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DESCRIPTION

TECHNICAL FIELD

[0001] The present invention relates to a highly sensitive, specific and reproducible real time RT-qPCR assay for the quantification of *PD-L1* expression in a RNA sample, such as an isolated RNA sample from Circulating Tumor Cells (CTCs) in peripheral blood of patients with solid cancers.

BACKGROUND OF THE INVENTION

[0002] The discovery of crucial molecular pathways that promote tumor growth and maintenance together with the development of drugs that specifically inhibit these pathways has changed much in the perennially limited panoply of options to treat many types of cancer. The promise of the emerging field of personalized medicine will increasingly be used to tailor therapeutics to defined sub-populations, and eventually, individual patients in order to enhance efficacy and minimize adverse side effects. However, the success of personalized medicine depends on having accurate, reproducible and clinically useful companion diagnostic tests to identify patients who can benefit from targeted therapies. According to this concept, the most recent paradigm is the successful co-development of a first-in-class selective inhibitor of oncogenic *BRAF* kinase, vemurafenib (ZELBORAF), which targets only the mutant BRAF protein, which is detected V600E positive by the approved companion diagnostic test, the Cobas 4800 BRAF V600 mutation test (Roche Molecular Diagnostics).

[0003] Despite the recent development of targeted therapies in many types of cancer, many patients do not benefit from these therapies. This fact led to an improved understanding of the mechanisms of protective anti-tumor immunity and the development of more efficacious immunotherapies that increase patient survival confirming the long-standing idea that immunity plays an important role in cancer pathogenesis. Immunotherapy is a type of cancer treatment designed to boost the body's natural defenses to fight cancer. It uses materials either made by the body or in a laboratory to improve, target, or restore the function of the immune system. It is now evident through intense research efforts that cancer cells can develop specific mechanisms to avoid immunosurveillance. One of these mechanisms is to present itself to the immune system in such a way that it fails to recognize it as something that should be killed. Another mechanism is to interfere with the abilities of T-cells, whose duty it is to carry out such killings and which, by hanging around for decades in the body, provide durable immunity to a given disease. Lastly, there are all sorts of ways in which the immune system as a whole can be suppressed.

[0004] Human cancers are characterized by high frequencies of genetic and epigenetic alterations, generating neo-antigens potentially recognizable by the immune system. The

ability of the immune system to recognise its normal cells from tumor cells and to attack against foreign invaders such as viruses provides the basis for the rapid and specific clearance of most infections. The immune system is able to detect and eliminate most tumors, which are at an early stage and clinically non-detectable by the concept of cancer immuno-editing. However, the cancer cells use a "cellular camouflage" in order to fool the immune system into thinking that they are normal cells; as a result some tumors are not completely destroyed and escape from the immune-surveillance. A basic hindrance for immunotherapeutic approaches is that the majority of mechanisms are active at the tumor site, which act together in order to balance effectively the anti-tumor immunity.

[0005] Despite the fact that an endogenous immune response to cancer has been observed in patients, this response seems to be ineffective, and the established cancers are tolerated by the immune system. Contributing to this state of tolerance, tumors may exploit several distinct mechanisms to actively suppress the host immune response. Among these mechanisms, endogenous "immune checkpoints" that normally terminate immune responses to mitigate collateral tissue damage can be co-opted by tumors to evade immune destruction. Recently, many specific immune checkpoint pathway inhibitors have been developed and approved by FDA to provide new immunotherapeutic approaches for treating cancer, including the development of the anti-CTLA-4 antibody (Ab), ipilimumab (Yervoy), for the treatment of patients with advanced melanoma and anti-PD-L1 antibody, nivolumab (Opdivo), for the treatment of patients with advanced squamous non-small cell lung cancer (NSCLC) who have progressed on or after platinum-based chemotherapy.

[0006] Programmed death 1 (*PD-1*) is an immune inhibitory receptor expressed on several immune cells, particularly cytotoxic T cells. This receptor interacts with two ligands, programmed death ligand 1 (*PD-L1*) (B7-H1, CD274) and *PD-L2* (B7-DC). The *PD-1* has greater affinity for *PD-L1*, which is widely expressed on tumor cells, as well as other immune cells, while *PD-L2* is expressed primarily on macrophages and dendritic cells [Keir M, Butte M, Freeman G, Sharpe A. PD-1 and its ligands in tolerance and immunity. *Annu Rev Immunol* 2008;26: 677-704]. When *PD-1* binds to tumor cells expressing *PD-L1*, T-cell activity and cytokine production are suppressed, leading to T-cell exhaustion. *PD-L1* ligation with *PD-1* during infection or inflammation in normal tissues is critically important in maintaining homeostasis of immune response to prevent autoimmunity. The PD-1/PD-L1 interaction in the tumor microenvironment, however, provides an immune escape for tumor cells by turning off cytotoxic T cells. Thus by blocking this interaction, it is expected that tumor cells will be attacked by cytotoxic T cells. The activation of the PD-1/PD-L1 pathway protects tumor cells from immunological responses mediated by T-cells. Inhibition of the PD-1/PD-L1 pathway reverses immune evasion by replenishing a plethora of activated non-exhausted T- cells. The development and clinical testing of immune blocking antibodies has resulted in until now clinical activity in a variety of malignancies including melanoma and lung cancer [Callahan MK, Wolchok JD. At the bedside: CTLA-4 and PD-1-blocking antibodies in cancer immunotherapy. *J Leukoc Biol.* 2013;94: 41-53].

[0007] Most recently, Larkin et al., presented a randomized, double-blind, phase 3 study, in

which the nivolumab (anti-PD-1 antibody) as monotherapy or the combination nivolumab plus ipilimumab (anti-CTLA-4 antibody) were compared to ipilimumab alone in patients with metastatic melanoma. The median progression-free survival was longer with nivolumab plus ipilimumab, as compared with ipilimumab or nivolumab as monotherapy. However, in patients with *PD-L1*-positive tumors, the median progression-free survival (PFS) was 14.0 months in the nivolumab-plus-ipilimumab group and in the nivolumab group, but in patients with *PD-L1*-negative tumors, PFS was longer with the combination therapy than with nivolumab alone. From these results it has become clear that the expression of *PD-L1* seems to be a significant predictive biomarker in anti-PD-L1 treatments. Thus the need for developing a new companion diagnostic test for detecting *PD-L1* positive or negative tumors, is increasing [Larkin J, Chiarion-Sileni V, Gonzalez R, Grob JJ, Cowey CL, Lao CD, et al. Combined Nivolumab and Ipilimumab or Monotherapy in Untreated Melanoma. *N Engl J Med*. 2015;373: 23-34].

[0008] US2007/0231264 A1 provides compositions, methods and kits related to proteins which function in controlling biology and physiology of mammalian cells, including cells of a mammalian immune system. WO2014/151006 A2 discloses biomarkers for patient selection and prognosis in cancer, as well as methods of using PD-L1/PD-1 pathway antagonists. Geng H et al., *International Journal of Cancer*, vol. 118, no. 11, 1 June 2006, pages 2657-2664 describes the involvement of B7-H1 in tumor evasion in the process of immunotherapy with HSP70 vaccine, suggesting a promising strategy of cancer treatment. Wu Y et al., *Biochemical and Biophysical Research Communications*, vol. 392, no. 4, 19 February 2010, pages 510-515 reveals that Dlk (human DAPk like kinase) overexpression could sensitize cells to apoptosis while overexpression of the kinase inactive mutant was able to rescue apoptotic cell death, supporting that the reconstitution of Dlk expression might bring a potential therapeutic approach to cervical carcinoma.

[0009] Recently, the "liquid biopsy" approach has a high potential to change significantly the therapeutic strategy in patients suffering from many types of cancer. The detection, enumeration and the molecular characterization of Circulating Tumor Cells (CTCs), cell-free circulating tumor DNA (ctDNA) and circulating microRNAs (miRNAs) provide an extremely powerful and reliable non-invasive source of blood-based biomarkers for the individual molecular profiling of each patient in real time, and especially before and after treatment. The applications of liquid biopsy are based on the identification of molecular targets, the assessment of prognosis, the diagnosis of recurrence/progression, the monitoring of response to therapy and monitoring of tumor genomic profiles in real time. Most importantly, these blood-based tests seem to be very challenging and highly important in case that tumor biopsies are not accessible (such as in the case of NSCLC). Moreover they can offer a close follow-up of disease biomarkers enabling the monitoring of the efficacy of treatment and potentially improve the choice of treatment options.

[0010] Recently, Mazel et al., using the CellSearch™ system (Veridex, J&J), an FDA-cleared platform for CTCs enumeration, by using an anti-PD-L1 specific antibody and the fourth channel for imaging in the CellSearch, found *PD-L1* positive CTCs in 11 out of 16 (68.8%) patients with metastatic breast cancer. More specifically, in their study, they have used the anti-human B7-

H1/PD-L1PE-conjugated monoclonal antibody for *PD-L1* expression, suggesting that this assay could be used for liquid biopsy for monitoring and stratification of cancer patients undergoing immune checkpoint blockade [Mazel M, Jacot W, Klaus P, Bartkowiak K, Topart D, Cayrefourcq L et al. Frequent expression of PD-L1 on circulating breast cancer cells. Mol Oncol. 2015, Article in press]. Moreover, Oliveira-Costa et al., found a strong cytoplasmatic expression of *PD-L1* in CTCs in oral squamous cell carcinoma using immunofluorescence and Nanostring [Oliveira-Costa JP, Fiorini de Carvalho A, Gobbi da Silveira G, Amaya P, Wu Y et al., Gene expression patterns through oral squamous cell carcinoma development: PD-L1 expression in primary tumor and circulating tumor cells. Oncotarget. 2015;6: 20902-20].

[0011] The detection of *PD-L1* expression in CTCs in a quantitative way could be used for monitoring the efficacy of immune checkpoint inhibitors as a "liquid biopsy" approach and could offer many advances in clinical practice. Thus, for this reason, an ultrasensitive and highly specific RT-qPCR based method for the quantification of *PD-L1* expression in CTCs was developed and validated, suitable for monitoring the efficacy of checkpoint inhibitors in peripheral blood of cancer patients. This assay has a very high analytical sensitivity and specificity in order to quantify the expression of *PD-L1* in CTCs, and is highly sensitive in comparison to other methods used in tumor tissues such as immunohistochemistry. Moreover, the developed method is a closed tube molecular diagnostic test that comprises a simple and high throughput clinical tool, which can easily be automated and used in most molecular diagnostic clinical laboratories since it does not require expensive instrumentation, and is easy to use. Moreover, the developed method is quantitative, thus enabling not only to recognize differences in the expression of *PD-L1* in clinical samples, but moreover to be subjected to daily quality control performance tests (robustness, reproducibility, within-run and between-run precision) that are very important for accreditation purposes.

[0012] For the first time a novel RT-qPCR based method with novel specifically designed primers and a hydrolysis probe for the quantification of *PD-L1* mRNA transcripts in a human clinical sample and especially in peripheral blood (CTCs) was designed. Especially for CTCs molecular characterization, highly sensitive, robust and specific methodologies are needed. Here it is provided evidence that this assay is suitable for selecting patients for immunotherapy based on the administration of checkpoint inhibitors, as well as for monitoring the efficacy of checkpoint inhibitors in peripheral blood of cancer patients.

