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(54) **Titre : MUTATIONS DE DDR2 EN TANT QUE CARACTERISTIQUES POUVANT ETRE CIBLEES D'UN MELANOME OU D'UN CARCINOME A CELLULES BASALES**
(54) **Title: DDR2 MUTATIONS AS TARGETABLE FEATURES OF MELANOMA OR BASAL CELL CARCINOMA**

DDR2 alignment (top lines) with DDR1 (bottom) showing conserved sequence between the two proteins at the sites of DDR2 mutations seen in extracellular-matrix domains (amino acids 22-200) and the kinase domain (amino acids 350 to 851).

Query 22 KAQVDEAIKXPLGSSQIPEEDITAGSQNSSTAAHYGRLSEEDDQAWCPZPUVED
81 K +PA QRY IGM 1RD DI-ASS NS+SAR++ RL+S +QJGAWCP V E
Sbjct 23 KGHFQEARCKTALGHQNTYFQSDISASSNSSTAAHRELESSDQGCANCPAGVTEK
82 RIUSC
Query 82 DLKRELIQDLMTLFTLFTLVTGQGRGAGGSIAPMYKINTFSDGTRN:SWNRHNGCVL
141 + +ELQ+DL LH + LVGTQGRGAGG G SE+ Y++ TSHG RN- W++R G++V+
Sbjct 83 E-SEVLQVQLRLVALVGTQGRSAGSLGKSPSEYRLATSEFGRRNWNKDRNGQVEI
141
Query 142 DGRSNFYDIPLDLEPPVAFVFRFIVTDSHSHVNCVRLYCCVWLGLVGYARACQ
201 GN +P + LKUL P+VAF VRF P D H+VC+RVLZYCC+H DGL+SY AP CG
Sbjct 142 SGRNEDESVVLADLGFPMFALVRFITRADRVMSVCLRVSLYCLNAGDLELYTAPVQOT
201
Query 202 FVLGGGIIYVLDSDVYDC ANGVNMTDGLQLTDCVGLDQFQITREYVWPGDYVWGR
360 N S +GYE+P FEEDH+K E M+YCNHNN G++ Y+G FR A HZ +
Sbjct 202 MYC--SEANTYHNTYDGTIVSGQLGRLGLADQVGLDQFSEGLSEWPGDYVWGRS
360
Query 360 NEGATNGVISHMEFDRIHNTFNK/ACNNHFMOLVTKRYQCYFR-SEASENEMHIS
420 N S +GYE+P FEEDH+K E M+YCNHNN G++ Y+G FR A HZ +
Sbjct 360 NHTSSGYSHEHFFDLRAFCANQ/ACNNHFMOLVTKRYQCYFR-SEASENEMHIS
420
Query 379 FFCVLDVWPGSARFVZVPLAHNMSALCQVIFADYHMFSEITFQSDANNYHNSALET
379 L + +P AR V+VPL R+R ++C++ EA H++FSEI+P SD + N+S AL
Sbjct 379 HNLGNLGDTRARAVGVPLQCFVARTLCREFLAPG+LLESEI+P SD -VNNSALGG
379
Query 380 S-----THAPPTVDNMLKDDSNTRILGICLVALIFILLAIIVILL
420 + +P E+ K + G T LKIGCLVALI: +IL II ++L
Sbjct 379 TFPDAPWPGPPPTNFSLELPRGQGVKAGDSPTALIGCLVALI: LLLLLIAILML
438
Query 421 NRQFQWMLKASRMMLDQMTVSLGLSDSDMTNDRSSSFGQNSYVDRIFPLRPD
480 NR W++L A SRA+L+SVIV LS-P D+ + NH P E P
Sbjct 439 WRSHWPLL A SRA+VLEELIIVSLVPGDTILIME--PGPEP-----PP
482
Query 481 YQEPPIIKRLPEFAP-----GEESGSCGVKPKQSGSP-----SVHYARADCVNL
525 YQEP R P AP G SG ++P +P P YHYARADCV L

Sbjct 483 YQEP-RFAGNPFMSAPCVENGSAISG---DTHREKFGAPLLFPFQNSVHYARADIVL
539 P574C
Query 539 QGVIGANTISVPAVTHLLSKNDVAVEEFHLLTFKXIGESQVQFVHLCEVGMERFK
589 QGVIGANTY+VPA+ + G +FPR L FFKLIGESQFQVHLCEV+ +
Sbjct 540 QGVIGANTIAVPAVPGAV-SGGPFVDFPSRLATFKEILGESQFQVHLCEVSSPQCLV
598
Query 590 DKDFALDVSANQVYAVVRLRADANNAHDFLEKIKMSLKPNIHLLSCVCTDDP
649 EF IAV P+VAVK+L R DA ENAHDFLEK+KMSLKPNIH LL YC+ GGP
Sbjct 599 SLETPAVVHGMPLVAVVILPDAENAHDFLEKIKMSLKPNIHLLSCVCTDDP
658
Query 650 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
700 LCKITHYHNGELNOLIS R+ P + ++ TASY L +A QIASQMY
Sbjct 659 LCKITDKHNGELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
718
Query 700 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
718
Query 701 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
718
Sbjct 701 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
718
Query 719 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
718
Sbjct 719 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
718
Query 761 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
820 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
820
Sbjct 779 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
838 LCKITEYHMKELAQFLERHE-----PNNSSSDVETVSYTHLKNATQIASQMY
838
Query 821 PDCVYHMLKSNRSTNINPSPQETILLQQ 851
Sbjct 839 PDCVYHMLKSNRSTNINPSPQETILLQQ 851

(57) **Abrégé/Abstract:**

Described herein are methods for diagnosing melanoma or basal cell carcinoma based on mutations in the DDR2 gene. Further, a distinct subgroup of BRAF- mutated melanomas have somatic mutations in the DDR2 gene as well. Applications of this finding to routine diagnostics include the molecular stratification of melanoma, and the tissue identification of targetable DDR2 kinase mutations in routine formalin-fixed paraffin-embedded sections. Described herein are methods, compositions and kits related to the discovery that DDR2 mutations may be markers for melanoma generally, and BRAF-mediated melanoma in particular, opening up the possibility of dual therapy for melanoma by targeting both DDR2 and BRAF.

