer, prostate cancer, neuroblastoma and leukaemia, through detection of the presence of autoimmune antibodies specific to BARD1 isoforms selected from the group comprising isoforms α, β, β', η, γ, ε, φ, δ, θ, π, π' and κ. For example the antigens selected from the group comprising SEQ ID NOs: 13, 14, 15, 23, 59-67, 69, 70, 75-80 can be useful for detecting breast cancer, ovarian cancer and prostate cancer.

Thus in a further embodiment, the present invention provides peptide selected from the group comprising SEQ ID NOs: 13 to 80 for use as antigen in a method for detecting the presence of BARD1 isoforms in a biological sample obtained from a subject, wherein the presence of said BARD1 isoforms is detected by detecting the presence of autoimmune antibodies specific to said BARD1 isoforms and wherein the presence of said BARD1 isoforms in said sample is an indication that said subject is afflicted with cancer. Said BARD1 isoforms are selected from the group comprising isoforms α, β, β', η, γ, ε, φ, δ, θ, π, π'and κ.

At least one antigen should be used for detecting the presence of autoimmune antibodies specific to BARD1 isoforms. Preferably at least four antigens are used; more preferably four to ten antigens are used; the most preferably four to six antigens are used.

The antigens of the present invention can also be contacted with negative control samples (healthy control blood samples) in order to obtain a base line, which facilitates discrimination between cancer subjects and healthy subjects (see Examples – Detection of anti-BARD1

autoimmune antibodies in blood of lung cancer patients). Optionally the antigens of the present invention can also be contacted with positive control samples (confirmed cancer blood samples) in order to obtain clear positive results.

In another embodiment, a blood sample from a subject can be contacted with BARD1 isoforms of the invention, preferably isoforms π and κ or fragments thereof. Then the specific binding between autoimmune antibody and said BARD1 isoforms can be detected allowing determination of the presence or absence of lung cancer and/or colorectal cancer based on the amount of the specific binding between autoimmune antibody and said BARD1 isoforms. The detection of autoimmune antibodies is preferably carried out in vitro on a blood sample obtained from a subject, preferably in serum.

Alternatively, according to an embodiment of the present invention, the presence of BARD1 isoforms of the invention is detected by

detecting the level of mRNA that encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, and

detecting the presence of autoimmune antibodies specific to said BARD1 isoforms in the blood sample obtained from the subject, and wherein at least four antigens selected from the group comprising SEQ ID NOs: 13 – 80 are used for detecting said autoimmune antibodies specific to said BARD1 isoforms.

The present invention further provides an isolated and/or purified polypeptide comprising SEQ ID NO: 1, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 1 for use as a biomarker in the method of the present invention; and an isolated and/or purified polypeptide comprising SEQ ID NO:2, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 2 for use as a biomarker in the method of the present invention.

The present invention also provides an antibody or fragment thereof which binds to an epitope as set forth in SEQ ID NO: 143 (DTKSRNEVVTPIKGDIPSVEYLLQNGS) on BARD1

isoform π. Preferably the present invention provides an antibody or fragment thereof which binds to an epitope as set forth in SEQ ID NO: 144 (NEVVTPIKGDIPSVEY).

The present invention further provides an antibody or fragment thereof which binds to an epitope as set forth in SEQ ID NO: 143 for use in a method for treating and/or preventing lung cancer and colorectal cancer. Preferably the present invention provides an antibody or fragment thereof which binds to an epitope as set forth in SEQ ID NO: 144 for use in a method for treating and/or preventing lung cancer and colorectal cancer

The present invention also encompasses polyclonal or monoclonal antibody or fragment thereof that specifically bind to at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, for use in a method for treating and/or preventing lung cancer and colorectal cancer, and wherein the following antibodies are excluded N19, C20, H300, PVC, WSF, BL, JH2, JH3, PGP, ELS, KPD, MIQ.

It is also encompassed by the present invention a combination of antibodies or fragments thereof that specifically bind to different epitopes of at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106 for use in a method for treating and/or preventing lung cancer and colorectal cancer, and wherein the following antibodies are excluded: N19, C20, H300, PVC, WSF, BL, JH2, JH3, PGP, ELS, KPD, MIQ.

The antibody of the present invention can be also used for detecting the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragment thereof, or sequence having at least 95% homology to SEQ ID NOs: 1-7, 105-106 in tissue samples of a subject, body fluids of a subject, or circulating cells in the blood of a subject.

Preferably said polyclonal or monoclonal antibodies or said combination of antibodies specifically bind to at least one of the BARD1 isoforms comprising amino acid sequences

selected from the group comprising SEQ ID NOs: 1 and 2, biologically active fragments thereof, or sequences having at least 95% homology SEQ ID NOs: 1-2.

As used herein, the term "antibody" refers to an immunoglobulin molecule having a specific structure, that interacts (i.e., binds) only with the antigen that was used for synthesizing the antibody (for example BARD1 isoforms of the invention) or with an antigen closely related thereto. Furthermore, an antibody can be a fragment of an antibody or a modified antibody, so long as it binds to one or more of the proteins encoded by the marker genes. For instance, the antibody fragment can be Fab, F(ab')2, Fv, or single chain Fv (scFv), in which Fv fragments from H and L chains are ligated by an appropriate linker (Huston J. S. et al., (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5879-83.). More specifically, an antibody fragment can be generated by treating an antibody with an enzyme, including papain or pepsin. Alternatively, a gene encoding the antibody fragment can be constructed, inserted into an expression vector, and expressed in an appropriate host cell (see, for example, Co M. S. et al., (1994) J. Immunol. 152:2968-76; Better M. and Horwitz A. H. (1989) Methods Enzymol. 178:476-96.; Pluckthun A. and Skerra A. (1989) Methods Enzymol. 178:497-515.; Lamoyi E. (1986) Methods Enzymol. 121 :652-63.; Rousseaux J. et al, (1986) Methods Enzymol. 121 :663-9.; Bird R. E. and Walker B. W. (1991) Trends Biotechnol. 9:132-7.).

An antibody can be modified by conjugation with a variety of molecules, for example, polyethylene glycol (PEG). The modified antibody can be obtained by chemically modifying an antibody. Such modification methods are conventional in the field.

Alternatively, an antibody can comprise a chimeric antibody having a variable region from a nonhuman antibody and a constant region from a human antibody, or a humanized antibody, comprising a complementarity determining region (CDR) from a nonhuman antibody, a frame work region (FR) and a constant region from a human antibody. Such antibodies can be prepared by using known technologies. Humanization can be performed by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody {see, e.g., Verhoeyen et al, (1988) Science 239:1534-6). Accordingly, such humanized antibodies are chimeric antibodies, wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non- human species. Fully human antibodies comprising human variable regions in addition to human framework and constant regions can

also be used. Such antibodies can be produced using various techniques known in the art. For example in vitro methods involve use of recombinant libraries of human antibody fragments displayed on bacteriophage (e.g., Hoogenboom & Winter, (1992) J. MoI. Biol. 227:381-8). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. This approach is described, e.g., in U.S. Patent Nos. 6,150,584; 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016. Such antibodies can be prepared by using known technologies.

The present invention also provides a recombinant siRNA molecule that binds to a single-stranded or double stranded RNA molecule, wherein said single-stranded or double stranded RNA molecule comprises an mRNA that encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequence having at least 95 % homology to SEQ ID NOs: 1-7, 105-106 and whereby the expression of said BARD1 isoforms are inhibited, for use in a method for treating and/or preventing lung cancer and colorectal cancer.

Preferably said mRNA encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1 and 2, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-2.

In the context of the present invention, the siRNA (RNA interferent or small interfering RNA) inhibits or reduces the expression of BARD1 isoforms. Preferably said isoforms are π, π', κ, β, β', δ, and γ; more preferably π, κ, β and the most preferably π and κ. Herein, the term "siRNA" refers to a double stranded RNA molecule which prevents translation of a target mRNA. Usually the siRNA comprises a sense nucleic acid sequence and an anti-sense nucleic acid sequence against expression of one or more of the BARD1 isoforms comprising amino acids sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106.

In general, siRNA can be isolated. An "isolated" siRNA is one that is removed from its original environment. For example, a siRNA is considered to be isolated if it is cloned into a vector that is not a part of the natural environment.

The siRNA can be constructed fully synthetically and consisting of two complementary single stranded RNA or biosynthetically. The siRNA is constructed such that a single transcript has both the sense and complementary antisense sequences from the target gene, (e.g. a single hairpin RNA or shRNA). Standard techniques for introducing siRNA into the cell can be used, including those in which DNA is a template from which RNA is transcribed.