SUMMARY OF THE INVENTION

[0013] It is an object to provide an improved method for quantifying *PD-L1* mRNA expression in a RNA sample such as an isolated RNA sample of CTCs in peripheral blood of patients with solid tumors. The object is wholly or partially achieved by a method according to claim 1. Embodiments and further details of the invention are set forth in the appended dependent claims, in the drawings and in the sequence listing. In particular the invention relates to an *in vitro* method for quantitative determination of the expression of Programmed Death Ligand 1 (*PD-L1*) in a liquid biopsy sample of Circulating Tumor Cells (CTC), said method comprising

the steps:

1. i. subjecting the sample to reverse transcription using RNA present in the sample as a template in order to synthesize a corresponding cDNA sequence,
2. ii. forming a reaction mixture comprising the sample, nucleic acid amplification reagents, a target primer pair, a target hydrolysis probe, said target primer pair and target hydrolysis probe being capable of hybridizing to *PD-L1* mRNA, and said target primer pair consisting of a forward target primer comprising the sequence 5'-GCTGAATTGGTCATCCCAGAA-3' (SEQ ID NO: 4) and a reverse target primer comprising the sequence 5'-TTTCACATCCATCATTCTCCCTT-3' (SEQ ID NO: 6)
3. iii. subjecting the reaction mixture to amplification conditions optimized to generate at least one copy of a nucleic acid sequence complementary to a target sequence, said target sequence being a mRNA transcript of the *PD-L1* mRNA sequence (SEQ ID NO: 1), and
4. iv. determining the amount of *PD-L1* mRNA in a said sample,
5. v. normalizing the expression of *PD-L1* with respect to an expression of a reference gene, whose expression levels remain constant between different cell types and
6. vi. comparing the amount of *PD-L1* mRNA expressed in a said sample to a positive control which is a sample comprising *PD-L1* mRNA and a negative control which is a sample without comprising *PD-L1* mRNA in order to estimate an overexpression of the *PD-L1* mRNA sequence.

[0014] The method is based on the quantitative determination of *PD-L1* mRNA expression in a sample. This assay may comprise a downstream analysis of *PD-L1* mRNA expression in a RNA sample, such as an isolated RNA sample of CTCs in peripheral blood of patients with solid cancers.

[0015] The CTCs isolation step could be performed by methods known to the skilled person, such as e.g. different microfluidic and filtration by size devices, density gradient centrifugation, positive and negative immunomagnetic selection, the CellSearchTM device, single cell analysis systems, or in-vivo CTC isolation systems such as the cell collector system (Gilupi, GmbH) or leukapheresis systems. It should be noted that CTC isolation is not limited to the listed methods.

[0016] In particular the target sequence in the method described herein is the mRNA-transcript of the *PD-L1* gene, which is derived after reverse transcription of the RNA present in the sample by using a commercially available cDNA kit.

[0017] The quantification of *PD-L1* mRNA expression may be used in many types of cancer such as breast, urothelial, colorectal, oesophageal, gastric, hepatocellular carcinoma, lung, melanoma, oropharyngeal squamous cell carcinoma, nasopharyngeal, multiple myeloma, renal cell carcinoma, cervical, glioblastoma, malignant mesotheliomas, lymphomas, ovarian and pancreatic. Advantageously, the quantification of *PD-L1* mRNA expression may be used in any

type of malignant neoplastic disease in order to quantify an expression of *PD-L1* mRNA.

[0018] The method according to the invention amplifies specifically only the *PD-L1* mRNA sequence, avoiding the amplification of genomic DNA. The method comprises a RT-qPCR, using a target primer pair, which comprises at least one intron-spanning site and a target hydrolysis probe. Advantageously the intron-spanning site may comprise only one base at either site of the intron resulting in that the target primers only bind to a sequence without introns under the conditions employed. The method utilizes a target primer pair that will only bind to a sequence in which the introns have been spliced-out, e.g. mRNA, cDNA. Moreover, the target hydrolysis probe is part of the amplification reaction mixture and hybridizes to the newly synthesized target sequence under select conditions, provided that this target sequence is present in the test sample.

[0019] According to the invention the main feature of the target primer pair is that it comprises at least one intron-spanning site. This provides a target primer pair that will only bind to a sequence in which the introns have been spliced out, e.g. mRNA, cDNA. It should be understood that said "splicing" may occur naturally i.e. to provide for the detection of mRNA in a biological sample. However, the term also encompasses an engineered sequence having the introns "spliced out" of the sequence, e.g. cDNA. The intron-spanning site may comprise only one base at either site of the intron provided that the target primer only binds the sequence without introns under the conditions employed. One or both of the forward and reverse target primers may comprise one or more intron-spanning site(s). In a preferred embodiment both target primers comprise an intron-spanning site.

[0020] In particular, the forward target primer is the primer that is extended in the same direction as the coding strand of the target nucleic acid. The forward target primer is designed to hybridize between exons 4 and 5 of the *PD-L1* mRNA sequence in order to enhance only the mRNA target sequence avoiding DNA genomic amplification. The forward target primer is complementary to the 3'-end. Conversely, the reverse target primer is the primer that is extended in the same direction as the non-coding strand of the target nucleic acid. The reverse target primer is designed to hybridize between exons 5 and 6 of the *PD-L1* mRNA sequence for amplification of only the target sequence avoiding non-specific products. Consequently, the target primers align with their 3'-ends facing each other.

[0021] More particularly, the "target primer pair", which is used in the method, is capable of hybridizing to a sequence of *PD-L1* mRNA.

[0022] In particular the target sequence is the mRNA-transcript of the *PD-L1* mRNA sequence (SEQ ID NO: 1). It should be noted that the DNA sequence for *PD-L1* (SEQ ID NO: 1) listed in the enclosed sequence listings correspond to the transcribed mRNA sequence of said protein. The forward target primer includes the sequence 5'-GCTGAATTGGTCATCCCAGAA-3' (SEQ ID NO: 4). The reverse target primer includes the sequence 5'-TTTCACATCCATCATTCTCCCTT-3' (SEQ ID NO: 6). The invention furthermore discloses sequences of specific probes, such as target hybridization probes, hydrolysis (TaqMan) probes

or molecular Beacon, or SCORPION type probes, for detection/quantification of the amplification PCR product. Furthermore, the probe may be used to ensure specificity. Said probe is a target hydrolysis probe. Preferably the target hydrolysis probe should include at least the sequence 5'-GCACATCCTCCA-3' (SEQ ID NO: 7), more preferably the target hydrolysis probe includes the sequence 5'-6FAM-ACCTCTGGCACATCCTCCAAATGAAAG-BBQ-3' (SEQ ID NO: 8) and two fluorescent particles. The probes are preferably labelled. The label can be either directly detectable with for example fluorophores, chemiluminophores, fluorescent particles and the like or indirectly detectable with specific binding partners and nucleic acids. Preferred labels are directly detectable, and particular preferred labels are fluorescent dyes, such as SYBR Green I, FAM, HEX, VIC, fluorescein LC Red 610, LC Red640, LC Red670, LC Red 705, and other fluorescent dyes known in the art.

[0023] In particular, the target hydrolysis probe is designed to hybridize to an internal region within the amplicon. Especially, the target hydrolysis probe which is used in this method is designed to hybridize to an internal region of exon 5 of the *PD-L1* mRNA sequence. It is typically a 20-30 bp oligonucleotide with a fluorescent reporter dye (i.e. 6-fluorescein, FAM) covalently attached to the 5' end and a fluorescent quencher dye (i.e. BlackBerry Quencher, BBQ). The proximally located quencher dye reduces the emission intensity of the reporter dye. The hydrolysis probe is added directly to the PCR mix, and conditions are virtually identical to those that are established for a standard PCR. During the extension phase of the PCR cycle, the Taq DNA polymerase cleaves the hydrolysis probe only when it is hybridized to the target, separating the reporter dye from the quencher dye. An increase in fluorescence intensity at 518 nm (when FAM is the reporter dye) (due to the release of the quenching effect on the reporter) is the result of hydrolysis probe hydrolysis and is quantitative for the initial amount of the template. The fluorescence intensity specific to the reporter dye increases because of its lack of proximity to the quencher dye. Repeated cycles of denaturation, annealing, and extension result in exponential amplification of the PCR product and of fluorescence intensity.

[0024] In another aspect, step (v) of the method may further comprise a reference primer pair that hybridizes to a reference mRNA sequence of a reference gene in order to ensure that amplifiable material is present in the test samples and in order to avoid false negative results.

[0025] A reference gene ideally should be stable, expressed in the cells and tissues of interest that do not show changes under the experimental conditions or disease state. These genes are used to normalize the mRNA levels of genes of interest before the comparison between different samples by the RT-qPCR. These reference genes are responsible for measuring and reducing the errors from variations among the samples, extraction and RNA quality and efficiency in cDNA synthesis, internal controls and the different experimental samples like in normal cells or tumor tissue. In the RT-qPCR method, an appropriate reference gene should be considered for accurate quantification of mRNA expression because the quantification cycle (C_Q) of the target genes is compared to the C_Q of the reference gene. The expression levels of the reference gene should remain constant between different cells types; otherwise the normalization to varying internal reference can result to increased errors. Several genes have been used as reference genes, including hypoxanthine phosphoribosyl transferase (*HPRT*),

β 2-microglobulin (*B2M*), glyceraldehyde 3-phosphate dehydrogenase (*GAPDH*) and β -actin (*ACTB*), 18S ribosomal RNA (*18S rRNA*), 28S ribosomal RNA (*28S rRNA*), α -tubulin (*TUBA*), albumin (*ALB*), ribosomal protein L32 (*RPL32*), TATA sequence binding protein (*TBP*), cyclophilin C (*CYCC*), Elongation factor 1 α (*EF1A*), RNA polymerase II (*RPII*) [Suzuki T, Higgins PJ, Crawford DR. Control selection for RNA quantitation. *Biotechniques*, 2000; 29:332-7].

[0026] In a preferred embodiment, *B2M* used as a reference gene in this invention, and advantageously said reference primer pair was designed to hybridize to the *B2M* (Beta-2-Microglobulin) mRNA sequence (SEQ ID NO: 2).

[0027] Therefore, in another aspect of the invention provides a reference primer pair of the *B2M* mRNA sequence (SEQ ID NO: 2). It should be noted that the DNA sequence *B2M* (SEQ ID NO: 2) listed in the enclosed sequence listings correspond to the transcribed mRNA sequence of said protein. In a preferred embodiment the forward reference primer should include at least the sequence 5'-GCCGTGTGAAC-3' (SEQ ID NO: 9), more preferably the forward reference primer includes sequence 5'-GCCTGCCGTGTGAACCATGT-3' (SEQ ID NO: 10). In a preferred embodiment the reverse reference primer should include at least the sequence 5'-CTTCAAACCTC-3' (SEQ ID NO: 11), more preferably the reverse reference primer includes the sequence 5'-AAATGCGGCATCTTCAAACCTC-3' (SEQ ID NO: 12).

[0028] In the context of the present invention "reference primer pair" and "target primer pair" are not the same. In the context of the present invention the term "reference primer pair" is intended to mean a primer pair, which is capable of hybridizing to a sequence of a gene, which is ubiquitous to a given cell. More particularly, the "reference primer pair", which is used in the method, is capable of hybridizing to a sequence of *B2M* mRNA sequence. In other words a "reference primer pair" can be used as an internal control in a method or kit of the invention.

[0029] In Real-time RT-qPCR a hybridization probe for the quantification of *B2M* expression may be used as described previously in relation to the *PD-L1* primer pair. In a preferred embodiment the reference hydrolysis probe should include at least the sequence 5'-CTCGATCCCAC-3' (SEQ ID NO: 13), more preferably the target hydrolysis probe includes the sequence 5'-6FAM-CATGATGCTGCTTACATGTCTCGATCCCAC-BBQ-3' (SEQ ID NO: 14) and two fluorescent particles.