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Abstract

Described herein are methods for diagnosing melanoma or basal cell carcinoma based on mutations in the DDR2 gene. Further, a distinct subgroup of BRAF-mutated melanomas have somatic mutations in the DDR2 gene as well. Applications of this finding to routine diagnostics include the molecular stratification of melanoma, and the tissue identification of targetable DDR2 kinase mutations in routine formalin-fixed paraffin-embedded sections. Described herein are methods, compositions and kits related to the discovery that DDR2 mutations may be markers for melanoma generally, and BRAF-mediated melanoma in particular, opening up the possibility of dual therapy for melanoma by targeting both DDR2 and BRAF.

DDR2 MUTATIONS AS TARGETABLE FEATURES OF MELANOMA OR BASAL CELL CARCINOMA

TECHNICAL FIELD

The present technology relates to novel mutations in the DDR2 gene in melanoma and basal cell carcinoma.

BACKGROUND

The following description is provided to assist the understanding of the reader. None of the information provided or references cited is admitted to be prior art to the present invention.

Melanoma and Basal Cell Carcinoma

Skin cancer is the most common of all cancers, afflicting more than one million Americans each year, a number that is rising rapidly. It is also the easiest to cure, if diagnosed and treated early. If allowed to progress to the point where it spreads to other sites, the prognosis is very poor. More than 8,000 melanoma deaths now occur per year.

Melanoma is a malignant tumor of melanocytes. Melanocytes predominantly occur in skin, between the outer layer of the skin (the epidermis) and the next layer (the dermis), but are also found in other parts of the body, including the bowel and the eye (see uveal melanoma). Melanoma can occur in any part of the body that contains melanocytes or as a metastatic tumor of unknown primary lesion. Melanoma is less common than other skin cancers but is much more dangerous and causes the majority (75%) of deaths related to skin cancer.

Melanoma arises from DNA damage to melanocytes. The early stage of the disease commonly begins with a radial growth phase when the tumor is confined to the epidermis followed by a dermal “vertical growth phase” (VGP). Some melanomas attain further invasive potential, growing into the surrounding tissue and may spread around the body through blood or lymph vessels to form metastases.

An immunological reaction against the tumor during the VGP may be judged by the presence and activity of the tumor infiltrating lymphocytes (TILs). These cells

sometimes attack the primary tumor, and in certain cases, the primary tumor regresses with diagnosis of only the metastatic tumor.

Multiple genetic events have been related to the pathogenesis (disease development) of melanoma. Some cases of melanoma have a clear genetic predisposition. Germline mutations in CDKN2A, CDK4, MC1R, MDM2 SNP309 and in genes associated with xeroderma pigmentosum (XP) predispose patients to developing melanoma. Other cases of familial melanoma are genetically heterogeneous, and putative loci for familial melanoma have been identified on the chromosome arms 1p, 9p and 12q.

Clinical and Pathological diagnosis

Melanoma is usually first detected by visual examination of pigmented lesions of the skin, notably those that show: (A) asymmetry, (B) a border that is uneven, ragged, or notched, (C) coloring of different shades of brown, black, or tan and (D) diameter that has recently changed in size. In contrast, non-neoplastic moles or nevi are symmetrical, have a regular border, even coloration, and show no change in size/diameter over time. The main diagnostic concern is in distinguishing between a benign nevus, a dysplastic nevus-which may show progression over time, and a melanoma. Moles that are irregular in color or shape undergo further workup for melanoma. Following a visual examination and a dermoscopic exam, or *in vivo* diagnostic tools such as a confocal microscope, a sample (biopsy) of the suspicious mole is usually obtained.

Sample Preparation

When an atypical mole has been identified, a skin biopsy takes place in order to best diagnose it. Local anesthetic is used to numb the area, then the mole is biopsied. The biopsy material is then sent to a laboratory to be evaluated by a pathologist. A skin biopsy can be a punch or shave biopsy, or complete excision. The complete excision is the preferred method, but a punch biopsy can suffice if the patient has cosmetic concerns (i.e. the patient does not want a scar) and the lesion is small. A scoop or deep shave biopsy is generally avoided due to risk of transecting a melanoma and thereby losing important prognostic information.

Most dermatologists and dermatopathologists use a diagnostic schema for classifying melanocytic lesions based on how symmetrical the lesion is and the degree of cytologic atypia in the melanocytes. In this classification, a nevus is classified as unequivocally benign, atypical/dysplastic, or clearly melanoma. A benign nevus exhibits no

significant cytologic atypia and symmetrical growth. An atypical mole is read as having either asymmetrical growth, and/or having (mild, moderate, or severe) cytologic atypia. Usually, cytologic atypia is of more important clinical concern than architectural atypia. Along with melanoma, nevi with moderate to severe cytologic atypia may require further excision to make sure that the surgical margin is completely clear of the lesion.

Important aspects of the skin biopsy report for melanoma, including the pattern (presence/absence of an in situ component, radial or vertical growth), depth of invasion, presence of lymphocyte infiltrate, presence/absence of vascular or lymphatic invasion, presence/absence of a preexisting benign melanoma and the mitotic index. A further important aspect of the skin biopsy report for atypical nevi and melanoma is for the pathologist to indicate if the excision margin is clear of tumor. If there is any atypical melanocytes at the margin or if a melanoma is diagnosed, a reexcision is performed. Lymph node dissection may also be performed based on the tumor parameters seen on the initial biopsy and on the reexcision.

Further molecular testing may be performed on melanoma biopsies, reexcision or lymph node metastatic samples to assess for targetable genetic changes to help select optimal therapy.

BRAF

BRAF is a human gene that makes a protein called B-Raf. The gene is also referred to as proto-oncogene B-Raf and v-Raf murine sarcoma viral oncogene homolog B1, while the protein is more formally known as serine/threonine-protein kinase B-Raf. B-Raf is a member of the Raf kinase family of serine/threonine-specific protein kinases. This protein plays a role in regulating the MAP kinase/ERK signaling pathway, which affects cell division, differentiation, and growth factor expression.