Usually, an siRNA that binds to a single-stranded RNA molecule, wherein said single-stranded RNA molecule comprises an mRNA that encodes at least one of the BARD1 isoforms comprising amino acids sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95 % homology to SEQ ID NOs: 1-7, 105-106, by associating with the normally single-stranded mRNA transcript, thereby interfering with translation and thus, expression of the BARD1 isoforms. Thus, siRNA molecules of the invention can be defined by their ability to hybridize specifically to mRNA or cDNA that encodes at least one of the BARD1 isoforms comprising amino acids sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95 % homology to SEQ ID NOs: 1-7, 105-106.

In the context of the present invention, an siRNA is preferably less than 500, preferably less than 200, more preferably less than 100, even more preferably less than 50, or most preferably less than 25 nucleotides in length. More preferably an siRNA is about 19 to about 25 nucleotides in length. In order to enhance the inhibition activity of the siRNA, one or more uridine ("u") nucleotides can be added to 3' end of the antisense strand of the target sequence. The number of "u's" to be added is at least 2, generally 2 to 10, preferably 2 to 5. The added "u's" form a single strand at the 3 'end of the antisense strand of the siRNA.

A siRNA of the present invention can be directly introduced into the cells in a form that is capable of binding to the mRNA transcripts. In these embodiments, the siRNA molecules of the invention are typically modified as know in the art. Other modifications are also possible, for example, cholesterol-conjugated siRNAs have shown improved pharmacological properties. Song, et al, Nature Med. 9:347-51 (2003). Alternatively, a DNA encoding the siRNA can be carried in a vector.

Several useful siRNA have been identified. For example siRNA in exon 9 (please refer to Fig. 1A and Fig. 4E) is efficient and lead to proliferation arrest. In another example, using siRNA within exon 4 is important for BARD1 isoform π (see Fig. 17). Some useful siRNA are:

K34: *CATTCTGAGAGAGCCTGTG* (SEQ ID NO. 107)

K423: *GTGCTCAGCAAGACTCATA* (SEQ ID NO. 108)

K401: *AAGTCTCTTTACCATTGGCTG* (SEQ ID NO. 109)

K78: *AAGTGTATGCTTGGGATTCTC* (SEQ ID NO. 110)

The present invention further provides a modulator of the biological activity of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, for use in a method for treating and/or preventing lung cancer and colorectal cancer. Preferably said BARD1 isoforms comprise amino acid sequences selected from the group comprising SEQ ID NOs: 1 and 2, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-2.

The modulator of the biological activity of the BARD1 isoforms can be a competitor. Preferably said competitor is a compound able to disturb interaction between said BARD1 isoforms and a receptor thereof. For example, the competitor can be also an inhibitor or an antagonist. The term “inhibitor” or "antagonist" refers to molecules that inhibit the function of the protein or polypeptide by binding thereto. The competitor, such as inhibitor or antagonist, can directly inhibit the interaction between BARD1 isoforms of the invention and its natural ligand and/or receptor resulting in disturbed biochemical or biological function of the receptor. Competitive inhibition is a form of inhibition where binding of the inhibitor prevents binding of the ligand and *vice versa*. In competitive inhibition, the inhibitor binds to the same active site as the natural ligand, without undergoing a reaction. The ligand molecule cannot enter the active site while the inhibitor is there, and the inhibitor cannot enter the site when the ligand is there. The “biological activity or function” of a protein refers to the ability to carry out diverse cellular functions and to bind other molecules specifically and tightly.

Also in the context of the present invention, a modulator of the biological activity of the BARD1 isoforms of the invention can be preferably microRNA (miRNA) which modulates gene expression. Applicants found that BARD1 can be target of many microRNAs. The

exogenous expression of specific microRNA represses BARD1 expression (see Fig. 18). More preferably in the context of the present invention, microRNAs are selected from the group comprising: hsa-mir-10a MI0000266: (SEQ ID NO. 111); hsa-mir-10b MI0000267 (SEQ ID NO. 112); hsa-mir-130a MI0000448 (SEQ ID NO. 113); hsa-mir-130b MI0000748 (SEQ ID NO. 114) ; hsa-mir-134 MI0000474 (SEQ ID NO. 115); hsa-mir-144 MI0000460 (SEQ ID NO. 116); hsa-mir-148a MI0000253 (SEQ ID NO. 117) ; hsa-mir-148b MI0000811 (SEQ ID NO. 118) ; hsa-mir-152 MI0000462 (SEQ ID NO. 119) ; hsa-mir-181a-2 MI0000269 (SEQ ID NO. 120) ; hsa-mir-181a-1 MI0000289 (SEQ ID NO. 121); hsa-mir-181b-1 MI0000270 (SEQ ID NO. 122) ; hsa-mir-181b-2 MI0000683 (SEQ ID NO. 123) ; hsa-mir-19a MI0000073 (SEQ ID NO. 124) ; hsa-mir-19b-1 MI0000074 (SEQ ID NO. 125) ; hsa-mir-19b-2 MI0000075 (SEQ ID NO. 126) ; hsa-mir-203 MI0000283 (SEQ ID NO. 127) ; hsa-mir-301a MI0000745 (SEQ ID NO. 128) ; hsa-mir-301b MI0005568 (SEQ ID NO. 129) ; hsa-mir-452 MI0001733 (SEQ ID NO. 130) ; hsa-mir-454 MI0003820 (SEQ ID NO. 131) ; hsa-mir-517a MI0003161 (SEQ ID NO. 132) ; hsa-mir-517c MI0003174 (SEQ ID NO. 133) ; hsa-mir-553 MI0003558 (SEQ ID NO. 134) ; hsa-mir-570 MI0003577 (SEQ ID NO. 135) ; hsa-mir-576 MI0003583 (SEQ ID NO. 136) ; hsa-mir-579 MI0003586 (SEQ ID NO. 137) ; hsa-mir-580 MI0003587 (SEQ ID NO. 138) ; hsa-mir-613 MI0003626 (SEQ ID NO. 139) ; hsa-mir-618 MI0003632 (SEQ ID NO. 140).

Usually microRNAs are short ribonucleic acid (RNA) molecules, having at least about 22 nucleotides, preferably about 60 to about 100 nucleotides, which can bind to complementary sequences on target messenger RNA transcript (mRNAs), usually resulting in translational repression or target degradation and gene silencing.

The present invention also includes a method for discriminating lung cancer and colorectal cancer from gynecological cancers, said method comprising the step of detecting in a biological sample obtained from a subject at least one of the BARD1 isoforms specific to lung cancer and colorectal cancer selected from the group comprising

isoform π comprising SEQ ID NO: 1, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 1, and

isoform κ comprising SEQ ID NO:2, a biologically active fragment thereof, or a sequence having at least 95% homology to SEQ ID NO: 2.

wherein the presence of said BARD1 isoforms specific to lung cancer and colorectal cancer is an indication for lung cancer and/or colorectal cancer.

Another feature useful to discriminate lung cancer and colorectal cancer from gynecological cancers, is that BARD1 isoform α is absent in lung cancer and colorectal cancer. The amino acid sequence of BARD1 isoform α is known from PCT/EP2008/053881. Thus optionally, said method further comprises detecting in said sample BARD1 isoform α, a biologically active fragment thereof, or a sequence having at least 95% homology BARD1 isoform α, wherein the absence of said BARD1 isoform α is an indication that said subject is not afflicted with lung cancer and/or colorectal cancer.

Preferably, gynaecological cancers are a group of different malignancies of the female reproductive system. The most common types of gynaecologic malignancies are cervical cancer, ovarian cancer, and endometrial (uterus) cancer. There are other less common gynaecological malignancies including cancer of the vagina, cancer of the vulva, gestational trophoblastic tumours, and fallopian tube cancer. In the context of the present invention, breast cancer is also included in gynaecological cancers.

The present invention further provides a kit for detecting the presence of BARD1 isoforms specific to lung cancer and colorectal cancer in a sample obtained from a subject, comprising

at least one polynucleotide primer or probe wherein said polynucleotide primer or probe is specific for a polynucleotide that encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, and/or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, and/or

combination of antibodies or fragments thereof that specifically binds to different epitopes of at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, and/or

at least one peptide selected from the group comprising SEQ ID NOs: 13 to 80.

Preferably said BARD1 isoforms comprises amino acid sequences selected from the group comprising SEQ ID NOs: 1-22, biologically active fragments thereof, or sequences having at least 95% homology to SEQ ID NO: 1-2.