[0030] In further aspect the present document also relates to a method for:

1. i. diagnosing and/or prognosing malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, and/or
2. ii. predicting efficacy of treatment of malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, and/or
3. iii. assessing outcome of treatment of malignant neoplastic disease in a subject during and after immunotherapy with checkpoint inhibitors, and/or
4. iv. assessing the recurrence of malignant neoplastic disease in a subject during and after

immunotherapy with checkpoint inhibitors,

wherein said method comprises the quantification of the *PD-L1* mRNA in a sample according to the steps for the *in vitro* method as described herein,

wherein the subject is a human being, who suffers from a malignant neoplastic disease,

wherein the checkpoint inhibitors may comprise the immune checkpoint blockade inhibitors, such as anti-PD-L1 inhibitors.

[0031] The *in vitro* method as described herein may advantageously be used for determining the amount of the *PD-L1* mRNA in a sample for:

1. i. diagnosing and/or prognosing malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, and/or
2. ii. predicting efficacy of treatment of malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, and/or
3. iii. assessing outcome of treatment of malignant neoplastic disease in a subject during and after immunotherapy with checkpoint inhibitors, and/or
4. iv. assessing the recurrence of malignant neoplastic disease in a subject during and after immunotherapy with checkpoint inhibitors,

wherein the sample analyzed may be a biological sample, and said biological sample may be obtained from a subject. Advantageously, the subject is a mammal such as a human being, who suffers from a malignant neoplastic disease.

[0032] The malignant neoplastic disease may be selected from the group consisting of breast, urothelial, colorectal, oesophageal, gastric, hepatocellular carcinoma, lung, nasopharyngeal, multiple myeloma, renal cell carcinoma, lymphomas, melanoma, oropharyngeal squamous cell carcinoma, cervical, glioblastoma, malignant mesotheliomas, ovarian and pancreatic cancer.

[0033] The *in vitro* method as described herein is advantageously used when the subject suffers from breast and non-small cell lung cancer.

[0034] When diagnosing and/or prognosing malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, the method comprises the steps of:

1. a) performing the *in vitro* method for quantification of the *PD-L1* mRNA in a sample as described herein,
2. b) determining the amount of *PD-L1* mRNA in a said sample,
3. c) normalizing the expression of *PD-L1* with respect to *B2M* expression, used as a reference gene,
4. d) comparing the amount of *PD-L1* mRNA detected in a said sample to a positive control and a negative control in order to estimate the over-expression of *PD-L1*, thereby deriving prognostic information.

[0035] The sample is advantageously obtained from a subject who is suffering from a malignant neoplastic disease and who has not been prescribed immunotherapy with checkpoint inhibitors. Further embodiments are wherein the positive control comprises peripheral blood mononuclear cells (PBMC) from healthy control samples since PBMC express as well *PD-L1* at very low levels.

[0036] Thus, an indication of prognostic information is a relative change in the amount of *PD-L1* mRNA in a said sample that identifies before immunotherapy with checkpoint inhibitors and may estimate the risk of future outcomes in an individual based on their clinical and non-clinical characteristics. In particular, a method of determining the prognosis as used herein refers to the prediction of the outcome of, or future course of, a subject. Prognosis includes the prediction of patient's survival. Moreover, prognosis may be used to predict the disease free survival time of an individual, progression-free survival time, disease specific survival time, survival rate, or survival time. Prognostic testing may be undertaken with (e.g. at the same time as) the diagnosis of a previously undiagnosed cancerous condition, or may relate to an existing (previously diagnosed) condition.

[0037] When predicting efficacy of treatment of malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, the method comprises the steps of:

1. a) performing the *in vitro* method for quantification of the *PD-L1* mRNA in a sample as described herein,
2. b) determining the amount of *PD-L1* mRNA in a said sample,
3. c) normalizing the expression of *PD-L1* with respect to *B2M* expression, used as a reference gene,
4. d) comparing the amount of *PD-L1* mRNA detected in a said sample to a positive and a negative control in order to estimate the overexpression of *PD-L1*, thereby predicting efficacy of treatment of malignant neoplastic disease in a subject.

[0038] The sample is advantageously obtained from a subject who is suffering from a malignant neoplastic disease and who has not been administered checkpoint inhibitors as immunotherapy. Thus, the prediction is associated with the amount of overexpression of *PD-L1* mRNA in a said sample that is identified before receiving immunotherapy with checkpoint inhibitors, such as anti-PD-L1 inhibitors and may indicate if the subject is likely to respond favourably to a treatment regimen, and can hence be used clinically to make treatment decisions by choosing the most appropriate treatment modality for any particular subject.

[0039] When assessing outcome of treatment of malignant neoplastic disease in a subject during and after immunotherapy with checkpoint inhibitors, the method comprises the steps of:

1. a) performing the *in vitro* method for the quantification of the *PD-L1* mRNA in a sample as described herein,
2. b) determining the amount of *PD-L1* mRNA in said sample,

3. c) normalizing the expression of *PD-L1* with respect to *B2M* expression, used as a reference gene,
4. d) comparing the amount of *PD-L1* mRNA detected in said sample to a positive control in order to estimate the overexpression of *PD-L1*,
5. e) repeating steps a) to d) at one or more time points during and after immunotherapy with checkpoint inhibitors of said subject, and wherein a change in relative amount of *PD-L1* mRNA in a said samples over time indicates the efficacy of treatment.

[0040] The sample is advantageously obtained from a subject who is suffering from a malignant neoplastic disease before and after said subject is being administered checkpoint inhibitors as immunotherapy. Thus, an indication of effective treatment is a relative change in decreasing amount of *PD-L1* mRNA in a said sample relative a previous sample analyzed in the steps of repeating the method.

[0041] When assessing recurrence of malignant neoplastic disease in a subject during and after immunotherapy with checkpoint inhibitors, the method comprises the steps of:

1. a) performing the *in vitro* method for the quantification of the *PD-L1* mRNA in a sample as described herein,
2. b) determining the amount of *PD-L1* mRNA in a said sample,
3. c) normalizing the expression of *PD-L1* with respect to *B2M* expression, used as a reference gene,
4. d) comparing the amount of *PD-L1* mRNA detected in a said sample to a positive and negative control in order to estimate the overexpression of *PD-L1*,
5. e) repeating steps a) to d) at one or more time points during and after immunotherapy with checkpoint inhibitors of said subject, and wherein a change in relative amount of *PD-L1* mRNA in a said samples over time indicates the risk of recurrence.

[0042] Thus, an indication of recurrence is a relative change in increasing amount of *PD-L1* mRNA in said samples that identify malignant neoplastic disease during immunotherapy with anti-PD-L1 inhibitors, i.e. an over-time increase in the amount of *PD-L1* mRNA in a sample relative a previous sample analyzed in the steps of repeating the method.

[0043] The invention also relates to a kit for determining the amount of *PD-L1* mRNA in a sample, the kit for the quantification of *PD-L1* in a sample may also be used for:

1. i. determining the expression of *PD-L1 mRNA* in a sample, and/or
2. ii. diagnosing and/or prognosing malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, and/or
3. iii. predicting efficacy of treatment of malignant neoplastic disease in a subject before immunotherapy with checkpoint inhibitors, and/or

4. iv. assessing outcome of treatment of malignant neoplastic disease in a subject during and after immunotherapy with checkpoint inhibitors, and/or
5. v. assessing the recurrence of malignant neoplastic disease in a subject during and after immunotherapy with checkpoint inhibitors.

[0044] The kit comprises

1. a) nucleic acid amplification reagents,
2. b) a target primer pair being capable of hybridizing to *PD-L1* mRNA and consisting of a forward target primer comprising the sequence 5'-GCTGAATTGGTCATCCCAGAA-3' (SEQ ID NO: 4) and a reverse target primer comprising the sequence 5'-TTTCACATCCATCATTCTCCCTT-3' (SEQ ID NO: 6),
3. c) a reference primer pair being capable of hybridizing to mRNA of a reference gene,
4. d) a target hydrolysis probe being capable of hybridizing to *PD-L1* mRNA
5. e) a reference hydrolysis probe being capable of hybridizing to mRNA of the reference gene,
6. f) optionally instructions for performing the *in vitro* method of the present invention.

[0045] The kit may comprise

- a forward target primer for determining the quantity of *PD-L1* in a sample, said forward target primer comprising the sequence 5'-GCTGAATTGGTCATCCCAGAA-3' (SEQ ID NO: 4), and
- a reverse target primer for determining the quantification of *PD-L1* in a sample, said reverse target primer comprising the sequence 5'-TTTCACATCCATCATTCTCCCTT -3' (SEQ ID NO: 6), and
- a hydrolysis target probe for determining the quantity of *PD-L1* in a sample, said hydrolysis target probe comprising or consisting of at least the sequence 5'-6FAM-GCACATCCTCCA-BBQ-3' (SEQ ID NO: 7), more preferably the target hydrolysis probe includes the sequence 5'-6FAM-ACCTCTGGCACATCCTCCAAATGAAAG-BBQ-3' (SEQ ID NO: 8) and two fluorescent particles (FAM, BBQ), and
- a forward reference primer for normalization the data for the quantification of *PD-L1* in respect to the expression of *B2M* as a reference gene, said forward reference primer comprising or consisting of at least the sequence 5'-GCCGTGTGAAC-3' (SEQ ID NO: 9), more preferably the forward reference primer includes the sequence 5'-GCCTGCCGTGTGAACCATGT-3' (SEQ ID NO: 10), and
- a reverse reference primer for normalization the data for the quantification of *PD-L1* in respect to the expression of *B2M* as a reference gene, said reverse reference primer comprising or consisting of at least the sequence 5'-CTTCAAACCTC-3' (SEQ ID NO: 11), more preferably the reverse reference primer includes the sequence 5'-AAATGCGGCATCTTCAAACCTC-3' (SEQ ID NO: 12), and

- a reference hydrolysis probe for normalization the data for the quantification of *PD-L1* in respect to the expression of *B2M* as a reference gene, said reference hydrolysis probe comprising or consisting of at least the sequence 5'-6FAM-CTCGATCCCAC-BBQ-3' (SEQ ID NO: 13), more preferably the target hydrolysis probe includes the sequence 5'-6FAM-CATGATGCTGCTTACATGTCTCGATCCCAC-BBQ-3' (SEQ ID NO: 14) and two fluorescent particles (FAM, BBQ).

BRIEF DESCRIPTION OF FIGURES

[0046]

Fig. 1: illustrates the procedure for the isolation of CTCs from peripheral blood and downstream RT-qPCR for *PD-L1* and *B2M*.

Fig. 2: depicts the hybridization sites for primers and hydrolysis probe for the amplification of *PD-L1* mRNA sequence. The primers -forward, reverse- and hydrolysis probe were depicted in bold and the exon-exon junction was depicted with a forward slash.

Fig. 3: depicts the hybridization sites for primers and hydrolysis probe for the amplification of *B2M* mRNA sequence. The primers -forward, reverse- and hydrolysis probe were depicted in bold and the exon-exon junction was depicted with a forward slash.

Fig. 4: RT-qPCR assay for *PD-L1*: experimental flowchart for *PD-L1* mRNA expression in clinical samples.

Fig. 5: presents the RT-qPCR calibration curves for *PD-L1* and *B2M* (copies/ μ L, all measured in triplicate).

Fig. 6: shows the quantitative expression of *PD-L1* in fresh frozen NSCLC primary tumors ($2^{-\Delta\Delta Cq}$ values).

Fig. 7: shows the ΔCq values between primary tissues of NSCLC and their adjacent normals.

Fig. 8: shows the quantitative expression of *PD-L1* in CTCs ($2^{-\Delta\Delta Cq}$ values).

Fig. 9: shows the ΔCq values between control group and CTCs isolated from breast cancer metastatic samples.

DEFINITIONS

[0047] The terms used in this invention are, in general, expected to adhere to standard definitions generally accepted by those having ordinary skill in the art of molecular biology. A few exceptions, as listed below, have been further defined within the scope of the present invention.

[0048] "At least one" as used herein means one or more, i.e. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 etc.