In 2002, BRAF was shown to be mutated in human cancers. More than 30 mutations of the BRAF gene associated with human cancers have been identified. The frequency of BRAF mutations varies widely in human cancers from approximately 60% of melanomas and some types of benign nevi, to approximately 1-10% of common carcinomas such as lung adenocarcinoma (ACA) and colorectal cancer. In 90% of BRAF-mutated tumors, thymine is substituted for adenine at nucleotide 1799. This leads to valine (V) being substituted for by glutamate (E) at codon 600 (V600E) in the activation segment. This mutation has been widely observed in papillary thyroid carcinoma, colorectal cancer,

melanoma and non-small-cell lung cancer. In June 2011, a team of Italian scientists used massively parallel sequencing to pinpoint mutation V600E as a likely driver mutation in 100% of cases of hairy cell leukemia. Less commonly, V600E mutation can also occur by a double nucleotide substitution.

BRAF mutations which have been found are R462I, I463S, G464E, G464V, G466A, G466E, G466V, G469A, G469E, N581S, E586K, D594V, F595L, G596R, L597V, T599I, V600D, V600E, V600K, V600R, K601E, E602K and A728V, etc. Most of these mutations are clustered in two regions of the gene: the glycine-rich P loop of the N lobe and the activation segment and flanking regions. Many of these mutations change the activation segment from an inactive state to an active state. For example in V600 mutations, the aliphatic side chain of Val600 interacts with the phenyl ring of Phe467 in the P loop. Replacing the medium-sized hydrophobic Val side chain with a larger and charged residue (such as the Val to Glu, Asp, Lys, or Arg changes seen in human tumors) can destabilize the interactions that maintain the DFG motif in an inactive conformation, resulting in conformational shift in the active position. Each BRAF kinase mutation has a variable effect on MEK phosphorylation activity, with most mutations having higher phosphorylation activity than the unmutated B-Raf protein, but some mutations show reduced or even absent kinase activity, termed “inhibitory” BRAF mutations. The effect of these inhibitory mutations appears to be to activate wild-type C-Raf, which then signals to ERK.

BRAF has also emerged as important drug target for tumor therapy. Drugs that treat cancers driven by BRAF mutations have been developed. On August 17, 2011, one of them, vemurafenib, was approved by FDA for treatment of advanced-stage melanoma. Other BRAF-directed kinase inhibitors include GDC-0879, PLX-4720, sorafenib tosylate, dabrafenib, and LGX818.

DDR2

Discoidin domain receptor family, member 2, also known as DDR2 or CD167b (cluster of differentiation 167b), is a receptor tyrosine kinase (RTK) that regulates cell growth, differentiation, and metabolism in response to extracellular signals. DDR2 mutation has been previously reported in 3-4% of squamous cell carcinoma (SCC) of the lung. In lung SCC, a few cases with DDR2 mutation were shown to have clinical response to treatment with the tyrosine kinase inhibitor dasatinib (*Cancer Discov.* 2011 April 3; 1(1): 78–89). The data suggested that DDR2 may be an important therapeutic target in SCC.

DDR2 protein comprises an extracellular discoidin (DS) domain, a transmembrane domain and a kinase domain. The kinase domain is located at amino acids 563 to 849 of the full length protein (which includes the signal peptide) and the DS domain is located at amino acids 22-399. The nucleotide sequence of human DDR2 mRNA variant 2 is shown in GenBank Accession no. NM_006182.

SUMMARY OF THE INVENTION

Methods of diagnosing melanoma in an individual are disclosed. In one aspect of the present invention, a method of diagnosing melanoma in an individual comprises

- (a) analyzing a biological sample from the individual,
- (b) detecting the presence of a nucleic acid encoding a DDR2 protein having a mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, and T836A in the sample, and
- (c) diagnosing the individual as having melanoma when the mutation is detected, thereby indicating that the individual has melanoma.

In another aspect, a method of diagnosing melanoma in an individual, comprises

- (a) analyzing a biological sample from the individual,
- (b) detecting the presence of a DDR2 protein having a mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, and T836A in the sample, and
- (c) diagnosing the individual as having melanoma when the mutation is detected, thereby indicating that the individual has melanoma.

In particular embodiments, the melanoma is advanced stage melanoma. The individual may have a skin lesion and/or may be suspected of having a skin disorder such as, for example, skin cancer, or melanoma.

Methods of diagnosing basal cell carcinoma in an individual are also disclosed. In one aspect of the invention, a method of diagnosing basal cell carcinoma in an individual comprises

- (a) analyzing a biological sample from the individual,
- (b) detecting the presence of a nucleic acid encoding a DDR2 protein having a mutation selected from the group consisting of N146K, R399Q, and S702F in the sample, and
- (c) diagnosing the individual as having basal cell carcinoma when the mutation is detected, thereby indicating that the individual has basal cell carcinoma.

In another aspect of the invention, a method of diagnosing basal cell carcinoma in an individual, comprising

- (a) analyzing a biological sample from the individual,
- (b) detecting the presence of a DDR2 protein having a mutation selected from the group consisting N146K, R399Q, and S702F in the sample, and
- (c) diagnosing the individual as having basal cell carcinoma when the mutation is detected, thereby indicating that the individual has basal cell carcinoma.

The individual may have a skin lesion and/or may be suspected of having a skin disorder such as, for example, skin cancer, or basal cell carcinoma.

Also disclosed are methods for determining likelihood that an individual with melanoma or basal cell carcinoma will respond to treatment with a kinase inhibitor, comprising

- (a) analyzing a biological sample from the individual,
- (b) detecting the presence of a DDR2 mutation that confers sensitivity to a kinase inhibitor in a DDR2 protein or nucleic acid in the sample, and
- (c) identifying the individual as likely to respond to treatment with a kinase inhibitor when one or more of the DDR2 mutations is present, thereby indicating the individual is likely to respond to treatment with a kinase inhibitor.

The DDR2 mutation may be a DDR2 protein mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, and T836A or a nucleic acid encoding a DDR2 protein having a mutation

selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, and T836A. The presence of any of these mutations may be in an individual with advanced stage melanoma.