Polynucleotide that encodes at least one of the BARD1 isoforms is a polynucleotide comprising nucleic acid sequences selected from the group comprising SEQ ID NO: 8 (isoform π), SEQ ID NO: 9 (isoform κ), SEQ ID NO: 10 (isoform β), SEQ ID NO: 11 (isoform δ), SEQ ID NO: 12 (isoform γ), SEQ ID NO: 141 (isoform π'), SEQ ID NO: 142 (isoform β'); preferably nucleic acid sequences selected from the group comprising SEQ ID NO: 8 and 9.

Primers, probes, and/or antibodies can be packaged together along with other necessary detection reagents in the form of a kit. For example, they can be packaged in separate containers, e.g., a nucleic acid or antibody (either bound to a solid matrix or packaged separately with reagents for binding them to the matrix), a control reagent (positive and/or negative), and/or a detectable label. Instructions (e.g., written, tape, VCR, CD-ROM, etc.) for carrying out the detection can also be included in the kit.

The present invention also encompasses vaccines and vaccination methods. For example, methods of treating or preventing lung cancer and/or colorectal cancer in a subject suffering from said cancer can involve administering to the subject a vaccine composition comprising

one or more of the BARD1 isoforms comprising amino acids sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, a biologically active fragment thereof, a sequence having at least 95% homology to SEQ ID NOs: 1-7, 105-106 or an immunologically active fragment thereof,

or one or more peptide (antigen) selected from the group comprising SEQ ID NO:13 to 80.

Preferably said BARD1 isoforms comprise amino acids sequences selected from the group comprising SEQ ID NOs: 1-2, a biologically active fragment thereof, a sequence having at least 95% homology to SEQ ID NOs: 1-2 and said peptide are selected from the group comprising SEQ ID NOs: 16, 17, 18, 23, 59-67, 68, 69, 74, 75, 76-80.

In the context of the present invention, an immunologically active fragment is a polypeptide that is shorter in length than the full-length naturally-occurring protein, for example one of

BARD1 isoforms, yet which induces an immune response analogous to that induced by the full-length protein. For example, an immunologically active fragment should be at least 8 residues in length and capable of stimulating an immune cell, for example, a T cell or a B cell. Immune cell stimulation can be measured by detecting cell proliferation, elaboration of cytokines (e.g., IL-2), or production of an antibody. See, for example, Harlow and Lane, Using Antibodies: A Laboratory Manual, 1998, Cold Spring Harbor Laboratory Press; and Coligan, et al., Current Protocols in Immunology, 1991-2006, John Wiley & Sons.

The present invention also includes a pharmaceutical composition for the treatment or prevention of lung cancer and/or colorectal cancer in a subject suffering from said cancer, wherein said composition comprises a pharmaceutically effective amount of an antibody of the present invention.

The present invention further includes a pharmaceutical composition for the treatment or prevention of lung cancer and/or colorectal cancer in a subject suffering from said cancer, wherein said composition comprises a pharmaceutically effective amount of a siRNA of the present invention.

The present invention further encompasses a pharmaceutical composition for the treatment or prevention of lung cancer and/or colorectal cancer in a subject suffering from said cancer, wherein said composition comprises a pharmaceutically effective amount of a modulator according to the present invention. Preferably said modulator is microRNA, which modulates gene expression.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder, such as lung and/or colorectal cancer, as well as those in which the disorder is to be prevented. Hence, the mammal, preferably human to be treated herein may have been diagnosed as having the disorder or may be predisposed or susceptible to the disorder, such as lung and/or colorectal cancer.

"Prevention" as used herein means that the administration of the modulator(s), siRNA and/or antibodies as described in the present invention results in a reduction in the likelihood or

probability that a subject at high risk for lung and/or colorectal cancer will indeed develop said cancer.

"A pharmaceutically effective amount" refers to an active ingredient (for example chemical or biological material) which, when administered to a human or animal organism induces a detectable pharmacologic and/or physiologic effect.

The respective pharmaceutically effect amount can depend on the specific subject to be treated, on the disease to be treated and on the method of administration. The treatment usually comprises a multiple administration of the pharmaceutical composition, usually in intervals of several hours, days or weeks. The pharmaceutically effective amount of a dosage unit of the active ingredient, such as antibody, siRNA or a modulator of the present invention, usually is in the range of 0.001 ng to 100 mg per kg of body weight of the subject to be treated. It is understood that the suitable dosage of an active ingredient of the present invention will be dependent upon the age, sex, health, and weight of the recipient, kind of concurrent treatment, if any and the nature of the effect desired.

For systemic administration, a therapeutically effective amount or dose can be estimated initially from *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC50 as determined in cell culture. Such information can be used to more accurately determine useful doses in humans.

Initial doses can also be estimated from in vivo data, e.g. animal models, using techniques that are well known in the art. One ordinarily skill in the art could readily optimise administration to humans based on animal data and will, of course, depend on the subject being treated, on the subject's weight, the severity of the disorder, the manner of administration and the judgement of the prescribing physician.

"Administering", as it applies in the present invention, refers to contact of the pharmaceutical compositions to the subject, preferably a human.

The pharmaceutical composition may be dissolved or dispersed in a pharmaceutically acceptable carrier well known to those skilled in the art, for parenteral administration by, e. g., intravenous, subcutaneous or intramuscular injection or by intravenous drip infusion.

As to a pharmaceutical composition for parenteral administration, any conventional additives may be used such as excipients, adjuvants, binders, disintegrants, dispersing agents, lubricants, diluents, absorption enhancers, buffering agents, surfactants, solubilizing agents, preservatives, emulsifiers, isotonizers, stabilizers, solubilizers for injection, pH adjusting agents, etc.

Acceptable carriers, diluents and adjuvants which facilitates processing of the active compounds into preparation which can be used pharmaceutically are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl orbenzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as TWEEN®, PLURONICS® or polyethylene glycol (PEG).

The form of administration of the pharmaceutical composition may be systemic or topical. For example, administration of such a pharmaceutical composition may be various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, buccal routes or via an implanted device, and may also be delivered by peristaltic means.

The pharmaceutical composition comprising an active ingredient of the present invention may also be incorporated or impregnated into a bioabsorbable matrix, with the matrix being

administered in the form of a suspension of matrix, a gel or a solid support. In addition the matrix may be comprised of a biopolymer.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g. films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and [gamma] ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT(TM) (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid.

The formulations to be used for in vivo administration must be sterile. This is readily accomplished for example by filtration through sterile filtration membranes.

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications without departing from the spirit or essential characteristics thereof. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations or any two or more of said steps or features. The present disclosure is therefore to be considered as in all aspects illustrated and not restrictive, the scope of the invention being indicated by the appended Claims, and all changes which come within the meaning and range of equivalency are intended to be embraced therein.

The foregoing description will be more fully understood with reference to the following Examples. Such Examples, are, however, exemplary of methods of practising the present invention and are not intended to limit the scope of the invention.

Examples

I - Patients – lung cancer

Tumor tissues from 100 NSCLC patients were collected at two different centres (Table 1). All patients were informed and approval obtained from the local ethics committees. Eight cases with benign lung diseases (five males and three females, ages ranging from 24 to 66 years (median age, 38 years); five cases of pulmonary emphysema, the rest pulmonary tuberculosis and carcinoid dysplasia) were used as control samples for BARD1 expression.

Follow-up records were available for 48 of 60 patients from Napoli; follow-up was from one to 69 months; two patients died during the perioperative period, and data on 10 patients were not available. Of 48 patients with follow-up records, 17 were treated with surgery only, four with chemotherapy post surgery, one with chemotherapy and radiotherapy post surgery, seven patients were treated with chemotherapy and radiotherapy, four with chemotherapy and one with radiotherapy only, and the remaining 14 were without treatment till last follow-up or death. Of these 48 patients, 35 were dead, and 13 were still alive during last follow-up period.

Seventeen of 40 patients from Cagliari had follow-up records; follow-up was from five to 95 months; 11 patients were still alive at the last follow-up period (Mar. 2010), and 6 patients died.

Overall survival was calculated from the date of surgery, beginning of chemotherapy or radiotheraphy, or the date of diagnosis for patients without treatment, to the last follow-up or death.