[0049] As used herein "target sequence" means a sequence that is detected, amplified, both amplified and detected or is complementary to the sequences provided herein or otherwise has at least one intron in its native state i.e. as genomic DNA or extra chromosomal DNA. While the term target sequence is sometimes referred to as single stranded, those skilled in the art will recognize that the target sequence may be double stranded. In particular, according to this text the "target sequence" is referred to the part of the *PD-L1* sequence, which is amplified, when a primer pair binds to the desired sequence.

[0050] As used herein, the term "primer" refers to an oligonucleotide which, produced synthetically, is capable of acting as a point of initiation of nucleic acid synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, i.e., in the presence of nucleotides and an agent for polymerization such as DNA polymerase, reverse transcriptase or the like, and at a suitable temperature and pH. The primer is preferably single stranded for maximum efficiency, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the agents for polymerization. The exact lengths of the primers will depend on many factors, including temperature and the source of primer. For example, depending on the complexity of the target sequence, a primer typically contains 15 to 25 or more nucleotides, although it can contain fewer nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with a template. In particular, the primers, which are used here, are preferably designed in a way that avoids amplification of genomic DNA or cDNA in order to avoid non-specific amplification of contaminating genomic DNA in the sample.

[0051] The optional reverse transcription step in the method of the invention is included wherever necessary in order to amplify the target sequence, i.e. when the nature of the target sequence is RNA. This process, designated reverse transcription, occurs under the direction of an RNA-dependent DNA polymerase enzyme called a reverse transcriptase. The process furthermore requires buffers and reagents, such as dNTPs, for the reverse transcription. Reverse transcription kits are commercially available and it is within the skill to perform this process. The nucleic acid amplification reagents used in the invention includes reagents which are well known and may include, but are not limited to, an enzyme with polymerase activity e.g. heat stable polymerases such as the Taq-polymerase (and, as necessary, reverse transcriptase activity e.g. when monitoring mRNA), enzyme cofactors such as magnesium or manganese; salts and deoxynucleotide triphosphates (dNTPs).

[0052] The term "amplification conditions" is generally defined as conditions, which promote hybridizing or annealing of primer sequences to a target sequence and subsequent extension of the primer sequence. It is well known in the art that such annealing is dependent on several parameters, including temperature, ionic strength, sequence length, complementarity and G:C content of the sequences. For example, lowering the temperature in the environment of complementary nucleic acid sequences promotes annealing. For any given set of sequences, melt temperature, or T_m , can be estimated by any of several known methods. Typically, diagnostic applications utilize hybridization temperatures, which are close to (i.e. within 10°C) the melt temperature. Ionic strength or "salt" concentration also impacts the melt temperature, since small cations tend to stabilize the formation of duplexes by negating the negative charge on the phosphodiester backbone. Typical salt concentrations depend on the nature and valency of the cation but are readily understood by those skilled in the art. Similarly, high G:C content and increased sequence length are also known to stabilize duplex formation because G:C pairings involve 3 hydrogen bonds where A:T pairs have just two, and because longer sequences have more hydrogen bonds holding the sequences together. Thus, a high G:C content and longer sequence lengths impact the hybridization conditions by elevating the melt temperature. Once sequences are selected for a given diagnostic application, the G:C content and length will be known and can be accounted for in determining precisely what hybridization conditions will encompass. Since ionic strength is typically optimized for enzymatic activity the only parameter left to vary is the temperature. Generally, the hybridization temperature is selected close to or at the T_m of the primers or probe. Thus, obtaining suitable hybridization conditions for a particular primer, probe, or primer and probe set is well within ordinary skill of one practicing this art. The amplification product produced as above can be detected during or subsequently to the amplification of the target sequence using any suitable method and a probe disclosed in greater detail below.

[0053] As used herein, the term "melting temperature" (T_m) in relation to an oligonucleotide is defined as the temperature at which 50% of the DNA forms a stable double-helix and the other 50% has been separated into single stranded molecules. As known to those of skill in the art, PCR annealing temperature is typically a few degrees less than the T_m , the latter of which is calculated based on oligo and salt concentrations in the reaction.

[0054] The terms "polynucleotide" and "oligonucleotide" are used interchangeably. "Oligonucleotide" is a term sometimes used to describe a shorter polynucleotide.

[0055] The terms "hybridized" and "hybridization" refer to the base-pairing interactions between two nucleic acids that result in formation of a duplex. It is not a requirement that two nucleic acids have 100% complementarity over their full length to achieve hybridization.

[0056] The term "external standard" as used herein means a synthetic DNA or RNA transcript in known amount(s) or concentration(s) that is tested separately from the test sample, i.e. through interpolation or extrapolation to a standard curve.

[0057] As used herein, "cycle threshold" (Ct) refers to quantification cycle values calculated

from the record fluorescence measurements of the real time quantitative PCR. "Cq" refers to the number of cycles required for the PCR signal to reach the significant threshold. The calculated Cq value is proportional to the log of the number of target copies present in the sample. The Cq quantification is performed with any method for the real time quantitative PCR amplification described in the art [Bustin SA. Absolute quantification of mRNA using real-time reverse transcription polymerase chain reaction assays. J Mol Endocrinol 2000;25: 169-193].

[0058] "Precision" is the measure of the degree of repeatability of an analytical method under normal operation and is normally expressed as the percent relative standard deviation for a statistically significant number of samples. The two most common precision measures are "repeatability" and "reproducibility". These are expression of two extreme measure of precision which can be obtained. Repeatability (the smallest expected precision) will give an idea of the sort of variability to be expected when a method is performed by a single analyst on one piece of equipment over a short time scale. If a sample is analyzed by a number of laboratories for comparative purposes then a more meaningful precision measure to use is reproducibility (this is the largest measure of precision).

[0059] "Limit of Detection" (LoD) is the lowest analyte concentration likely to be reliably distinguished from the blank and at which detection is feasible. LoD is determined by utilizing both the measured LoB and test replicates of a sample known to contain a low concentration of analyte.

[0060] "Limit of Quantification" (LoQ) refers to the lowest concentration at which the analyte can not only be reliably detected but at which some predefined goals for bias and imprecision are met. The LoQ is defined as three times the LOD.

[0061] "Linearity" is the ability of the method to elicit test results that are directly proportional to analyte concentration with in a given range. Linearity is generally reported as the variance of the slope of the regression line. Traditionally linearity was regarded as a desirable property of methods as only linear curves could be easily interpreted. With the ready availability of computing power this is now of little importance and non-linear calibrations can readily be dealt with.

[0062] "False negative" refers to a test result indicates a subject does not suffer from a malignant neoplastic disease when the subject actually does have it. In the context of this application the "false negative" refers to a test result that is incorrect because the method failed to determine the overexpression of *PD-L1* in a sample from a subject.

[0063] "False positives" refers to a test result that that indicates a subject who suffers from a malignant neoplastic disease when the subject actually does not have it. In the context of this application the "false positive" refers to a test result that is incorrect because the method indicates to determine the overexpression of *PD-L1* in a sample, which does not exist.

[0064] "Healthy" refers to a subject possessing good health. Such a subject demonstrates an

absence of any malignant or non-malignant disease. In the context of this application, a "healthy individual" is only healthy in that they have an absence of any malignant or non-malignant disease; a "healthy individual" may have other diseases or conditions that would normally not be considered "healthy".

[0065] "Prognosis" as used herein to refer to the prediction of the likelihood of progression, including recurrence, metastatic spread, and drug resistance, of a malignant neoplastic disease. For example, a patient having an expression profile, which correlates with an invasive phenotype, may exhibit a high proliferative activity, and therefore may be demonstrative of a favourable response to therapy, as the invasive phenotype can be a histologic characteristic used to indicate a therapy-sensitive neoplastic disease.

[0066] A "malignant" neoplasm is generally poorly differentiated (anaplasia), has characteristically rapid growth accompanied by progressive infiltration, invasion, and destruction of the surrounding tissue. Furthermore, a malignant neoplasm has the capacity to metastasize to distant sites. The term "metastasis" refers to the spread or migration of cancerous cells from a primary (original) tumor to another organ or tissue, and is typically identifiable by the presence of a "secondary tumor" or "secondary cell mass" of the tissue type of the primary (original) tumor and not of that of the organ or tissue in which the secondary (metastatic) tumor is located. For example a carcinoma of the lung that has migrated to bone is said to be metastasized lung cancer, and consists of cancer cells originating from epithelial lung cells growing in bone tissue.

[0067] As used herein, the expression "clinical outcome" or "outcome" is meant to be expressed in terms of different endpoints such as Disease-Free Survival (DFS), Relapse-Free Survival (RFS), Time-to-Recurrence (TR), Cancer-Specific Survival (CSS) or Overall Survival (OS), in accordance with the recommendations of Punt CJ, Buyse M, Köhne C-H, Hohenberger P, Labianca R, Schmoll HJ, et al. Endpoints in Adjuvant Treatment Trials: A Systematic Review of the Literature in Colon Cancer and Proposed Definitions for Future Trials. J. Natl. Cancer Inst. 2007;13: 998-1003.

[0068] As used herein, the expression "Relapse-Free Survival" or "Recurrence-Free Survival" (RFS) is defined as the time to any event, irrespective of the cause of this event, except for any second primary cancer. Recurrence of or death from the same cancer and all treatment-related deaths or deaths from other causes are events. Second primary from the same cancers and other primary cancers are ignored, and loss to follow-up is censored.

[0069] As used herein, the expression "Disease-Free Survival" (DFS) is defined as the time to any event, irrespective of the cause of this event. All events are included, except loss to follow-up which is censored. As used herein, the "Overall Survival" (OS) is defined as the time to death, irrespective of cause, whether or not the death was due to cancer. Local regional recurrence, distant metastases, second primary cancers, and second other primary cancers are ignored. Loss to follow-up is censored.

[0070] "Subject" as used herein includes humans, nonhuman primates such as chimpanzees and other apes and monkey species, farm animals such as cattle, sheep, pigs, goats and horses, domestic mammals such as dogs and cats, laboratory animals including rodents such as mice, rats and guinea pigs, and the like. The term does not denote a particular age or sex. Thus, adult and newborn subjects, as well as fetuses, whether male or female, are intended to be covered. In preferred embodiments, the subject is a mammal, including humans and non-human mammals. In the most preferred embodiment, the subject is a human.

[0071] As used herein a "biological sample" encompasses a variety of sample types obtained from any subject having or not having malignant neoplasm. A typical subject is a human. For example, biological samples include samples obtained from a tissue or blood fluids collected from an individual suspected of having a malignant neoplasm.

[0072] "Immunotherapy" is treatment that uses certain parts of a person's immune system to fight diseases such as cancer. This can be done either stimulating the immune system to work harder or smarter to attack cancer cells or giving the immune system components, such as man-made immune system proteins. Some types of immunotherapy are also sometimes called biologic therapy or biotherapy. In the last few decades immunotherapy has become an important part of treating some types of cancer. Immunotherapy includes treatments that work in different ways. Some boost the body's immune system in a very general way. Others help train the immune system to attack cancer cells specifically.

[0073] "Checkpoint inhibitors" (also known as immune checkpoint modulators) are designed to lessen the effectiveness of checkpoint proteins. They could have a variety of mechanisms of action, but if effective they let the immune system see the other molecules on the surface of the cancer cells. There are many kinds of immune checkpoint inhibitors, such as anti-PD-L1 inhibitors, anti-CTLA4 inhibitors etc.

[0074] As used herein the term circulating tumor cells (CTC) are cells that have shed into the vasculature from a primary tumor and circulate in the bloodstream. CTCs thus constitute seeds for subsequent growth of additional tumors (metastasis) in vital distant organs, triggering a mechanism that is responsible for the vast majority of cancer-related deaths.