The method further may comprise detecting the presence of a BRAF mutation such as V600E or V600K in BRAF from the individual.

In some embodiments, the DDR2 mutation is a DDR2 protein mutation selected from the group consisting of N146K, R399Q, and S702F; or a DDR2 nucleotide sequence encoding a DDR2 mutation selected from the group consisting of N146K, R399Q, and S702F. The presence of any of these mutations may be in an individual with basal cell carcinoma.

In one embodiment, the step of analyzing a biological sample comprises sequencing the DDR2 gene for the presence of mutations known to confer sensitivity to DDR2 inhibitors. In some embodiments, the DDR2 nucleic acid sequence is examined for one or more mutations encoding N146K, R399Q, S702F, R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, or T836A in DDR2.

Methods of identifying an individual having melanoma or basal cell carcinoma as a candidate for therapy with a DDR2 inhibitor are also disclosed. In some embodiments, a method of identifying an individual having melanoma or basal cell carcinoma as a candidate for therapy with a DDR2 inhibitor, comprises sequencing the DDR2 gene for the presence of mutations known to confer sensitivity to DDR2 kinase inhibitors. In some embodiments, the DDR2 sequence is examined for a sequence encoding at least one mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q and T836A. In an alternate method, the candidate for therapy with a DDR2 inhibitor is identified by the expression levels of DDR2, wherein low expression levels of DDR2 such as GAPDH-normalized relative DDR2 transcript levels below 0.025 indicate the individual is a candidate for therapy.

The invention comprises a method for treating melanoma or basal cell carcinoma in an individual comprising administering to the individual a therapeutically effective amount of a DDR2 inhibitor. In some embodiments, the melanoma is advanced stage melanoma. Suitable DDR2 inhibitors include kinase inhibitors, siRNA, shRNA, and an antibody that specifically binds to DDR2 or to a DDR2 having at least one mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F,

S674F, R680L, L701F, R742Q, and T836A. In some embodiments, the DDR2 inhibitor is a tyrosine kinase inhibitor that inhibits kinase activity of DDR2. In some embodiments, the kinase inhibitor inhibits tyrosine kinase activity of DDR2 having at least one mutation in the kinase domain. In some embodiments, the kinase inhibitor inhibits tyrosine kinase activity of DDR2 having at least one mutation in the discoidin (DS) domain. In some embodiments, the tyrosine kinase inhibitor inhibits kinase activity of DDR2 having at least one mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, and T836A.

Methods disclosed herein may be used to treat melanoma or basal cell carcinoma in an individual with a DDR2 mutation selected from the group consisting of a mutation in the DDR2 discoidin domain, a mutation in the DDR2 intracellular interacting domain, and a mutation in the DDR2 kinase domain. The DDR2 mutation may be a germline mutation or a somatic cell mutation. In some embodiments the DDR2 mutation is a N146K, R399Q, or S702F mutation. The DDR2 mutation may be encoded by a mutated DDR2 gene.

In relation to therapy, the individual may be examined for mutations in DDR2 protein, comprising sequencing a DDR2 nucleic acid from the individual to determine if the nucleic acid encodes a DDR2 protein with a mutation, and subsequently the likelihood that the individual will respond to therapy with a DDR2 inhibitor. In particular embodiments, the DDR2 sequence of the individual may be determined before the start of treatment or during treatment.

An individual with melanoma or basal cell carcinoma may harbor a mutation in a DDR2 nucleic acid sequence and/or a mutation in a BRAF nucleic acid sequence. The mutation may be in the individual's genomic DNA and/or in RNA. In some embodiments, the methods for treating melanoma or basal cell carcinoma disclosed herein are performed in an individual who does not harbor a mutation in a DDR2 or a BRAF nucleic acid or in an individual carrying a mutated DDR2 and/or BRAF gene or RNA.

In another embodiment, an individual with melanoma or basal cell carcinoma is also treated with a BRAF inhibitor, such as an inhibitor that inhibits activity of BRAF with a mutation at codon 600 (such as a V600E or V600K mutation) or other sensitive BRAF mutations in addition to being treated with a DDR2 inhibitor. Suitable BRAF inhibitors

include BRAF kinase inhibitors such as, for example, vemurafenib, GDC-0879, PLX-4720, sorafenib tosylate, dabrafenib, and LGX818.

Compositions for treating melanoma and/or basal cell carcinoma also are provided. In one embodiment, a composition for the treatment of melanoma or basal cell carcinoma comprises a DDR2 inhibitor alone, or with a BRAF inhibitor. The DDR2 inhibitor may be a kinase inhibitor or one or more inhibitors selected from the group consisting of siRNA directed to a DDR2 nucleic acid, shRNA directed to a DDR2 nucleic acid, and an antibody that specifically binds to a DDR2 polypeptide and inhibits DDR2 kinase activity. In some embodiments, the DDR2 kinase inhibitor inhibits DDR2 having mutations in the kinase domain. In some embodiments, the inhibitor inhibits DDR2 having mutations in the discoidin domain. In some embodiments, the composition comprises a DDR2 kinase inhibitor that inhibits kinase activity of DDR2 having one or more of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q and T836A mutations. The BRAF inhibitor may be, for example, a kinase inhibitor such as vemurafenib, GDC-0879, PLX-4720, sorafenib tosylate, dabrafenib, and LGX818.