Table 1. Patient Characteristics – lung cancer

Samples		Napoli	Cagliari	Total
Cases		60	40	100
Gender	Male	54	20	74
	Female	6	20	26
Age	Range	34-77	33-77	33-77
	Median	63	60	62
Normal (peri-tumor)		0	20	20
Tumor		60	40	100
Histology	Adenocarcinoma	26	40	66
	Squamous Cell Carcinoma	21	0	21

	Large Cell Carcinoma	9	0	9
	Adenosquamous Carcinoma	4	0	4
Grade	Well-differentiated	2	10	12
	Moderately differentiated	20	12	32
	Poorly differentiated	26	18	44
	Undifferentiated	1	0	1
	Unspecified	11	0	11
Stage	IA	14	18	32
	IB	19	8	27
	IIA	1	5	6
	IIB	9	3	12
	IIIA	11	2	13
	IIIB	4	1	5
	IV	1	3	4
	Unknown	1	0	1

Patients characteristics – colorectal cancer

Pathologic diagnoses were made by experienced pathologists based on WHO criteria and staged according to American Joint Committee on Cancer classification. All patients were informed and compliance was obtained as well as approval of the local ethical committees. A total of 168 cases with colorectal cancer containing 20 cases from Cagliari and 148 cases from Germany were examined (Table 2). Twenty cases from Cagliari including both tumor tissue and their adjacent morphologically normal tissue (peri-tumor) samples were used for reverse-transcriptase PCR detection. 148 cases with colorectal cancer from Germany were used for immunohistochemistry on tissue arrays. These 168 cases were composed of 106 colon cancers and 62 rectal cancers, they were all adenocarcinomas. The patients were 93 males and 75 females, with age at diagnosis ranging from 33 to 78 years (median age, 61 years). 21 patients had stage I disease, 34 stage II, 50 stage III, and 23 stage IV; the remaining 40 patients were of unknown stage since the primary tumor or/and the regional lymph nodes or/and distant metastasis could not be assessed. Ten patients had well differentiated (G1), 116 moderately differentiated (G2), and 38 poorly differentiated (G3) tumors; the remaining 2 patients were unspecified (GX).

The sections used for immunochemical staining were tissue microarrays with tetramerous for each case. 75 of 148 cases had follow-up records, follow-up was from one to 72 months, and

remaining 73 patients had no survival data. Of these 75 patients with follow-up records, 22 were dead, 48 were lost, and five were still alive during last follow-up period.

Table 2. Patient characteristics of colorectal cancer

Samples		Germany	Cagliari	Total
Cases		148	20	168
Gender	Male	83	10	93
	Female	65	10	75
Age	Range	41-97	33-73	33-97
	Median	73	60.5	71
Normal (peri-tumor)		0	20	20
Tumor		148	20	168
Histology	Adenocarcinoma	148	20	168
Grade	Well-differentiated	10	0	10
	Moderately differentiated	105	12	117
	Poorly differentiated	32	6	38
	Undifferentiated	0	0	0
	Unspecified	1	2	3
Tumor	T1	3	1	4
	T2	32	4	36
	T3	69	13	82
	T4	42	2	44
	TX	2	0	2
Node	N0	74	7	81
	N1	34	7	41
	N2	36	6	42
	N3	1	0	1
	NX	3	0	3
Metastasis	M0	101	15	116
	M1	44	5	49

	MX	3	0	3
Stage	I	26	4	30
	II	38	3	41
	III	35	9	44
	IV	44	4	48
	Unknown	5	0	5

Immunohistochemistry

Immunohistochemistry was performed on adjacent sections with antibodies against different regions of BARD1 and against BRCA1.

Antibodies against different regions of BARD1 used, namely N19 (exon 1) (sc-7373) and C20 (exon 11) (sc-7372), were purchased from Santa Cruz (Santa Cruz Biotechnology, Santa Cruz, CA), PVC (exon 3) and WSF (begin of exon 4) were generated and applied as described previously (Irminger-Finger I et al., Mol Cell 8:1255-66, 2001 ; Feki A et al., Oncogene 24:3726-36, 2005 ; Hayami R et al., Cancer Res 65:6-10, 2005 ; Li L et al., Int J Biochem Cell Biol 39:1659-72, 2007 ; Redente EF et al., Anticancer Res 29:5095-101, 2009 ; Fabbro M et al., J Biol Chem 277:21315-24, 2002). Antibodies against BRCA1 were from Santa Cruz (D16; Santa Cruz Biotechnology, Santa Cruz, CA). Staining was visualized by secondary antibodies (goat antirabbit or rabbit antigoat) conjugated with HRP were applied in 1:100 dilutions at room temperature for 1 hr. DAB staining was for 2 to 15 min at room temperature. Slides were counterstained with hematoxylin before dehydration and mounting. To ascertain sensitivity and specificity, immunohistochemistry was performed omitting the primary antibodies on control sections. To quantify expression of BARD1 or BRCA1, 4 different regions were chosen for each tumor section; the percentage of positive cells and intensity of staining were combined to calculate an average score of each sample. Three persons performed this quantification independently and without any knowledge of clinical data.

For immunohistochemistry performed on mice with induced lung cancer, treated and age-matched untreated mice were sacrificed after 16, 24, and 32 weeks, and tumors dissected and analyzed by immunohistochemistry using antibodies PVC, WFS, and C20 on two control and three tumor bearing mice. Analysis and quantification was as described for human samples.

Formalin-fixed and paraffin-embedded 5 μm tissues sections were de-paraffinized in xylene and re-hydrated through descending ethanol concentrations (100% alcohol, 95% alcohol, 70%

alcohol, dH2O). The sections were boiled for 5 min in a microwave for antigen retrieval, and endogenous peroxidases were blocked. Slides were incubated overnight at 4°C in a humidifying chamber with the first antibody after BSA (bovine serum albumin) blocking of the non-specific epitopes. The primary antibodies used for BARD1 detection were N19 (sc-7373, Santa Cruz Biotechnology) (1: 25 diluted), PVC (1: 100 diluted), WFS (1: 100 diluted), and C20 (sc-7372, Santa Cruz, CA) (1: 20 diluted), which recognize epitopes in exons 1, 3, 4, and 11, respectively; BRCA1 antibody was C20 (sc-642, Santa Cruz Biotechnology) (1:100 diluted), recognizing BRCA1 C-terminal epitopes. Secondary antibodies (goat anti-rabbit or rabbit anti-goat) conjugated with horse radish peroxidase (HRP) were applied in 1:100 dilutions at room temperature for 1 hour. Then diaminobenzidine (DAB) staining was permitted for maximum 15 minutes at room temperature. Slides were counter-stained with hematoxylin before de-hydration and mounting. To ascertain sensitivity and specificity, immunohistochemistry was performed omitting the primary antibodies on control sections. Expression levels of BARD1 and BRCA1 were measured semi-quantitatively. Staining was scored using intensity and percentage of the stained tumor cells. The value of the staining intensity and positive cell percentage were multiplied to get the final staining score. The total staining score of each antibody is from 0 to 100, 25 or less staining score is definited negative staining ("-"), more than 25 is definited positive staining ("+"), and it was distinguished "+", "++", and "+++" according to the total staining score more than 25 to 50, more than 50 to 75, and more than 75. For statistical analysis, only positive versus negative cases were considered, except the correlation of different antibodies staining using staining score. Four different regions were chosen for each tumor section and scored independently by three observers (Y,Z; L,L and J,W) without knowledge of clinical data.

RNA / RT-PCR analysis

RT-PCR was performed to qualitatively determine the expression of different isoforms and to investigate their structure. RNA was isolated from frozen tissue sections using Trizol reagent. Chloroform (0.1 ml) was added and samples centrifuged at 14,000 g for 15 min at 4 °C to separate the phases. The aqueous phase was transferred to an RNase-free Eppendorf tube, and an equal volume of isopropanol added for RNA precipitation. The RNA pellet was washed with 75 percent ethanol and dissolved in 20 μl RNase-free water. Concentrations were measured to ascertain that D260/D280 ratios were at least 1.8.

For reverse transcription, 1 μg of RNA was used in 21 μl of reverse transcriptase buffer containing 1 μl of dNTPs (10 mM), 1 μl of oligo dT, 2 μl of DTT (0.1 M), 4 μl of first-stand buffer and 1 μl of Superscript II. Reactions were performed at 65 °C for 5 min, followed by 42 °C for 2 min, 42 °C for 50 min, and 70 °C for 15 min. Two μl cDNA was used as a template for PCR with different primers.

Estrogen Receptor α (ERα) was amplified using annealing temperature 56°C and extension times 1 min with primers 5'-ACAAGCGCCAGAGAGATGAT-3' (SEQ ID NO: 81) and 5'-GATGTGGGAGAGGATGAGGA-3' (SEQ ID NO: 82). Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was amplified as internal control with primers 5'-AGCCACATCGCTCAGACACC-3' (SEQ ID NO: 83) and 5'-GTATCTAGCGCCAGCATCG-3' (SEQ ID NO:84). The same volume of PCR product was used on agarose/TBE gels (0.8% for FL, 1% for others) containing 0.1μg/ml ethidium bromide (EtBr) for analysis the same size fragment of BARD1 (20 μl for exon 1-11, 10 μl for exon 1-4, 5 μl for others) and visualization under UV light.