[0075] As used herein, the term *PD-L1* refers to the official name of the gene "Programmed death-ligand 1" (*PD-L1*; also called B7-H1 or CD274). The "Programmed death-ligand 1" gene is expressed on many cancer and immune cells and plays an important part in blocking the "cancer immunity cycle" by binding programmed death-1 (*PD-1*) and B7.1 (CD80), both of which are negative regulators of T-lymphocyte activation. Binding of *PD-L1* to its receptors suppresses T-cell migration, proliferation and secretion of cytotoxic mediators, and restricts tumour cell killing. The PD-L1-PD-1 axis protects the host from overactive T-effector cells not only in cancer but also during microbial infections. Blocking *PD-L1* should therefore enhance anticancer immunity, but little is known about predictive factors of efficacy. More especially, the term "target sequence", as used herein refers to *PD-L1* mRNA sequence.

[0076] As used herein, the term *B2M* refers to the official name of the gene "beta-2-microglobulin", which encodes a serum protein found in association with the major histocompatibility complex (MHC) class I heavy chain on the surface of nearly all nucleated cells. The protein has a predominantly beta-pleated sheet structure that can form amyloid fibrils in some pathological conditions. The encoded antimicrobial protein displays antibacterial activity in amniotic fluid. More especially, the term "reference sequence", as used herein refers to *B2M* mRNA sequence.

[0077] As used herein, the term "reference gene" refers to any particular known genome sequence, whether partial or complete, of any organism or virus which may be used to reference identified sequences from a subject. For example, a reference genome used for human subjects as well as many other organisms is found at the National Center for Biotechnology Information at www.ncbi.nlm.nih.gov. A "genome" refers to the complete genetic information of an organism or virus, expressed in nucleic acid sequences. More especially, the term "reference gene", as used herein refers to *B2M* gene.

DETAILED DESCRIPTION

[0078] The present invention provides a highly sensitive, specific and reproducible real time RT-qPCR method for the quantification of *PD-L1* expression in a biological sample, such as an isolated RNA sample from CTC in peripheral blood of patients with solid cancers. The clinical importance of *PD-L1* mRNA expression is associated with the response to targeted immunotherapies in many types of cancers.

MATERIALS AND METHODS

Patients

[0079] As a first group, a total of 31 primary NSCLC carcinomas and their corresponding 31 adjacent non-neoplastic tissues were analyzed. As a second group, a total of 32 peripheral blood samples were obtained from 22 patients with metastatic breast cancer and 10 from healthy female blood donors, used as control group in order to define the specificity of the assay. The tissue samples were collected at the time of surgery and were immediately flash frozen in liquid nitrogen and stored at -80 °C. All samples were analyzed histologically to access the account of tumor component (at least 70% of tumor cells) and the quality of material (i.e., absence of necrosis).

CTC isolation from peripheral blood with positive immunomagnetic selection

[0080] CTC were isolated from 20 mL peripheral blood as previously described [Strati A, et al. Gene expression profile of circulating tumor cells in breast cancer by RT-qPCR. BMC Cancer 2011;11: 422]. This procedure is outlined in Figure 1. Moreover, the developed RT-qPCR assay for *PD-L1* can be applied in CTC samples isolated with different methodologies as well. To reduce blood contamination by epithelial cells from the skin, the first 5 ml of blood were discarded, and the collection tube was at the end disconnected before withdrawing the needle. After collection, peripheral blood was diluted with 20 mL phosphate buffered saline (PBS, pH 7.3) and peripheral blood mononuclear cells (PBMCs) were isolated by gradient density centrifugation using Ficol-Paque TM PLUS (GE Healthcare, Bio-Sciences AB) at 670 g for 30 min at room temperature. The interface cells were removed, washed twice with 40 mL of sterile PBS (pH 7.3, 4°C), at 530 g for 10 min, and resuspended in 1 mL of PBS. CTC were enriched using immunomagnetic Ber-EP4 coated capture beads (Dynabeads® Epithelial Enrich, Invitrogen), according to manufacturer's instructions. Two fractions were isolated for each sample: the EpCAM-positive CTC fraction (CTC fraction) and the corresponding EpCAM-negative fraction containing the PBMC (PBMC fraction).

RNA isolation from tumor tissues and cDNA synthesis

[0081] Total cellular RNA was isolated with the Qiagen RNeasy Mini Reagent Set (Qiagen), according to the manufacturers' instructions. All preparation and handling steps of RNA took place in a laminar flow hood under RNase-free conditions. The isolated RNA was dissolved in RNA storage buffer (Ambion) and stored at -70°C until use. RNA concentration was determined in the NanoDrop® ND-1000 spectrophotometer (NanoDrop Technologies). The amount of 1µg of total RNA was used to perform reverse transcription of RNA with the High-Capacity RNA-to-cDNA™ Kit (Applied Biosystems, USA) in a total volume of 20µL, according to the manufacturer's instructions.

RNA isolation from CTCs and cDNA synthesis

[0082] Total RNA isolation was performed using the TRIZOL-LS reagent (Invitrogen, USA). All RNA preparation and handling steps took place in a laminar flow hood, under RNase-free conditions. The isolated RNA was dissolved in 20µL of RNA storage buffer (Ambion, USA) and stored at -70°C until use. RNA concentration was determined by absorbance readings at 260 nm using the Nanodrop-1000 spectrophotometer (NanoDrop, Technologies, USA). mRNA was isolated from the total RNA, using the Dynabeads mRNA Purification kit (Invitrogen, USA) according to the manufacturer's instructions. cDNA synthesis was performed using the High-Capacity RNA-to-cDNA™ Kit (Applied Biosystems, USA) in a total volume of 20µL according to the manufacturer's instructions.

Primer and probe designs

[0083] Primers and hydrolysis probes for *PD-L1* and *B2M* used as reference gene were de novo *in-silico* designed (Table 1). *In-silico* design was performed by using Primer Premier 5.0 software (Premier Biosoft, CA, USA) to avoid primer-dimer formation, false priming sites and formation of hairpin structures. Hybridization to genomic DNA was completely avoided. Moreover, the primers and probes were designed, so as to amplify specifically *PD-L1* or *B2M* target genes according to the search in the BLAST Sequence Similarity Search tool (NCBI, NIH). The hydrolysis probes included a 5'-fluorescein (FAM) as a fluorophore covalently attached to the 5'-end of the oligonucleotide probe and a BlackBerry® Quencher (BBQ) as a quencher at the 3'-end. The position of primers and hydrolysis probes for each target gene are shown in Figures 2 and 3.

Table 1. RT-qPCR assay for *PD-L1* and *B2M* expression; sequences of primers and hydrolysis probes

Gene (Accession No)	Sequence (5'-3')	Tm(°C)	Amplicon Size (bp)
<i>PD-L1</i> (NM_014143)			
Target forward primer	5'-GCTGAATTGGTCATCCCAGAA-3' (SEQ ID NO: 4), S1	59.8	147
Target reverse primer	5'-TTTCACATCCATCATTCTCCCTT-3' (SEQ ID NO: 6), S1	60.2	
Hydrolysis target probe	5'-6FAM- ACCTCTGGCACATCCTCCAAATGAAAG- BBQ-3' (SEQ ID NO: 8), S1	69.8	
<i>B2M</i> (NM_004048)			
Reference forward primer	5'-GCCTGCCGTGTGAACCATGT-3' (SEQ ID NO: 10), S2	63.7	99
Reference reverse primer	5'-AAATGCGGCATCTTCAAACCTC-3' (SEQ ID NO: 12), S2	63.2	
Hydrolysis reference probe	5'-6FAM- CATGATGCTGCTTACATGTCTCGATCCCAC- BBQ-3' (SEQ ID NO: 14), S2	73.4	

[0084] For each gene, a primer pair and a hydrolysis probe were designed. For *PD-L1*, a primer set S1 was designed to amplify the region (147 bp) that comprises at least one intron-spanning site. This provides a primer pair that will only bind to a sequence in which the introns have been spliced out, e.g. mRNA, cDNA. In particular, the forward primer is designed between exons 4 and 5 (intron exon junction) and the reverse primer is designed between exons 5 and 6 (intron exon junction) of *PD-L1* mRNA sequence in order to enhance only the mRNA target sequence avoiding DNA genomic amplification and non-specific products. The hydrolysis probe is designed to hybridize to an internal region within the amplicon. For *B2M*, a

primer pair and a hydrolysis probe were designed. For *B2M*, a primer set S2 was designed to amplify the region (99 bp) that comprises at least one intron-spanning site. This provides a primer pair that will only bind to a sequence in which the introns have been spliced out, e.g. mRNA, cDNA. In particular, the forward primer is designed in internal region of exon 9 of *B2M* mRNA sequence and the reverse primer is designed between exons 2 and 3 of *B2M* mRNA sequence for amplification only the target sequence avoiding non-specific products. In this case, the hydrolysis probe is designed to be hybridized between exons 3 and 4 (intron exon junction). All primers and probes sequences are shown in detail in Table 1.

RT-qPCR assay

[0085] RT-qPCR reaction was performed in the LightCycler 2.0 (IVD instrument, Roche, Germany) using glass capillary tubes (Roche Applied Science, Germany). As positive control used PBMC from healthy control samples since PBMC express as well *PD-L1*. The cycling protocol was identical for both *PD-L1* and *B2M* and consisted of an initial 2-min denaturation step at 95 °C, followed by 45 cycles of denaturation at 95 °C for 10 s, annealing at 58 °C for 20 s, and extension at 72 °C for 20 s. Real-time-PCR was performed in a total volume of 10 µL per reaction. The PCR reaction mix for *PD-L1* and *B2M* are described in detail IN Table 2.

Table 2. Reaction components for *PD-L1* and *B2M* RT-qPCR

Reagents	<i>PD-L1</i>			<i>B2M</i>		
	Initial conc	V(µL)	Final conc	Initial conc	V(µL)	Final conc
Buffer	5X	3	1.5X	5X	1	0.5X
Mg	25mM	1	2.5mM	25mM	1.2	3mM
dNTPs	10mM	0.2	200 µM	10mM	0.15	150 µM
BSA	10 µg/µL	0.6	0,6 µg/µL	10 µg/µL	0.3	0,3 µg/µL
Forward primer	10µM	0.3	0,3 µM	10µM	0.25	0,25 µM
Reverse primer	10µM	0.3	0,3 µM	10µM	0.25	0,25 µM
Hydrolysis Probe	3µM	0.83	0,25 µM	3µM	0.83	0,25 µM
Taq polymerase	5U/µL	0.1	0,05U/µL	5U/µL	0.1	0,05U/µL
Volume of reaction	-	10	-	-	10	-

EXAMPLE 1

Development and analytical validation of the assay

[0086] The experimental flowchart of the study is outlined in Figure 4.

[0087] **Protocol optimization.** A RT-qPCR based methods for the quantification of *PD-L1* and *B2M* expression were optimized in a number of experiments, using as positive control cDNA samples from peripheral blood mononuclear cells (PBMC) of healthy control samples and negative control of PCR reaction mix, with respect to: PCR annealing temperature, cycling parameters, primers and probe concentrations, Mg^{+2} and dNTPs concentrations.

[0088] Single RT-qPCR was performed for *PD-L1* and *B2M* expression. Quantification is based on real-time monitoring during PCR of labelled specific hydrolysis probe for *PD-L1*. The cycle where the fluorescence signal rises above background noise (quantification cycle, Cq) is best quantified through the LightCycler software as the second derivative maximum of the curve. Real-time RT-PCR for *PD-L1* mRNA was performed using the LightCycler system (Roche Diagnostics). For the developed protocol, the primers and hydrolysis probes were used as previously described.