The invention also includes kits. For example, a kit for identifying the presence of DDR2 and/or BRAF mutations, the kit comprising at least one primer selected from

Exon3F	TCCAGTTCCAACACCATCTTC
Exon 4F	TTTCTCTTTGGTTTCTCTTGGTC
Exon 5-1F	CCCAACCCTCACCTCTCAAG
Exon 5-2F	CCAGTGGAACCTGATGACCT
Exon 5-3F	CCATGCAGGAGGTCATGG
Exon 6-1F	CACTCATTCTCTTCTCTCTCCTCA
Exon6-2F	CCATTGTAGCCAGATTGTGCC
Exon 7F	CTTGGCTGTGTTTCCTTTGC
exon 8-1F	CTCTTCTCCTGGCCTGAGC
Exon 8-2F	CCCAGACCCATGAATACCAC
Exon 9-1F	TCACATGCCTCTTTCTCTACCA
Exon 9-2F	CAGTGCTACTTCCGCTCTGA
Exon 9-3F	CCCAGTGCTCGGTTTGTC
Exon 10F	GCTCTGACTCACCCCTTGTTTT
Exon 11-1F	CCTTCTCTCCCTGGTCACAG

Exon 11-2F	GGATCCTGATTGGCTGCTT
Exon 12-1F	TCTCCTTGCTCTTCTCTTCCA
Exon 12-2F	ACCGCTCCTCATCACCTAGT
exon 13-1F	CTCGTTGCCCTTGTCTTCC
Exon 13-2F	GAGGGGGTGCCCCACTAT
Exon 13-3F	AGTGCCTGCCGTCACCAT
exon 14-1F	TGATGCTGAGACTAGATGACTTTTG
Exon 14-2F	GGGAATGGAAAAATTCAAAGA
exon 15-1F	TTTATCTATGTCTGTATCCTCCCAAG
Exon 15-2F	CCATCTATTAGCTGTGTGTATCACTG
Exon 16-1F	CCTTCTGTCTTCTTGTCTATTTCTC
Exon 16-2F2	TCTCTTAATTTTGTTACCGAGA
Exon 16-3F2	CTTTGGAATGAGCAGGAACC
Exon 17-1F	TGATTTCCTCTCTTTCTTTACTT
Exon 17-2F	TTTGTGGGAGACTTTCACCTTT
Exon 18-1F	TTTCCTTTATTTTTGTTCCTCAAAG
Exon 18-2F	GCTGCTGGAGAAGAGATACGA
BRAF11-1F	TCTGTTTGGCTTGACTTGACTT
BRAF11-2F	GACGGGACTCGAGTGATGAT
Exon 12-1R	GCGATCGTAAGTCGAGTTGG
Exon 12-2R	CCCACCACATCATCCTCAC
exon 13-1R	TGTGTTGCCTCCTGTCACTC
Exon 13-2R	TGGGGAACCTCTCCACAG
Exon 13-3R	AAGGGAATCAAAGAATCAACTCA
exon 14-1R	GCTCGGAGCATTTTCACA
Exon 14-2R	GGAAAATTCAAATGTAGACCACAG
exon 15-1R	CATGTATTCAGTGATCATAAGAGAGG
Exon 15-2R	AGAAGGAAGACCTGGCTTGTT
Exon 16-1R	TGTGTAGTTCTTACCCACTAAACAGT
Exon 16-2R2	GCCCTGGATCCGGTAATAGT
Exon 16-3R2	CAGGGCTTTAAAATGCTGAGA
Exon 17-1R	TCTGACAGCTGGGAATAGGG
Exon 17-2R	CCATTCATCCCCAACAGTTC
Exon 18-1R	GCAGAAAGGTGGATTCTTGG
Exon 18-2R	AGGACCTGAGCCGTAGGAAC

BRAF11-1R	TCCAATTCTTTGTCCCACTG
BRAF11-2R	TGTCACAATGTCACCACATTACA
BRAF15-1R	GACCCACTCCATCGAGATTT and
BRAF15-2R	TCAGTGGAAAAATAGCCTCAA

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a sequence alignment of the DDR2 protein (top lines) compared with DDR1 (bottom) showing conserved sequence between the two proteins at the sites of DDR2 mutations seen in extracellular-DS domains (amino acids 22-399) and the kinase domain (amino acids 563 to 849) including F574C, S667F, R680L, L701F , R742Q and T836A.

Figure 2 shows a sequence alignment of three mutations in the DDR2 kinase domain, F574C, S667F and L701F, identified by Ion Torrent sequencing of genomic DNA extracted from macrodissected formalin-fixed paraffin-embedded (FFPE) sections of melanomas; middle panels show mutation confirmations by bidirectional Sanger sequencing; bottom panels show alignment of the mutations in the DDR2 kinase domain with the homologous locations in other kinases, including BRAF, EGFR and ALK.

Figure 3 shows DDR2 expressed at low levels in DDR2-mutated melanoma.

Figure 4 shows an S702F kinase domain mutation in basal cell carcinoma.

Figure 5 shows N146K and R399Q biallelic DDR2 mutations in basal cell carcinoma.

DETAILED DESCRIPTION

Definitions

Certain terms employed in this description have the following defined meanings. Terms that are not defined have their art-recognized meanings. That is, unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

As used herein, unless otherwise stated, the singular forms “a,” “an,” and “the” also include the plural. Thus, for example, a reference to “an oligonucleotide” includes a plurality of oligonucleotide molecules, a reference to label is a reference to one or more

labels, a reference to probe is a reference to one or more probes, and a reference to “a nucleic acid” is a reference to one or more polynucleotides.

As used herein, unless indicated otherwise, when referring to a numerical value, the term “about” means plus or minus 10% of the enumerated value.

As used herein, the terms “isolated,” “purified” or “substantially purified” refer to molecules, such as nucleic acid, that are removed from their natural environment, isolated or separated, and are at least 60% free, preferably 75% free, and most preferably 90% free from other components with which they are naturally associated. An isolated molecule is therefore a substantially purified molecule.

A “fragment” in the context of a gene fragment or a chromosome fragment refers to a sequence of nucleotide residues which are at least about 10 nucleotides, at least about 20 nucleotides, at least about 25 nucleotides, at least about 30 nucleotides, at least about 40 nucleotides, at least about 50 nucleotides, at least about 100 nucleotides, at least about 250 nucleotides, at least about 500 nucleotides, at least about 1,000 nucleotides, at least about 2,000 nucleotides.

The terms “identity” and “identical” refer to a degree of identity between sequences. There may be partial identity or complete identity. A partially identical sequence is one that is less than 100% identical to another sequence. Partially identical sequences may have an overall identity of at least 70% or at least 75%, at least 80% or at least 85%, or at least 90% or at least 95%.

The term “detectable label” as used herein refers to a molecule or a compound or a group of molecules or a group of compounds associated with a probe and is used to identify the probe hybridized to a genomic nucleic acid or reference nucleic acid.