PCR products (10 μl) were analyzed on 1% of agarose/TAE gels supplemented with ethidium bromide and visualized under UV light. Please refer to Table 3 for a complete list of primers and conditions.

The QIAEX II kit (Qiagen, Hombrechtikon, Switzerland) was used for DNA purification. Sequencing was performed with internal BARD1 primers.

Table 3

Forward primer		Reverse primer		PCR product (bp)	Anealing Tem (°C)	Extension (sec)
Sequence	Position (bp) (Exon)	Sequence	Position (bp) (exon)			
5' GAGGAGCCTTTCATCCGAAG 3' (SEQ ID NO: 85)	-28 (Ex 1)	5' ATTGCAGGCTGGGTTTGCACTGAAG 3' (SEQ ID NO: 95)	506 (Ex 4)	534	56	60
5' GAGGAGCCTTTCATCCGAAG 3' (SEQ ID NO: 86)	-28 (Ex 1)	5' TTTTGATACCCGGTGGTGTT 3' (SEQ ID NO: 96)	1481 (Ex 6)	1509	56	90
5' GAGGAGCCTTTCATCCGAAG 3' (SEQ ID NO: 87)	-28 (Ex 1)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 97)	2252 (Ex11)	2280	56	120
5' GTTTAGCCCTCGAAGTAAGAAAG 3' (SEQ ID NO: 88)	438 (Ex 4)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 98)	2252 (Ex11)	1815	56	120
5'GTCAGATATGTTGTGAGTAAAGCTTC3' (SEQ ID NO: 89)	461 (Ex 4)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 99)	2252 (Ex11)	1792	56	120
5' AGCAAGTGGCTCCTTGACAG 3' (SEQ ID NO: 90)	783 (Ex 4)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 100)	2252 (Ex11)	1470	56	90
5' CCAGTCCCATTTCTAAGAGATGTAG 3' (SEQ ID NO: 91)	986 (Ex4)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 101)	2252 (Ex11)	1267	56	90
5' GAGGAGAGACTTTGCTCC 3' (SEQ ID NO: 92)	1280 (Ex4)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 102)	2252 (Ex11)	973	56	60
5' GCTGGATGGACACCATTG 3' (SEQ ID NO: 93)	1378 (Ex5)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 103)	2252 (Ex11)	875	56	60
5' CTCCAGCATAAGGCATTGGT 3' (SEQ ID NO: 94)	1441 (Ex 6)	5' CGAACCCTCTCTGGGTGATA 3' (SEQ ID NO: 104)	2252 (Ex11)	812	56	60

Image analysis for PCR

Images were manipulated by ImageJ, Java-based image processing software (National Institutes of Health, http://rsbweb.nih.gov/ij/). PCR products were subjected to agarose gel, visualized with Ethidium bromide staining and photographed. Images were saved as JPG files before being converted to greyscale for analysis. The image was opened in ImageJ, calibration function was set to un-calibrated OD for each image before measurement. The rectangle tool was used to draw the area for measurement of the same size of PCR bands. The same size of band in DNA ladder closing the size of interest bands in samples were used to get the relative accurate values in different gels based on adjusting the area of rectangle. The area of the peak was outlined. The proportion of the peak area as a percentage of the total area under the curve was used for statistical analysis.

Total RNA extraction, reverse transcription and PCR

RT-PCR was performed to qualitatively show expression of different isoforms and to determine their structure. RNA isolation from frozen tissue sections was obtained using Trizol reagent according to the protocol of RNA isolation. Chloroform (0.1 ml) was added, and samples were centrifuged at 14,000 g for 15 min at 4 °C to separate the phases. The aqueous phase was transferred to an RNase-free Eppendorf tube, and an equal volume of isopropanol was added for RNA precipitation. RNA pellet was washed with 75 percent ethanol and dissolved in 20 µl RNase-free water. Concentrations were measured to ascertain that D260/D280 ratios were at least 1.8.

For reverse transcription, 1.5 µg of RNA was used in final volume of 25 µl, containing M-MLV RT 5x Reaction Buffer 5 µl, 2 µl of oligo dT (500µg/ml), 1.5 µl of 10 mM dNTP's, Recombinant RNasin Ribonuclease Inhibitor 1µl (25 u/µl) and 1 µl of M-MLV Reverse Transcriptase (200 u/µl). The reaction was incubated at 70°C 5 minutes followed by 42°C 60 minutes and 70°C 10 minutes. Three µl of cDNA were used as a template for amplification of FL BARD1, and 2 µl of cDNA were used for amplification of various fragments of BARD1. PCR was performed with *Taq polymerase* in a final volume of 50 µl. Primary denaturation (94°C, 2 min) and final extension (72°C, 10 min) were the same for all PCR reactions. Annealing temperatures and extension times were variable according to different primers and length of the expected product for BARD1 (Table 3).

Estrogen Receptor α (ERα) was amplified using annealing temperature 56°C and extension times 1 min with primers 5'-ACAAGCGCCAGAGAGATGAT-3' (SEQ ID NO: 81) and 5'-GATGTGGGAGAGGATGAGGA-3' (SEQ ID NO: 82). Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was amplified as internal control with primers 5'-AGCCACATCGCTCAGACACC-3' (SEQ ID NO:83) and 5'-GTATCTAGCGCCAGCATCG-3' (SEQ ID NO:84). The same volume of PCR product was loaded on agarose/TBE gels (0.8% for FL, 1% for others) containing 0.1μg/ml ethidium bromide (EtBr) for visualization of fragment of BARD1 (20 μl for exon 1-11, 10 μl for exon 1-4, 5 μl for others) under UV light.

The QIAEX II kit (Qiagen, Hombrechtikon, Switzerland) was used for DNA purification of RT-PCR products according to the manufacturer's instruction followed by sequencing with forward and reverse primers used for PCR, or additional primers within the fragments if no overlapped sequence was produced.

Mouse model

Lung tumors were chemically induced in BALB/c mice as described in Redente EF, Dwyer-Nield LD, Barrett BS, et al: Lung tumor growth is stimulated in IFN-gamma-/- mice and inhibited in IL-4Ralpha-/- mice. Anticancer Res 29:5095-101, 2009. Male mice, 6 – 8 weeks of age, were injected intraperitoneally with one mg urethane per g body weight once weekly for seven weeks. Mice were sacrificed 16, 24 and 32 weeks after treatment. Lung tissue and tumors were dissected and processed for immunochemistry analysis. Tissues from three mice were analyzed for each time point.

Statistical analysis

The Spearman's correlation coefficient ρ was used to assess the correlation between expression levels of BARD1 and BRCA1 epitopes. The $\chi 2$ test was used to compare the percentage of positive cases in tumor versus peritumor tissues, and correlation of positive cases of BARD1 expression with clinical variables. The T-test was used to measure the correlation of BARD1 expression level with clinical variables. For associations with survival, patients were further placed into two groups according to their BARD1 expression levels. Survival differences were estimated using Kaplan–Meier method and compared by the log-rank test. For all calculations, the tests were two-sided, and a value of $P < 0.05$ was considered

statistically significant. Analyses were performed using Statistical Package for the Social Sciences (SPSS) for Windows version 13 (SPSS Inc, Chicago, IL).

II - Results

Immunohistochemistry on sections of tumors was performed, comprising different types, grades, and stages from 100 patients (Table 1). Antibodies recognizing four different epitopes of BARD1 (mapping to exons 1, 3, 4, and 11) were used, which could theoretically result in 16 different staining patterns. Surprisingly, only few distinct patterns were observed, and staining for all four antibodies was observed in the majority of tumors (Fig. 1A-E). Staining of adjacent sections showed that different epitopes were expressed in different regions of tumor sections and in different sub-cellular compartments (Fig. 1B-D), suggesting that different isoforms of BARD1 were expressed within a single tumor. Typically, BARD1-N19 (exon 1) and C20 (exon 11) showed cytoplasmic granular staining and were co-localized to the same regions of a tumor. BARD1 PVC (exons 3) and WFS (exon 4) immunostainings were diffuse and in the cytoplasm. These differences in intensity and intracellular localization of stainings suggested that expression of all four epitopes did not reflect the expression of wild type BARD1, but rather the simultaneous expression of different isoforms.