[0089] Real-time RT-PCR was performed in a total volume of 10 μ L in the LightCycler glass capillaries. For the PCR, 1 μ L of cDNA was placed into a 9 μ L reaction volume containing a PCR reaction mix, which is described in Table 3. Moreover, the PCR conditions protocol was used as previously described.

[0090] The method can be also applied to any other real time PCR instrument, such as LightCycler 1.5 instrument, LightCycler 2.0 instrument, LightCycler 480 (Roche Diagnostics) and Applied Biosystems Real-Time PCR Instrument.

EXAMPLE 2

RT-qPCR quantification using external calibrators

[0091] Firstly, individual PCR amplicons specifically for *PD-L1* and *B2M* were generated in order to be used as external quantification calibrators. For this purpose, total RNA was extracted from PBMC pool from normal samples since PBMC express as well *PD-L1*. cDNA was synthesized and served as a template for the amplification of *PD-L1* and *B2M* by the above described RT-qPCR. PCR products were purified using MinElute PCR Purification Kit (Qiagen, Germany) and the amplicons were quantified in the Nanodrop-1000 spectrophotometer (NanoDrop, Technologies, USA).

[0092] DNA concentration was converted to copies/ μ L by use of the Avogadro number and the molecular weight of the amplicon number of bases of the PCR product multiplied by the mean molecular weight of a pair of nucleic acids which is 660. A standard stock solution

corresponding to 10^{10} copies/ μL for each gene transcript was prepared. Serial dilutions of this stock amplicon solution in DNase/RNase-free water ranging from 10^5 copies/ μL to 10 copies/ μL served as quantification calibrators throughout the study. For the quantification of *PD-L1* and *B2M* gene transcripts, an external calibration curve was obtained by plotting the concentration of each quantification calibrator expressed as copies/ μL vs the corresponding quantification cycle (Cq).

EXAMPLE 3

The limit of detection and linearity of assay

[0093] The limit of detection (LOD) of the developed RT-qPCR assay for both *PD-L1* and *B2M* as copies/ μL in the reaction was evaluated. To estimate LOD, the quantification calibrators containing a known number of copies/ μL were prepared as described below in detail: For each gene target a calibration curve was generated using serial dilutions of these standards in triplicate for each concentration, ranging from 10^5 copies/ μL to 10 copies/ μL . The calibration curves showed linearity from 10 copies/ μL up to 10^5 copies/ μL , with correlation coefficients larger than 0.99 in both cases, indicating a precise log-linear relationship (Figure 5). None of the primers and hydrolysis probes gave any signal for any of the gene target transcripts when 50 ng/ μL of 10 different genomic DNAs was analyzed.

[0094] The LOD for both of these assays was found to be 3 copies/ μL and the limit of quantification (LOQ) was found to be 9 copies/ μL , (estimated according to the MIQE Guidelines, S. Bustin et.al. Clin Chem. 2009). The characteristics of the calibration curves are given below in Table 3.

Table 3. Characteristics of the calibration curves for *PD-L1* and *B2M* RT-qPCR

Gene	mean slope n=3	Intercept n=3	PCR efficienc y ^a (%)	LOD, copies/ μL	LOQ, copies/ μL
<i>B2M</i>	-3.237 +0.013	37.67 +0.031	104	3 copies/ μL	9 copies/ μL
<i>PD-L1</i>	-3.506 +0.14	38.43 +0.32	93	3 copies/ μL	9 copies/ μL
a: PCR efficiency is expressed as $E=[10^{-1/\text{slope}}]-1$					

EXAMPLE 4

Evaluation of intra and inter-assay precision

[0095] Repeatability or intra-assay variance (within-run precision) of the *PD-L1* RT-qPCR, was evaluated by repeatedly analyzing 3 cDNA samples corresponding to low, medium and high mRNA expression, while for *B2M* was evaluated by repeatedly analyzing 4 cDNA samples corresponding to 1, 10, 100 and 1000 cells equivalents per μL of cDNA in the same assay, in 3 parallel determinations.

[0096] Intra-assay variance expressed as the CVs (%) of the Cq variance for *PD-L1*, ranged from 0.84 to 1.2, while for *B2M* ranged from 0.21 to 0.72 (Table 4). Intra-assay variance expressed as within-run CVs of copies/ μL ranged for *PD-L1*, from 16% to 20% and for *B2M* from 3.7% to 14% (Table 4). Reproducibility or inter-assay variance (between-run precision) of the RT-qPCR assays, was evaluated by analyzing the same cDNA sample, representing 100 SKBR-3 cells for *B2M* and PBMCs for *PD-L1* and kept frozen in aliquots at -20°C , over a period of one month on 4 separate assays performed in 4 different days. Between-run CVs were 17% for *B2M*, and 15% for *PD-L1* (Table 4).

Table 4. RT-qPCR for *PD-L1* and *B2M*: Evaluation of intra and inter-assay precision

<i>B2M</i>	Cq (SD)	CV%	Copies (SD)	CV%
SKBR-3	<i>Intra-assay precision (n=3)</i>			
1	32.56 (0.11)	0.34	$3.8(\pm 0.29) \times 10$	7.9
10	29.29 (0.21)	0.72	$3.8 (\pm 0.55) \times 10^2$	14
100	25.79 (0.053)	0.21	$4.5 (\pm 0.15) \times 10^3$	3.7
1000	22.40 (0.10)	0.45	$4.9 (\pm 0.36) \times 10^4$	7.3
	<i>Inter-assay precision (n=5)</i>			
100	25.73 0.26	1.0	$4.7 (\pm 0.85 \times 10^3$	17
<i>PD-L1</i>				
	<i>Intra -assay precision (n=3)</i>			
cDNA 1	35.63 (0.30)	0.84	$6.5 (\pm 1.3)$	20
cDNA 2	31.48 (0.25)	0.79	$0.97 (\pm 0.14) 10^2$	16
cDNA 3	24.45 (0.29)	1.2	$1.0 (\pm 0.18) \times 10^4$	19
	<i>Inter-assay precision (n=5)</i>			
cDNA 4	29.57 (0.21)	0.71	$5.32 (\pm 0.82) \times 10^2$	15

EXAMPLE 5

Normalization of data for the quantification of *PD-L1* expression in primary tumors and

CTCs

[0097] The normalization of data for the quantification of *PD-L1* expression has performed in respect to the expression of *B2M* as a reference gene, and using the $2^{-\Delta\Delta C_t}$ method (Livak and Schmittgen, Methods 2001).

[0098] In primary tumors two samples were available for each patient: a) the primary tumor and the corresponding non-cancerous tissue. In this case for each sample, the expression of *PD-L1* is estimated as a relative ratio to *B2M* used as a reference gene in both the primary tumor and its adjacent non-cancerous tissue, used as a calibrator. Then by using the $2^{-\Delta\Delta C_t}$ approach, the normalization of analytical signal (Cq) of *PD-L1* in each primary tumor sample to the corresponding analytical signal (Cq) of *PD-L1* in the adjacent non-cancerous sample.

[0099] In the case of CTCs for each sample, the expression of *PD-L1* is estimated as a relative ratio to *B2M* used as a reference gene in both the EpCAM-positive CTC fraction and in the corresponding EpCAM-positive CTC fraction in the group of healthy blood donors used as a calibrator. Then by using the $2^{-\Delta\Delta C_t}$ approach, the overexpression of *PD-L1* in the EpCAM-positive CTC fraction of peripheral blood samples was evaluated.

[0100] In the EpCAM-positive CTC fraction, one sample was defined as *PD-L1* overexpressed based on the fold change of *PD-L1* expression in respect to the group of ten healthy individuals used as a control group. More specifically, a cut-off value was estimated according to the expression of *PD-L1* in the EpCAM-positive fraction of ten healthy individuals analysed in exactly the same way as the patient's peripheral blood samples. For these ten control samples, the difference of the Cq value ($\Delta C_{q_{control}}$) for *PD-L1* from the respective Cq value for *B2M* ($C_{q_{PD-L1}} - C_{q_{B2M}}$) was measured. The median value of these 10 ΔC_q values was 15.78 ± 0.83 (Table 5).

Table 5. Expression of *PD-L1* in PBMC (control group). (ΔC_q values: $C_{q_{PD-L1}} - C_{q_{B2M}}$)

A/A	Cq <i>PD-L1</i>	Cq <i>B2M</i>	ΔC_q
1	38,68	22,06	16.62
2	38,70	22,70	16.00
3	36,58	20,63	15.95
4	35,38	19,77	15.61
5	41,24	25,74	15.50
6	40,60	23,16	17,44
7	40,40	23,81	16,59
8	38,90	24,12	14,78
9	39,34	22,67	16,67

A/A	Cq <i>PD-L1</i>	Cq <i>B2M</i>	ΔCq
10	38,93	23,99	14,94
		SD	0.83
		Median	15.78
		Cut off	14.70

Example 6

Expression of *PD-L1* in primary tumors (NSCLC)

[0101] In this group, the quantification of *PD-L1* expression was performed in 31 pairs of NSCLC tissues and their adjacent non-neoplastic tissues using RT-qPCR. *PD-L1* was expressed in all tissues, and its expression was normalized with respect to *B2M* gene expression and by using the relative quantification approach described by Livak and Schmittgen as previously described. In this study demonstrated that *PD-L1* was overexpressed in 14/31 (45.2%) of NSCLC tissues (Figure 6). The ΔCq values between primary tissues of NSCLC and their adjacent normal samples are shown in Figure 7.

EXAMPLE 7

Expression of *PD-L1* expression in CTCs

[0102] In this group, the quantification of *PD-L1* in the EpCAM-positive CTC fraction (isolated from peripheral blood from metastatic breast cancer patients) was performed. For each patient sample, the corresponding $Cq_{PD-L1} - Cq_{B2M}$ value (ΔCq_{sample}) was calculated. Then each individual ΔCq_{sample} value was evaluated by finding its difference from the median $\Delta Cq_{control}$ value ($\Delta \Delta Cq = \Delta Cq_{sample} - \Delta Cq_{control}$) (Table 6). The median value of the $2^{-\Delta \Delta Cq}$ for the patients group analysed was 2.20. The samples with a $2^{-\Delta \Delta Cq}$ value above 2.20 or a ΔCq value below 14.7 were defined as positive for *PD-L1* mRNA overexpression (Table 6). Moreover, the ΔCq values in all of the samples from healthy individuals were above 14.7 (Figure 8).

[0103] According to the results, *PD-L1* was found to be overexpressed in 8/22 (36.4%) patients with verified metastasis (Figure 8). The ΔCq values between control group and CTCs isolated from breast cancer metastatic samples are shown in Figure 9.