As used herein, the term “detecting” refers to observing a signal from a detectable label to indicate the presence of a target. More specifically, detecting is used in the context of detecting a specific sequence.

The term “multiplex PCR” as used herein refers to an assay that provides for simultaneous amplification and detection of two or more products within the same reaction vessel. Each product is primed using a distinct primer pair. A multiplex reaction may further include specific probes for each product that are detectably labeled with different detectable moieties.

The term “nested polymerase chain reaction” is a modification of polymerase chain reaction which, in the present context, is performed to add sequences to an amplicon. Nested polymerase chain reaction involves two sets of primers, used in two successive runs of polymerase chain reaction, the second set intended to amplify the target from the first run product.

As used herein, the term “oligonucleotide” refers to a short polymer composed of deoxyribonucleotides, ribonucleotides, or any combination thereof. Oligonucleotides are generally between about 10, 11, 12, 13, 14, 15, 20, 25, or 30 to about 150 nucleotides (nt) in length, more preferably about 10, 11, 12, 13, 14, 15, 20, 25, or 30 to about 70 nt

As used herein, the term “subject” or “individual” refers to a mammal, such as a human, but can also be another animal such as a domestic animal (*e.g.*, a dog, cat, or the like), a farm animal (*e.g.*, a cow, a sheep, a pig, a horse, or the like) or a laboratory animal (*e.g.*, a monkey, a rat, a mouse, a rabbit, a guinea pig, or the like).

The terms “complement,” “complementary” or “complementarity” as used herein with reference to polynucleotides (*i.e.*, a sequence of nucleotides such as an oligonucleotide or a genomic nucleic acid) related by the base-pairing rules. The complement of a nucleic acid sequence as used herein refers to an oligonucleotide which, when aligned with the nucleic acid sequence such that the 5' end of one sequence is paired with the 3' end of the other, is in “antiparallel association.” For example, for the sequence 5'-A-G-T-3' is complementary to the sequence 3'-T-C-A-5'. Certain bases not commonly found in natural nucleic acids may be included in the nucleic acids of the present invention and include, for example, inosine and 7-deazaguanine. Complementarity need not be perfect; stable duplexes may contain mismatched base pairs or unmatched bases. Those skilled in the art of nucleic acid technology can determine duplex stability empirically considering a number of variables including, for example, the length of the oligonucleotide, base composition and sequence of the oligonucleotide, ionic strength and incidence of mismatched base pairs. Complementarity may be “partial” in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be “complete,” “total,” or “full” complementarity between the nucleic acids.

“Detecting” a mutation in a gene or protein may be accomplished by performing an appropriate assay. To detect a mutation in a gene or protein in a biological sample, the biological sample is assayed to determine the presence or absence of the mutated

gene or mutated protein. The assay may include extracting nucleic acid (such as, for example, total genomic DNA and/or RNA) from the sample and analyzing the extracted nucleic acid by methods known in the art. An assay may involve isolating protein from the biological sample and analyzing the protein. However, an assay need not involve either extraction of nucleic acid or isolation of protein. That is, some assays may be employed that directly analyze a biological sample without extracting or isolating nucleic acid or protein.

Methods of Diagnosis

In one embodiment, a method for diagnosing melanoma in an individual is described, comprising (a) analyzing a biological sample from the individual, (b) detecting the presence of a DDR2 protein having a mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, and T836A or a nucleic acid encoding such a DDR2 protein in the sample, and (c) diagnosing the individual as having melanoma when the mutation is detected, thereby indicating that the individual has melanoma. The melanoma may be a particular subset of melanoma. In some embodiments, the method is for diagnosing advanced stage melanoma.

Methods for diagnosing basal cell carcinoma in an individual are also disclosed. A method for diagnosing basal cell carcinoma in an individual, comprises (a) analyzing a biological sample from the individual, (b) detecting the presence of a DDR2 protein having a mutation selected from the group consisting of N146K, R399Q, and S702F, or a DDR2 nucleic acid that encodes the mutated DDR2 protein in the sample, and (c) identifying the individual as having basal cell carcinoma when the mutation is present, thereby indicating the individual has basal cell carcinoma.

The nucleic acid may be DNA and/or RNA.

Methods of diagnosis may be performed in an individual with a skin lesion. A "skin lesion" is an area of variation in skin color and/or texture. Alternatively or in addition, the individual may be suspected of having a skin disorder such as, for example, skin cancer, melanoma or basal cell carcinoma.

Methods of Screening/Predicting Response to Treatment

Another aspect of the present invention provides a method for determining likelihood of responding to treatment with a kinase inhibitor in an individual with melanoma or basal cell carcinoma, comprising: (a) analyzing a biological sample from the individual to detect the presence of a DDR2 mutation that confers sensitivity to a kinase inhibitor, and (b)

identifying the individual as likely to respond to treatment with a kinase inhibitor when one or more DDR2 mutations is present, thereby indicating the individual is likely to respond to treatment with a kinase inhibitor. In some embodiments, the DDR2 mutation is an amino acid mutation in a DDR2 protein selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q and T836A. In other embodiments, the DDR2 mutation is a nucleic acid sequence encoding a DDR2 protein having a mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, and T836A.

In some embodiments the DDR2 mutation is a DDR2 protein mutation selected from the group consisting of N146K, R399Q, and S702F. In some embodiments the DDR2 mutation is a DDR2 nucleic acid sequence encoding a DDR2 mutation selected from the group consisting of N146K, R399Q, and S702F.

The method further may comprise detecting the presence of a V600E or V600K mutation in BRAF from the individual. The individual may have advanced stage melanoma.