The expression levels of N19 and C20 strongly correlated with each other, as was the case for PVC and WFS (Fig. 1F), but other antibody staining patterns did not correlate. Thus it could be concluded that N-terminally and C-terminally truncated forms, as well as forms with internal deletions, are expressed in NSCLC. Particularly, the WFS (5'end of exon 4) staining was upregulated in many lung cancers, in contrast to the epitope expression pattern observed for ovarian cancers, where WFS staining was rare.

BRCA1 and BARD1 co-expression in adjacent tissue sections (Fig. 1B-D) was investigated. BRCA1 was expressed in 66.7% of NSCLC samples, but it did not correlate with expression of any the BARD1 epitopes. As BRCA1 is not co-expressed with BARD1, these data suggest that functions of the BRCA1-BARD1 heterodimer are lost in NSCLC.

BARD1 expression in tumor and normal peri-tumor tissue was observed, although more elevated in tumors (Fig. 2A; Fig. 5). Expression was generally higher in tumors from female than from male patients (Fig. 2B).

The expression of specific BARD1 epitopes was less frequent in adenocarcinomas than in non-adenocarcinomas (including squamous cell carcinoma and large cell carcinoma) (Fig. 2C). However, no correlation of antibody staining with tumor grade and stage was found (data not shown).

Individual epitopes of BARD1 expression and expression pattern with disease free survival (DFS) and overall survival (OS) in 65 patients with follow-up data was also evaluated. Patients with individual PVC and WFS positive staining had significantly shorter DFS and shorter OS than those with negative staining. Most importantly, patients with PVC and WFS simultaneously positive staining pattern showed a very shorter survival compared with those who had different combinations. No correlations were observed between N19, C20, and other staining patterns and either DFS or OS.

Univariate and multivariate analysis using Cox's proportional hazards model were performed to evaluate whether the markers analyzed have an independent prognostic significance. In the univariate analysis, pathologic stage also showed prediction of DFS and OS (Table 5). The pathologic stage and another two possible prognostic factors, histologic type and patient gender, were entered into a multivariate model. This latter analysis showed that individual PVC and WFS positive staining, PVC and WFS simultaneously positive staining pattern, and pathologic stage preserve independent prognostic significance for both DFS and OS (Table 5).

Table 4. Univariate analysis of survival in 65 NSCLC patients with follow-up data

	DFS				OS		
Predictors	HR	95% CI	*P*		HR	95% CI	*P*
N19 pos vs neg	1.08	0.50-2.32	0.849		1.11	0.46-2.67	0.811
PVC pos vs neg	3.84	1.50-9.87	0.005		4.79	1.41-16.2	0.012
WFS pos vs neg	3.39	1.50-7.67	0.003		2.47	1.01-6.00	0.047
C20 pos vs neg	1.26	0.53-2.98	0.602		1.45	0.51-4.12	0.481
N19 and C20 pos vs others	1.08	0.50-2.32	0.849		1.11	0.46-2.67	0.811
PVC and WFS pos vs others	3.22	1.49-6.96	0.003		3.02	1.22-7.46	0.017
4 Abs pos vs others	2.04	1.11-3.77	0.123		1.86	0.91-3.81	0.091
Stage III, IV vs I, II	3.04	1.61-5.72	0.001		3.60	1.85-7.02	0.000
AC vs non-AC	0.72	0.41-1.24	0.232		0.62	0.33-1.14	0.124
Grade 3, 4 vs 1, 2	1.50	0.84-2.66	0.167		1.87	0.96-3.66	0.068
Age (years) ≤ 60 vs > 60	1.06	0.61-1.83	0.837		1.21	0.64-2.28	0.557
Male vs female	1.35	0.65-2.80	0.414		0.89	0.35-2.27	0.804

Note: *HR*, hazard ratio; 95% CI, 95% confidence interval; *P*, *P* – value; *pos,* positive staining; *neg*, negative staining. *AC*, adenocarcinoma; *non-AC*, including squamous cell carcinoma and large cell carcinoma; *others*, all other combinations.

Table 5. Multivariate analysis of survival in 65 NSCLC patients with follow-up data

	DFS				OS		
Predictors	HR	95% CI	*P*		HR	95% CI	*P*
PVC pos vs neg*	2.94	1.09-7.94	0.034		3.36	0.93-12.1	0.064
Stage III, IV vs I, II	2.47	1.26-4.85	0.009		2.96	1.46-6.00	0.003
AC vs non-AC	1.34	0.73-2.48	0.348		1.51	0.76-3.01	0.238
Male vs female	1.42	0.66-3.03	0.367		1.09	0.41-2.90	0.865
WFS pos vs neg*	3.81	1.61-9.04	0.002		2.52	0.98-6.53	0.056
Stage III, IV vs I, II	3.71	1.86-7.41	0.000		3.97	1.94-8.15	0.000
AC vs non-AC	1.14	0.62-2.11	0.668		1.41	0.70-2.85	0.336
Male vs female	1.58	0.74-3.39	0.242		1.26	0.47-3.39	0.645
PVC and WFS pos vs others*	3.50	1.54-7.95	0.003		3.03	1.16-7.94	0.024
Stage III, IV vs I, II	3.56	1.79-7.06	0.000		3.93	1.92-8.04	0.000
AC vs non-AC	1.12	0.60-2.08	0.718		1.31	0.65-2.65	0.449
Male vs female	1.52	0.70-3.26	0.287		1.23	0.46-3.31	0.678

Note: *HR*, hazard ratio; 95% CI, 95% confidence interval; *P*, *P* – value; *pos*, positive staining; *neg*, negative staining. *AC*, adenocarcinoma; *non-AC*, including squamous cell carcinoma and large cell carcinoma; *others*, all other combinations. * HR adjusted for all the other predictors in the model (pathology, stage and sex)

In another example of the present invention, a correlation of BARD1 isoforms with initiation and progression of lung cancer was showed, wherein BARD1 expression in experimentally induced lung cancer was monitored. Multiple injections of urethane into BALB/c mice induce primary lung tumors progressing into adenocarcinomas. This treatment leads to macroscopic tumors at 16 weeks; they become larger at 24 weeks, and invade into normal adjacent tissue after 32 weeks. Normal tissues and tumor regions at all stages were selected and scored the antibody staining (Fig. 3). Consistently, expression of PVC and WFS was weak, and C20 was strong in control animals. This pattern was similar in 16 weeks tumors. However, in 24 week tumors, PVC and WFS expressions increased in comparison to C20 and were highly upregulated in 32 week tumors. These experiments demonstrate that the BARD1 expression pattern changes during different stages of tumorigenesis and suggest that BARD1 epitopes mapping to exons 3 and 4 may be involved in tumor promotion and progression towards an invasive stage.

The structure of different isoforms expressed in NSCLC was determined by RT-PCR with primers amplifying the entire BARD1 coding region from samples of 10 female and 10 male patients. RNA was extracted from tumor tissue and from normal peri-tumor tissue. Normal lung control tissue was obtained from patients with benign respiratory pathologies. BARD1 expression in normal lung was absent or very low; only weak expression of BARD1 was found in controls by RT-PCR (Fig. 4A) and by immunohistochemistry (data not shown). RT-PCR from NSCLC patients showed expression of FL BARD1 and several different isoforms thereof in most tumor and peri-tumor samples. In most cases, the specific expression pattern of FL BARD1 and isoforms were identical in normal peri-tumor and tumor tissues (Fig. 4B). To distinguish isoforms of similar molecular weight, RT-PCR was performed with primers amplifying the exons 1 and 4, or 1 and 6. It was found, in addition to FL BARD1, the expression of already know isoform β, but not α (WO 2008/119802) and additional two new isoforms κ and π (Fig. 4B, C, E, Fig. 6 and Fig. 7).

The expression of isoforms obtained by RT-PCR in female and male cases was quantified. FL and isoforms were similarly expressed in tumors and in peri-tumor tissue, in contrast to the significant upregulation of BARD1 isoforms at the protein level (Fig. 1A and Fig. 5). Expression of isoforms BARD1β and κ was significantly upregulated in males as compared to

females ($P < 0.05$), while expression of isoforms BARD1η, BARD1γ, and BARD1ε was upregulated in females as compared to males (Fig. 7).

In another example of the present invention, ERα expression was found in all lung tissues from females and males, both in normal and peri-tumor tissues (Fig. 4D), which suggests that BARD1 isoforms might be related to estrogen signalling in NSCLC.