Table 6. Expression of *PD-L1* in the EpCAM-positive CTC fraction ($2^{-\Delta \Delta Cq}$ values)

A/A	Cq PD-L1	Cq B2M	$\Delta Cq_{Cq_{PD-L1} - Cq_{B2M}}$	$\Delta\Delta Cq_{\Delta Cq_{sample} - \Delta Cq_{control\ median}}$	$2^{-\Delta\Delta Cq}$	Result
1	38,47	22,32	16,15	0.37	0,77	Negative
2	36,32	19,49	16,83	1.05	0,48	Negative
3	38,71	21,31	17,40	1.62	0,33	Negative
4	37,51	21,92	15,59	-0.19	1,14	Negative
5	39,24	24,24	15.00	-078	1,72	Negative
6	39,52	22,74	16,78	1.00	0,50	Negative
7	34,81	20,82	13,99	-1.79	3,46	Positive
8	40,39	23,2	17,19	1.41	0,38	Negative
9	38,45	21,89	16,56	0.78	0,58	Negative
10	34,89	22,09	12,8	-2.98	7,89	Positive
11	36,10	21,25	14,85	-0.93	1,91	Negative
12	39,30	25,16	14,14	-1.64	3,12	Positive
13	38,63	24,66	13,97	-1.81	3,51	Positive
14	40,98	23,51	17,47	1.69	0,31	Negative
15	35,78	21,21	14,57	-1.21	2,31	Positive
16	38,86	24,58	14,28	-1,5	2,83	Positive
17	39,26	24,55	14,71	-1,07	2,10	Negative
18	38,57	21,35	17,22	1,44	0,37	Negative
19	39,82	25,54	14,28	-1,5	2,83	Positive
20	39,23	20,97	18,26	2,48	0,18	Negative
21	38,82	21,51	17,31	1,53	0,35	Negative
22	35,37	20,91	14,46	-1,32	2,50	Positive
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REFERENCES CITED IN THE DESCRIPTION

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Patentkrav

- 1.** *In vitro*-fremgangsmåde til kvantitativ bestemmelse af udtrykket af programmeret død-ligand 1 (*PD-L1*) i en flydende biopsiprøve af cirkulerende tumorceller (CTC), hvor nævnte fremgangsmåde omfatter trinnene:
- i. at udsætte den flydende biopsiprøve til revers transkription under anvendelse af RNA til stede i prøven som en template for at syntetisere en tilsvarende cDNA-sekvens,
 - ii. at danne en reaktionsblanding omfattende prøven,
nukleinsyreforstærkningsreagenser, et målprimerpar, en
målhydrolysesonde, hvor nævnte målprimerpar og målhydrolysesonde er i stand til at hybridisere til *PD-L1* mRNA, og nævnte målprimerpar består af en fremad-målprimer omfattende sekvensen 5'-
GCTGAATTGGTCATCCCAGAA-3' (SEQ ID NO: 4) og en revers-målprimer
omfattende sekvensen 5'-TTTCACATCCATCATTCTCCCTT-3' (SEQ ID NO: 6)
 - iii. at udsætte reaktionsblandingen for amplifikationsforhold optimeret til at generere mindst én kopi af en nukleinsyresekvens komplementær til en målsekvens, hvor nævnte målsekvens er et mRNA-transkript af *PD-L1* mRNA-sekvensen (SEQ ID NO: 1), og
 - iv. at bestemme mængden af *PD-L1* mRNA i den flydende biopsiprøve,
 - v. at normalisere udtrykket af *PD-L1* i forhold til et udtryk af et referencegen hvis udtryksniveauer forbliver konstante mellem forskellige celletyper,
 - vi. at sammenligne mængden af *PD-L1* mRNA udtrykt i den nævnte prøve med en positiv kontrol, hvilken er en prøve omfattende *PD-L1* mRNA og en negativ kontrol, hvilken er en prøve uden *PD-L1* mRNA for at estimere et overudtryk af *PD-L1* mRNA-sekvensen.
- 2.** Fremgangsmåde ifølge krav 1, til
- i. at diagnosticere og/eller prognosticere ondartet neoplastisk sygdom hos et individ før immunterapi med checkpoint-inhibitorer, og/eller
 - ii. at forudsige virkningsgraden af behandling af ondartet neoplastisk sygdom hos et individ før immunterapi med checkpoint-inhibitorer, og/eller
 - iii. at vurdere udfald af behandling af ondartet neoplastisk sygdom hos et individ under og efter immunterapi med checkpoint-inhibitorer, og/eller

iv. at vurdere tilbagevendelsen af ondartet neoplastisk sygdom hos et individ under og efter immunterapi med checkpoint-inhibitorer, hvor individet er et pattedyr, som har eller er mistænkt for at have en ondartet neoplastisk sygdom.

5

3. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 2, hvor mål-*PD-L1*-hydrolysesonden omfatter mindst sekvensen 5'-6FAM-GCACATCCTCCA-BBQ-3' (SEQ ID NO: 7), fortrinsvis mål-*PD-L1*-hydrolysesonden omfatter sekvensen 5'-6FAM-ACCTCTGGCACATCCTCCAAATGAAAG-BBQ-3' (SEQ ID NO: 8) og to fluorescerende partikler.

4. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 3, hvor referencegenet vælges fra gruppen bestående af hypoxanthinphosphoribosyltransferase (*HPRT*), β 2-microglobulin (*B2M*), glycerinaldehyd-3-phosphatdehydrogenase (*GAPDH*) og β -actin (*ACTB*), 18S ribosomal-RNA (18S *rRNA*), 28S ribosomal-RNA (28S *rRNA*), α -tubulin (*TUBA*), albumin (*ALB*), ribosomalprotein L32 (*RPL32*), TATA-sekvensbindingsprotein (*TBP*), cyklophilin C (*CYCC*), Eelongeringsfaktor 1 α (*EF1A*), RNA-polymerase II (*RPII*).

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5. Fremgangsmåde ifølge krav 4, hvor referencegenet er β 2-microglobulin (*B2M*)-mRNA-sekvens (SEQ ID NO: 2) og fremad-*B2M*-referenceprimeren omfatter mindst sekvensen af 5'-GCCGTGTGAAC-3' (SEQ ID NO: 9) eller fremad-*B2M*-referenceprimeren omfatter sekvensen 5'-GCCTGCCGTGTGAACCATGT-3' (SEQ ID NO: 10) og hvor revers-*B2M*-referenceprimeren omfatter mindst sekvensen af 5'-CTTCAAACCTC-3' (SEQ ID NO: 11) eller revers-*B2M*-referenceprimeren omfatter sekvensen 5'-AAATGCGGCATCTTCAAACCTC -3' (SEQ ID NO: 12).

6. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 5, hvor mål- eller referencehydrolysesonden omfatter fluorescerende partikler.

7. Fremgangsmåde ifølge krav 6, hvor de fluorescerende partikler af mål- eller referencehydrolysesonden er en fluorescerende reporter kovalent fastgjort til 5'-enden af mål- eller referencehydrolysesonden og et fluorescerende quencher-farvestof fastgjort til 3'-enden.

35

8. Fremgangsmåde ifølge krav 7, hvor fluorescerende reporterfarvestof er 6-fluorescein (FAM) og det fluorescerende quencherfarvestof er BlackBerry Quencher (BBQ).

- 5 **9.** Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 8, hvor reference-B2M-hydrolysesonden omfatter mindst sekvensen af 5'-6FAM-CTCGATCCCCAC-BBQ-3' (SEQ ID NO: 13), fortrinsvis hvor reference-B2M-hydrolysesonden omfatter sekvensen 5'-6FAM-CATGATGCTGCTTACATGTCTCGATCCCCAC -BBQ-3' (SEQ ID NO: 14) og to fluorescerende partikler.

10

10. Fremgangsmåde ifølge et hvilket som helst krav fra 2 til 9, hvor den ondartede neoplastiske sygdom vælges fra gruppen bestående af bryst-, urotelial-, kolorektal-, spiserørs-, mave-, hepatocellulær karcinom, lunge-, melanom, næsesvælgs-, multipel myelom, nyrecellekarcinom, lymfomer, orofaryngeal
15 pladeepitelkarcinom, livmoderhals-, glioblastom, ondartede mesoteliomaer, æggestoks- og bugspytkirtelkræft.

11. Kit til at amplificere en *PD-L1* målsekvens og at bestemme udtrykket af *PD-L1* mRNA i en prøve omfattende;

20

a) nukleinsyreforstærkningsreagenser,

b) et målprimerpar, som er i stand til at hybridisere til *PD-L1* mRNA og som består af en fremad-målprimer omfattende sekvensen 5'-GCTGAATTGGTCATCCCAGAA-3' (SEQ ID NO: 4) og en revers-målprimer

omfattende sekvensen 5'-TTTCACATCCATCATTCTCCCTT-3' (SEQ ID NO: 6),

25

c) et referenceprimerpar, som er i stand til at hybridisere til mRNA af et referencegen,

d) en målhydrolysesonde, som er i stand til at hybridisere til *PD-L1* mRNA

e) en referencehydrolysesonde som er i stand til at hybridisere til mRNA af referencegenet,

30

f) eventuelt instruktioner til at udføre *in vitro*-fremgangsmåden som defineret i kravene 1 til 10.

DRAWINGS

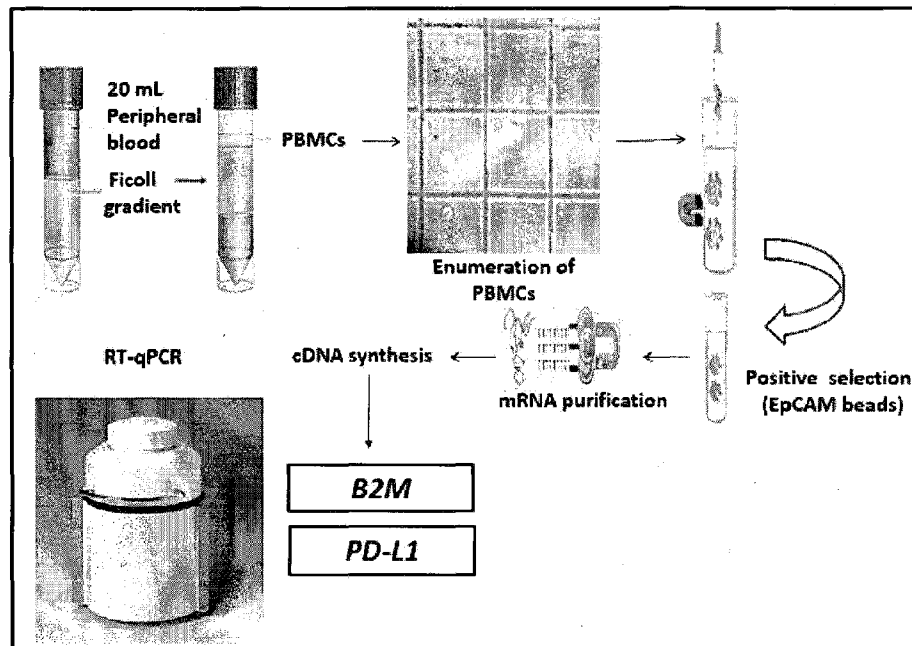


Fig. 1

PD-L1 mRNA sequence**Forward PD-L1**

actgcacttttaggagattagatcctgaggaaaaccatacagctgaattggtcatcccag/
 |||||
 cgacttaaccagtagggtc

Hydrolysis probe PD-L1

aactacctctggcacatcctccaaatgaaaggactcacttggtaattctgggagccatct
 || |||||
 ttgatggagaccgtgtaggaggtttactttc

Reverse PD-L1

ttc cctcttactacc
 ||| |||||
 tattatgccttgggtgtagcactgacattcatcttcogtttaagaaaag/ggagaatgatgg

tacacttt

|||||

atgtgaaaaaatgtggcatccaagatacaaaactcaaagaagcaaagtgat

Fig. 2**B2M mRNA sequence****Forward B2M**

tactacactgaattcaccocccactgaaaaagatgagtatgcctgccgtgtgaaccatgt
 |||||
 cggacggcacacttggtaga

Hydrolysis probe B2M

caccc tagctctgtacattcgtcgtagtag
 ||||| |||||
 gactttgtcacagcccaagatagttaagtggg/atcgagacatgtaagcagcatcatg