Yet another aspect of the present invention discloses a method for stratifying early and late stage melanoma, comprising (a) analyzing a biological sample from an individual with melanoma or suspected of having melanoma, (b) detecting the presence of a DDR2 mutation, such as R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q or T836A in the sample, and (c) identifying the melanoma as later stage when the DDR2 mutation is detected. The presence of these mutations is indicative of later stage melanoma given their absence in primary cutaneous melanomas and their presence in secondary cutaneous nodules or metastatic lesions which have adverse prognosis (Balch CM et al. Prognostic Factors Analysis of 17,600 Melanoma Patients: Validation of the American Joint Committee on Cancer Melanoma Staging System. JCO August 15, 2001 vol. 19 no. 16 3622-3634, Balch CM et al. Final Version of 2009 AJCC Melanoma Staging and Classification. JCO December 20, 2009 vol. 27 no. 36 6199-6206).

In one aspect of the present invention, an individual is identified as likely to respond to therapy with a DDR2 inhibitor such as, for example, a DDR2 kinase inhibitor, when GAPDH-normalized relative DDR2 transcript levels in a biological sample from the individual are below 0.025.

The term “biological sample” as used herein refers to a sample containing a nucleic acid of interest. A biological sample may comprise a clinical sample (*i.e.*, obtained directly from a patient) or isolated nucleic acids and may be cellular or acellular fluids and/or tissue (*e.g.*, biopsy) samples. In some embodiments, a sample is obtained from a tissue or bodily fluid collected from a subject. Sample sources include, but are not limited to, sputum (processed or unprocessed), bronchial alveolar lavage (BAL), bronchial wash (BW), whole blood or isolated blood cells of any type (*e.g.*, lymphocytes), bodily fluids, cerebrospinal fluid (CSF), urine, plasma, serum, or tissue (*e.g.*, biopsy material). Methods of obtaining test samples and reference samples are well known to those of skill in the art and include, but are not limited to, aspirations, tissue sections, drawing of blood or other fluids, surgical or needle biopsies, collection of paraffin embedded tissue, collection of body fluids, collection of stool, and the like. In the present context the biological sample preferably is blood, serum or plasma. The term “patient sample” as used herein refers to a sample obtained from a human seeking diagnosis and/or treatment of a disease, especially prostate disease.

To detect the presence of a DDR2 or BRAF mutation, nucleic acid samples or target nucleic acids may be amplified and sequenced by various methods known to the skilled artisan including Sanger sequencing and so-called Next Generation Sequencing (NGS). Next-generation sequencing lowers the costs and greatly increases the speed over the industry standard dye-terminator methods. Examples of NGS include

- (a) Massively Parallel Signature Sequencing (MPSS)
- (b) Polony sequencing combined an in vitro paired-tag library with emulsion PCR
- (c) 454 pyrosequencing
- (d) Solexa sequencing
- (e) SOLiD technology
- (f) DNA nanoball
- (g) Heliscope single molecule
- (h) Single molecule real time (SMRT) and
- (i) Ion semiconductor sequencing

Ion semiconductor sequencing couples standard sequencing chemistry with a novel, semiconductor based detection system that detects hydrogen ions that are released during the polymerization of DNA, as opposed to the optical methods used in other sequencing systems. A microwell containing a template DNA strand to be sequenced is flooded with a single type of nucleotide. If the introduced nucleotide is complementary to the

leading template nucleotide it is incorporated into the growing complementary strand. This causes the release of a hydrogen ion that triggers a hypersensitive ion sensor, which indicates that a reaction has occurred. If homopolymer repeats are present in the template sequence multiple nucleotides will be incorporated in a single cycle. This leads to a corresponding number of released hydrogens and a proportionally higher electronic signal.

The terms “amplification” or “amplify” as used herein includes methods for copying a target nucleic acid, thereby increasing the number of copies of a selected nucleic acid sequence. Amplification may be exponential or linear. A target nucleic acid may be either DNA or RNA. The sequences amplified in this manner form an “amplification product,” also known as an “amplicon.” While the exemplary methods described hereinafter relate to amplification using the polymerase chain reaction (PCR), numerous other methods are known in the art for amplification of nucleic acids (*e.g.*, isothermal methods, rolling circle methods, etc.). The skilled artisan will understand that these other methods may be used either in place of, or together with, PCR methods. *See, e.g.*, Saiki, “Amplification of Genomic DNA” in *PCR Protocols*, Innis *et al.*, Eds., Academic Press, San Diego, CA 1990, pp. 13-20; Wharam *et al.*, *Nucleic Acids Res.*, 29(11):E54-E54, 2001; Hafner *et al.*, *Biotechniques*, 30(4):852-56, 858, 860, 2001; Zhong *et al.*, *Biotechniques*, 30(4):852-6, 858, 860, 2001.

A key feature of PCR is “thermocycling” which, in the present context, comprises repeated cycling through at least three different temperatures: (1) melting/denaturation, typically at 95°C (2) annealing of a primer to the target DNA at a temperature determined by the melting point (T_m) of the region of homology between the primer and the target and (3) extension at a temperature dependent on the polymerase, most commonly 72°C. These three temperatures are then repeated numerous times. Thermocycling protocols typically also include a first period of extended denaturation, and end on an extended period of extension.

The T_m of a primer varies according to the length, G+C content, and the buffer conditions, among other factors. As used herein, T_m refers to that in the buffer used for the reaction of interest.

An oligonucleotide (*e.g.*, a probe or a primer) that is specific for a target nucleic acid will “hybridize” to the target nucleic acid under suitable conditions. As used herein, “hybridization” or “hybridizing” refers to the process by which an oligonucleotide

single strand anneals with a complementary strand through base pairing under defined hybridization conditions. It is a specific, *i.e.*, non-random, interaction between two complementary polynucleotides. Hybridization and the strength of hybridization (*i.e.*, the strength of the association between the nucleic acids) is influenced by such factors as the degree of complementarity between the nucleic acids, stringency of the conditions involved, and the T_m of the formed hybrid.

Methods of Treatment

In one aspect of the invention, a method of treating melanoma or basal cell carcinoma in an individual comprises administering to the individual a therapeutically effective amount of a DDR2 inhibitor. A “DDR2 inhibitor” is a compound that inhibits DDR2 function (including DDR2 kinase activity) and includes kinase inhibitors that inhibit DDR2 kinase activity as well as siRNA specific for DDR2 nucleic acid, shRNA specific for DDR2 nucleic acid and an antibody that binds to DDR2 and inhibits associated DDR2 kinase activity.