III - Results

BARD1 expression in colorectal cancer was investigated by performing IHC on tumor sections from 148 paraffin-embeded tissue samples of colorectal cancer presented as tissue microarray with tetramerous for each of the cases (Table 2). One hundred and forty-five cases were eligible for analysis after IHC assay, and they were analyzed in this study. Four antibodies (N19, PVC, WFS and C20) against different regions of BARD1 (exon 1, exon 3, exon 4 and exon 11, respectively) were used to distinguish different BARD1 epitopes on adjacent tissue sections (Fig. 1A). BRCA1 expression was also investigated using BRCA1 C20 antibody against C-terminal epitope of BRCA1.

The positive staining for each of the four antibodies was variable in colorectal cancer (Fig. 9A). BARD1 N19, PVC, WFS and C20 staining were classified as positive in 36 (24.8%), 122 (84.1%), 129 (89%) and 61 (42.1%) cases of colorectal cancer, respectively. 142 cases were observed with at least one antibody positive staining, and no expression of BARD1 was found in only three cases (Fig. 9B). In other words, 97.9% (142 of 145) of colorectal cancer cases expressed at least one epitope of BARD1.

Although in principle 16 different combinations for expressing of the 4 epitopes are possible, only three major combinations were found (Fig. 9B). These 3 BARD1 expression patterns in colorectal cancer included: expression of only the middle epitopes was the most frequent (38.6%) (Fig. 2B, D), staining for all four antibodies was the second (18.6%) (Fig. 8B, C, E), loss of the N-terminal epitope was third (17.9%) (Fig. 8B, F) most frequently observed expression pattern.

Like BARD1 expression in NSCLC tissues, it was found that all four antibodies staining were cytoplasmic but in different regions. BARD1 N19 and C20 showed granular staining, while

PVC and WFS showed diffuse staining, and they were colocalized to the same cells or same regions, respectively (Fig. 8C-F). To investigate this further, the expression pattern obtained with each antibody was quantified and compared the results. Strong correlation was observed between expression levels of N19 and C20 ($\rho = 0.71$; $P = 0.000$). Others, comparisons such as PVC and WFS ($\rho = 0.39$; $P = 0.000$), PVC and C20 ($\rho = 0.36$; $P = 0.000$), and WFS and C20 ($\rho = 0.27$; $P = 0.001$) showed weak correlations. No correlation was found between N19 and PVC, and N19 and WFS staining (Fig. 10A).

From the different epitope expression levels, the intracellular localization, the intensity of staining with different antibodies, the correlated or uncorrelated expression of different BARD1 epitopes, and the expression patterns with four antibodies against different BARD1 epitopes, it was possible to conclude that N-terminally and C-terminally truncated forms, loss of the N-terminus forms, as well as forms which contain the four epitopes reactive with antibodies used in this study, were expressed in colorectal cancer.

IV - Non-coordinate expression of BARD1 and BRCA1

Unlike BARD1, BRCA1 staining showed both cytoplasmic and nuclear granular staining within the same cell (Fig. 8C). BRCA1 positive staining was observed in 22.1% (32 of 145) of colorectal cancer cases, while N19 positive staining was observed in 24.8% (36 of 145) cases. Interestingly, only 7 of 61 cases (11.5%) that were N19 positive were also BRCA1 positive. Moreover, no correlations were found between BRCA1 expression and distinct epitopes of BARD1 expression (Fig. 10B). These results demonstrated that BRCA1 expression was not coordinated with BARD1 in colorectal cancer.

V - Correlation of BARD1 protein expression with clinicopathological characteristics and patients prognosis

Frequency of N19 positive staining was significantly associated with female sex ($P = 0.014$) (Fig. 11A), this is consistent with the results that BARD1 N19 over expressed in female than in male in NSCLC (Fig. 2a-B). BARD1 different epitopes expression and BRCA1 expression were not correlated with any of other clinicopathologic variables, e.g. tumor grade, primary tumor, lymph node and distant metastasis status, and tumor stage (Fig. 4B-F). In addition, no significant correlation was obtained between different expression patterns and clinicopathological variables (data not shown).

The correlation of BARD1 and BRCA1 expression with survival was also assessed by comparing different BARD1 expression patterns (Fig. 9B) and expression of individual four epitopes of BARD1 and BRCA1 with survival in 75 colorectal cancer cases with follow-up data. It was found (Table 6) that patients with BARD1 N19 positive staining had higher 1-year, 2- year and 3- year survival rates, patients with C20 positive staining had higher 1- year and 3- year survival rates, as compared with their negative staining. No differences were obtained from comparison of BARD1 PVC and WFS (negative staining cases were not enough for further analysis), and BRCA1 positive and negative staining with survival.

When expression pattern was used as comparison (Table 7), it was found that the expression pattern of all four antibodies positive staining correlated with higher 1- year, 2- year and 3-year survival rates as compared with expression patterns of only the middle epitopes expression and other expression patterns in group. However, expression pattern of only the middle epitopes expression (detected with PVC and WFS) was correlated with lower 1- year, 2- year and 3- year survival rates as compared with other expression patterns in group, as well as comparison with all four antibodies positive staining pattern. No correlation was found between expression pattern of loss of the N-terminus epitope and other expression patterns, including expression pattern of all four antibodies positive staining (with the exception of 1-year survival rate), only the middle epitopes expression pattern, and all the other expression patterns in group.

Taken together it was possible to conclude that BARD1 expression pattern of all four antibodies positive staining is a positive prognostic factor, as well as expression of N-terminal epitope of BARD1; inversely, only the middle two epitopes simultaneous expression is a negative prognostic factor, but not their individual epitopes expression in colorectal cancer.

Table 6. Correlation of distinct epitopes of BARD1 and BRCA1 expression with survival in 75 colorectal cancer patients

Abs	Expression level	No.of patients	Median survival (m)	1- Year survival		2- Year survival		3- Year survival	
				%	*P-Value*	%	*P-Value*	%	*P-Value*
N19	"-" : "+"	55:20	11:26	47.3:85.0	0.0035	21.8:50.0	0.0178	12.7:40.0	0.009
PVC	"-" : "+"	14:61	14:15	57.1:57.4	0.9873	28.6:29.5	0.9446	21.4:19.7	0.8822
WFS	"-" : "+"	4:71							
C20	"-" : "+"	42:33	9:17	45.2:72.7	0.0169	21.4:39.4	0.0898	11.9:30.3	0.048
BRCA1	"-" : "+"	60:15	16:12	60.0:46.7	0.3504	31.7:20.0	0.3747	23.3:6.7	0.1489

Note: "-", negative staining; "+", positive staining.

For WFS, negative staining cases were not enough for further analysis.

Table 7. Correlation of BARD1 expression patterns with survival in 75 colorectal cancer patients

Expression pattern	No.of patients	Median survival (m)	1- Year survival		2- Year survival		3- Year survival	
			%	*P-Value*	%	*P-Value*	%	*P-Value*
++++ : -++-	17:31	27:9	88.2:41.9	0.0019	52.9:16.1	0.0073	41.2:6.5	0.0032
++++ : -+++	17:11	27:12	88.2:45.5	0.0144	52.9:18.2	0.0659	41.2:9.1	0.0664
++++ : others	17:58	27:12	88.2:48.3	0.0034	52.9:22.4	0.0151	41.2:13.8	0.0131
-++- : -+++	31:11	9:12	41.9:45.5	0.839	16.1:18.2	0.875	6.5:9.1	0.7702
-++- : others	31:44	9:16.5	41.9:68.2	0.0236	16.1:38.6	0.035	6.5:29.5	0.0138
-+++ : others	11:64	12:15.5	45.5:59.4	0.3885	18.2:31.3	0.3792	9.1:21.9	0.3274

Note: ++++, four Abs positive staining; -++-, only PVC and WFS positive staining; -+++, only N19 negative staining; others, other than the expression pattern which is compared.

VI - Structure of BARD1 isoforms expressed in colorectal cancer

BARD1 mRNA level expression was assessed by RT-PCR in 20 tumor tissues and peri-tumor tissues, including 10 male and 10 female cases. RNA was extracted from frozen tissue sections. RT-PCR was performed using forward primer in exon 1 and reverse primers in exon 11 and exon 4 to amplify the BARD1 coding regions (exon 1 to exon 11, and exon 1 to exon 4), GAPDH was amplified as control. Together, ERα was also amplified from these series of samples, as did in NSCLC (Fig. 11A).