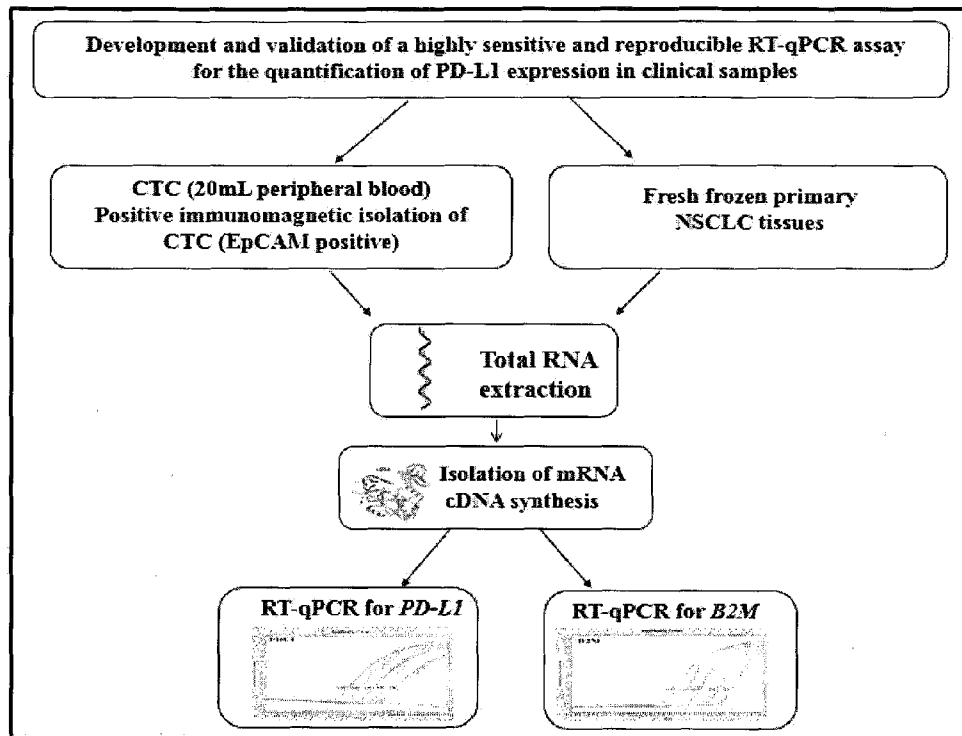
Reverse B2M

ctc caaacttctacggcgtaaa

||| |||||

gag/gtttgaagatgccgcatttggattggatgaattccaaattctgctt

Fig. 3

**Fig. 4**

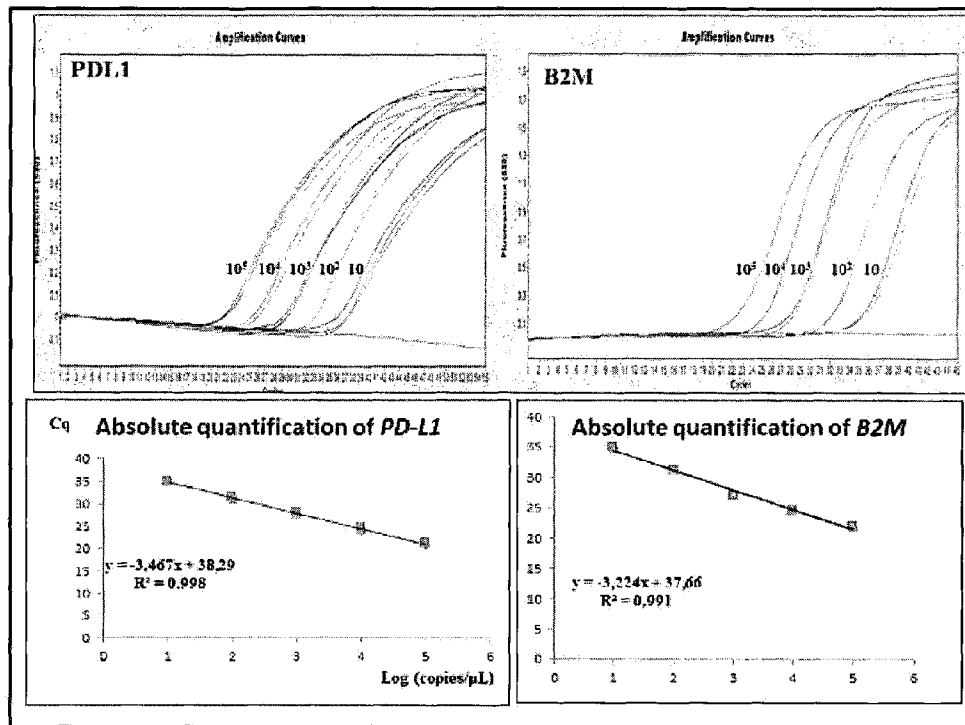
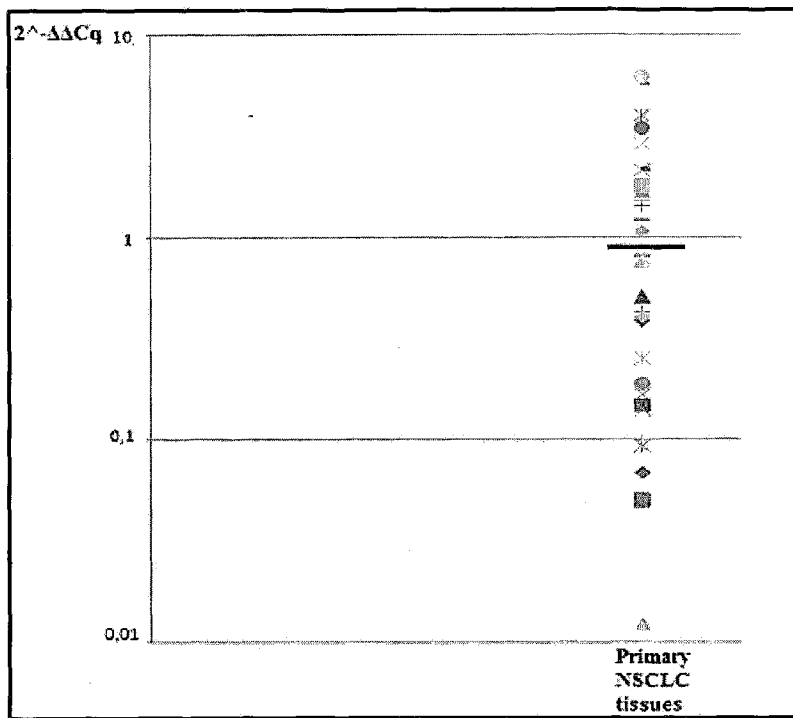


Fig. 5

**Fig. 6**

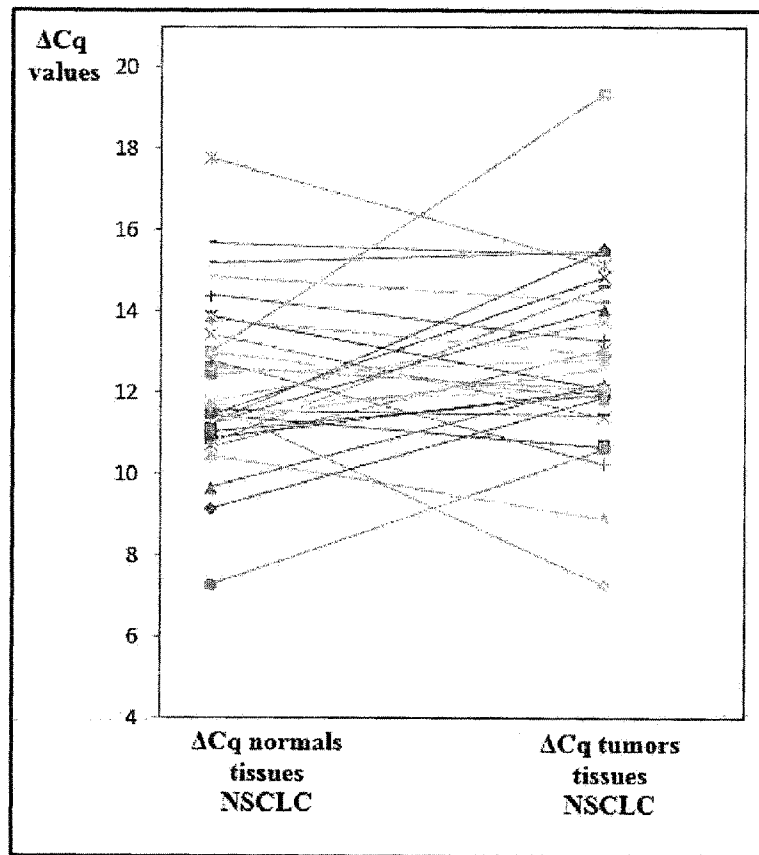
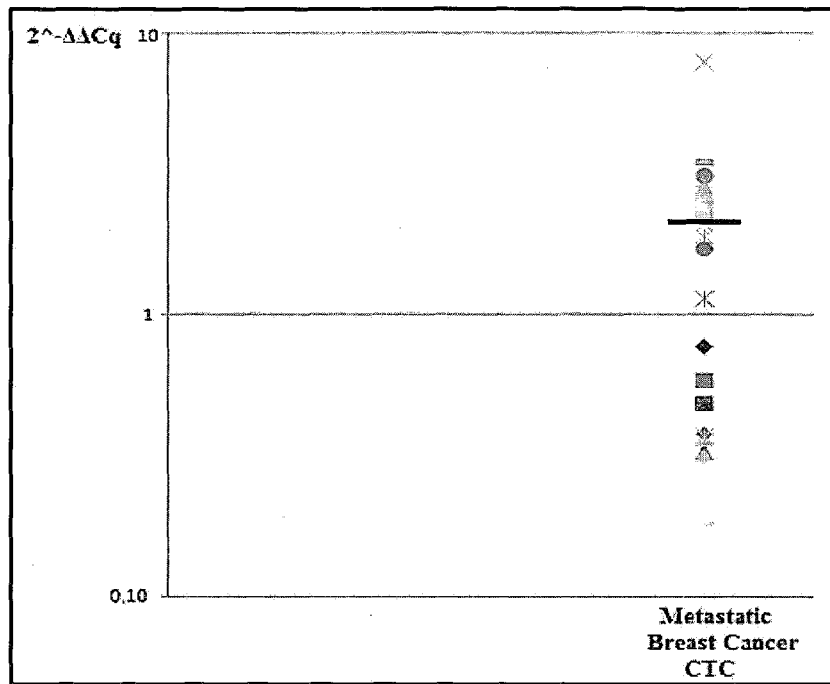
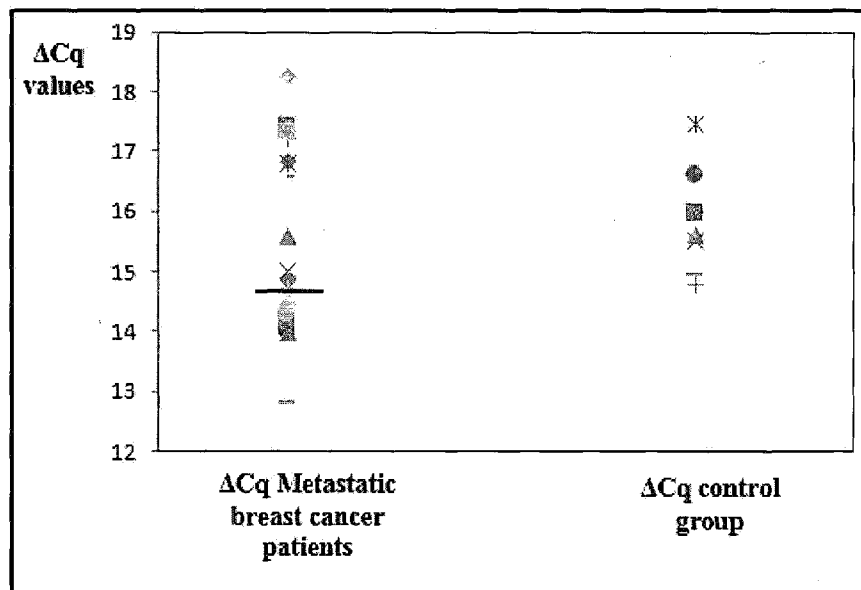


Fig. 7

**Fig. 8****Fig. 9**