Unlike in NSCLC, BARD1 mRNA expression pattern were quite different in tumor tissues and peri-tumor tissues of the colorectum. FL BARD1 and isoforms were frequently expressed in most of tumor samples (90%, 18 of 20 cases); but in peri-tumor tissues, no BARD1 expression was frequent (65%, 13 of 20 cases), 7 cases (35%) expressed FL BARD1 only and/or less isoforms. This was statistically significant ($P = 0.0003$). The similar results were also observed in males (8/10 vs 4/10, respectively) ($P = 0.0679$) and in females (10/10 vs 3/10, respectively) ($P = 0.0010$) (Fig. 12A). All BARD1 isoforms, which were expressed in NSCLC tissues including new isoform κ, with a deletion of exon 3, and new isoform π with a deletion of 408 bp within the 3' end of exon 4, were also expressed in colorectal cancer tissues. To accentuate, FL BARD1 and all BARD1 isoforms were frequently expressed in tumor tissues, but less or no expression in peri-tumor tissues ($P < 0.05$ for all). (Fig. 12B).

VII - Similar BARD1 expression pattern observed in tissue from males and females

BARD1 isoforms β and κ were significantly up regulated in lung tissue from males and isoforms η, γ and ε were high expressed in lung tissue from females. Unlike in lung tissue, frequency of FL BARD1 and isoforms expression were similar in colorectal tissue from males and females, including in peri-tumor tissues ($P > 0.05$ for all) (Fig. 12C) and in tumor tissues ($P > 0.05$ for all) (Fig. 12D).

No ERα expression was found in colorectal tissues in the series samples, including in peri-tumor tissues and tumor tissues, in males and females (Fig. 11B). This result could, at least partially, explain that there was no correlation of BARD1 expression with males and females in colorectal tissues, as compared BARD1 expression in lung tissues.

VIII - Correlation of BARD1 isoforms expression with clinical variables

It was found that FL BARD1 and BARD1 isoforms were more frequently expressed in patients with age more than 60 years than equal or less than 60 years. Specially, frequency of BARD1 isoforms φ, δ and π expression were significantly associated with older age patients ($P < 0.01$) (Figure 13A). Moreover, BARD1 isoform κ expression in frequency was significantly associated with large tumor size or nearby tissue invasion (T3 and T4) ($P = 0.0098$), lymph node involvement (N1 and N2) ($P = 0.0422$), and advanced stages (stage III and IV) ($P = 0.0422$) (Fig. 6B-D). No correlation was observed between BARD1 expression and tumor histopathological grade (Fig. 13E).

IX - Detection of anti-BARD1 autoimmune antibodies in blood of lung cancer patients

Method

A test was developed based on immune absorption assays using the antigens of the present invention (BARD1 peptides) for capturing autoimmune antibodies in the blood of lung cancer patients. Method used for tests performed is an adaptation of a standard ELISA antibody capturing test. Specifically the following protocol was applied:

- Microtiter plates (96 wells) are coated with BARD1 peptides [10 microgram/ ml] diluted in PBS and incubation over night at 4°C.
- Wells are blocked with Phosphat-buffered saline (PBS) substituted with blocking agent (e.g. 5% BSA) for one hour at room temperature with agitation.
- Serum of patients and controls diluted in PBS containing 1% blocking agent is added to wells and incubated for two hours is performed with agitation at room temperature.
- Wells are rinsed three times with PBS.
- Secondary anti-human antibody coupled to HRP or Sulfo-Tag or equivalent detection reactive, diluted in PBS and 1 % blocking agent, is added to wells and incubated for one hour at room temperature with agitation.
- Wells are washed with PBS three times.
- Read out is performed by adding HRP substrate or substrates for equivalent methods of detection, reactions are measured immediately.

Test

The following antigens (peptides) were tested on serum samples from lung cancer patients and on controls samples from healthy blood donors: SEQ ID NOs: 46, 33, 48, 20, 50, 19, 22, 16, 32, 26

Results

See Figure 14. Healthy controls were compared with lung cancer patients. Values measured are arbitrary values. Values are generally higher in cancer patients than in controls. Combined values for several peptides results in a clear distinction between controls and cancer cases: sensitivity 100% and specificity 95% if 11 peptides are used.

Test description

For example it is possible to use serum from patients to detect autoimmune antibodies against BARD1 isoforms. In control samples (healthy blood donors) the reaction values are significantly lower than in the cancer samples. Individual peptides can give high values for one control, but the use of a combination of peptides leads to exclusion of false positives.

CLAIMS

1. A method for detecting the presence of a BARD1 isoform specific to lung cancer and colorectal cancer in a biological sample obtained from a subject comprising the step of detecting in the sample at least one of the BARD1 isoforms specific to lung cancer and colorectal cancer selected from the group comprising

isoform π comprising SEQ ID NO: 1, or a sequence having at least 95% homology to SEQ ID NO: 1, and

isoform κ comprising SEQ ID NO: 2, or a sequence having at least 95% homology to SEQ ID NO: 2,

in which the presence of the BARD1 isoforms specific to lung cancer and colorectal cancer in a sample from the subject is an indication that the subject is afflicted with lung cancer and/or colorectal cancer, has an increased risk of lung cancer and/or colorectal cancer, and/or has a risk of recurrence after a treatment for lung cancer and/or colorectal cancer.

2. A method according to Claim 1, in which the method comprises the step of detecting in the biological sample BARD1 isoform π consisting of SEQ ID NO: 1 and BARD1 isoform κ consisting of SEQ ID NO: 2.

3. A method according to Claim 1 or 2, in which the method further comprises detecting in the biological sample at least one of the BARD1 isoforms selected from the group comprising

isoform π' comprising SEQ ID NO: 105, or a sequence having at least 95% homology to SEQ ID NO: 105,

isoform β comprising SEQ ID NO: 5, or a sequence having at least 95% homology to SEQ ID NO: 5,

isoform δ comprising SEQ ID NO: 6, or a sequence having at least 95% homology to SEQ ID NO: 6, and

isoform γ comprising SEQ ID NO: 7, or a sequence having at least 95% homology to SEQ ID NO: 7,

isoform β' comprising SEQ ID NO: 106, or a sequence having at least 95% homology to SEQ ID NO: 106,

4. A method according to Claim 3, in which the method comprises detecting in the biological sample BARD1 isoform π consisting of SEQ ID NO: 1, BARD1 isoform κ consisting of SEQ ID NO: 2 and BARD1 isoform β consisting of SEQ ID NO: 5.

5. A method according to any preceding claim, in which the biological sample is selected from the group comprising a biopsy sample, a histology sample, lung liquids, frozen tissue sample, tumor tissue sample, feces sample, cerebrospinal fluid (CSF), circulating tumour cells (CTC) and blood sample.

6. A method according to any preceding claim, in which the subject is a human.

7. A method according to any preceding claim, in which the presence of the BARD1 isoforms is detected by using antibodies specific to the BARD1 isoforms.

8. A method according to Claim 7, in which the antibodies are a combination of antibodies or fragments thereof that specifically bind to different epitopes of at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106.

9. A method according to any of Claims 1 to 6, in which the presence of the BARD1 isoforms is detected by detecting the level of mRNA that encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106.

10. A method according to any of Claims 1 to 6, in which presence of the BARD1 isoforms is detected by detecting the presence of autoimmune antibodies specific to the BARD1 isoforms in the blood sample obtained from the subject, and in which at least four antigens selected from the group comprising SEQ ID NOs: 13 – 80 are used for detecting the autoimmune antibodies specific to the BARD1 isoforms.

11. A method according to any of Claims 1 to 6, in which the presence of the BARD1 isoforms is detected by

detecting the level of mRNA that encodes at least one of the BARD1 isoforms comprising amino acid sequences selected from the group comprising SEQ ID NOs: 1-7, 105-106, or sequences having at least 95% homology to SEQ ID NOs: 1-7, 105-106, and

detecting the presence of autoimmune antibodies specific to the BARD1 isoforms in the blood sample obtained from the subject, and in which at least four antigens selected from the group comprising SEQ ID NOs: 13 – 80 are used for detecting the autoimmune antibodies specific to the BARD1 isoforms.

12. A method for discriminating lung cancer and colorectal cancer from gynecological cancers, the method comprising the step of detecting in a biological sample obtained from a subject at least one of the BARD1 isoforms specific to lung cancer and colorectal cancer selected from the group comprising

isoform π comprising SEQ ID NO: 1, or a sequence having at least 95% homology to SEQ ID NO: 1, and

isoform κ comprising SEQ ID NO: 2, or a sequence having at least 95% homology to SEQ ID NO: 2.

in which the presence of the BARD1 isoforms specific to lung cancer and colorectal cancer is an indication for lung cancer and/or colorectal cancer, and not gynecological cancers.