An “antibody” includes a polyclonal antibody, a monoclonal antibody, an antigen-binding fragments thereof such as F(ab').sub.2 and an Fab fragments, and a single chain antibody.

As used herein, a “kinase inhibitor” is a composition that inhibits kinase activity of a protein kinase. A “tyrosine kinase inhibitor” is a composition that inhibits tyrosine kinase activity of a protein tyrosine kinase, and a “serine/threonine kinase inhibitor” is a compound that inhibits serine/threonine kinase activity of a protein serine/threonine kinase. Exemplary kinase inhibitors include imatinib, nilotinib, dasatinib, GDC-0879, PLX-4720, sorafenib, tosylate, dabrafenib, vemurafenib and LGX818. Imatinib mesylate (also known as STI571 or 2-phenylaminopyrimidine or “imatinib” for short; marketed as a drug under the trade name “Gleevec” or “Glivec”) is an ATP competitive inhibitor of tyrosine kinase activity. Other kinase inhibitor drugs include bosutinib (SKI-606) and the aurora kinase inhibitor VX-680.

A “DDR2 kinase inhibitor” is a compound that inhibits DDR2 kinase activity, including kinase activity of a DDR2 having at least one mutation selected from the group consisting of R105C, P321L, R458H, S467F, P476S, I488S, F574C, S667F, S674F, R680L, L701F, R742Q, T836A, N146K, R399Q, and S702F. A DDR2 kinase inhibitor may inhibit activity of a DDR2 protein directly, or it may act upstream by inhibiting DDR2

nucleic acid (e.g., by inhibiting transcription or translation). Exemplary DDR2 kinase inhibitors include imatinib, nilotinib and dasatinib.

In one embodiment of this aspect of the invention, the method comprises administering to the individual a therapeutically effective amount of a BRAF inhibitor, in addition to the DDR2 inhibitor. A "BRAF inhibitor" is any compound that inhibits BRAF function (including BRAF kinase activity) and includes kinase inhibitors that inhibit BRAF kinase activity as well as siRNA specific for BRAF nucleic acid, shRNA specific for BRAF nucleic acid and antibodies that bind to BRAF and inhibit associated BRAF kinase activity. The BRAF inhibitor may be a serine/threonine kinase inhibitor. A "BRAF kinase inhibitor" is a compound that inhibits BRAF kinase activity. Exemplary BRAF kinase inhibitors include GDC-0879, PLX-4720, sorafenib, vemurafenib, tosylate, dabrafenib, and LGX818

Routes and frequency of administration of the therapeutic agents disclosed herein, as well as dosage, will vary from individual to individual as well as with the selected drug, and may be readily established using standard techniques. In general, the pharmaceutical compositions may be administered, by injection (e.g., intracutaneous, intratumoral, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. In a particular embodiment, the pharmaceutical composition is administered orally. In one example, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster treatments may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. In one embodiment, 2 intradermal injections of the composition are administered 10 days apart.

A "solid oral dosage form," "oral dosage form," "unit dose form," "dosage form for oral administration," and the like are used interchangeably, and refer to a pharmaceutical composition in the form of a tablet, capsule, caplet, gelcap, geltab, pill and the like.

Dosage forms typically include an "excipient," which as used herein, is any component of an dosage form that is not an API. Excipients include binders, lubricants, diluents, disintegrants, coatings, barrier layer components, glidants, and other components. Excipients are known in the art (see HANDBOOK OF PHARMACEUTICAL EXCIPIENTS, FIFTH EDITION, 2005, edited by Rowe et al., McGraw Hill). Some excipients serve multiple functions or are so-called high functionality excipients. For example, talc may act as

a lubricant, and an anti-adherent, and a glidant. See Pifferi et al., 2005, "Quality and functionality of excipients" *Farmaco*. 54:1-14; and Zeleznik and Renak, Business Briefing: Pharmagenics 2004.

A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-cancer immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored using conventional methods. In general, for pharmaceutical compositions, the amount of each drug present in a dose ranges from about 100 µg to 5 mg per kg of host, but those skilled in the art will appreciate that specific doses depend on the drug to be administered and are not necessarily limited to this general range. Likewise, suitable volumes for each administration will vary with the size of the patient.

In the context of treatment, a "therapeutically effective amount" of a drug is an amount of or its pharmaceutically acceptable salt which eliminates, alleviates, or provides relief of the symptoms for which it is administered. The disclosed compositions are administered in any suitable manner, often with pharmaceutically acceptable carriers. Suitable methods of administering treatment in the context of the present invention to a subject are available, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route. The dose administered to a patient, in the context of the present invention, should be sufficient to effect a beneficial therapeutic response in the patient over time, or to inhibit disease progression. Thus, the composition is administered to a subject in an amount sufficient to elicit an effective response and/or to alleviate, reduce, cure or at least partially arrest symptoms and/or complications from the disease. An amount adequate to accomplish this is defined as a "therapeutically effective dose."

In general, an appropriate dosage and treatment regimen involves administration of the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients.

In some embodiment, IC₅₀ for inhibition of wild-type DDR2 kinase activity is in the range of 600 nM for imatinib, 50 nM for nilotinib and 1.5 nM for dasatinib (Day E, et al. Inhibition of collagen-induced discoidin domain receptor 1 and 2 activation by imatinib,

nilotinib and dasatinib. Molec Cell Pharm 2008;599:44-53), which are below the achievable plasma trough concentrations of the drugs in their current daily oral dosing (4 uM, 2 uM and 100nM respectively, see Braden et al. Blood 2006;108:2332-2338).

The DDR2 inhibitor and BRAF inhibitor, if both administered, can be administered sequentially or concurrently, and may be formulated separately or as a single composition.

Kits

In one embodiment of the invention, a kit may be used for conducting the diagnostic and prognostic methods described herein. Typically, the kit should contain, in a carrier or compartmentalized container, reagents useful in any of the above-described embodiments of the diagnostic method. The carrier can be a container or support, in the form of, e.g., bag, box, tube, rack, and is optionally compartmentalized. The carrier may define an enclosed confinement for safety purposes during shipment and storage. A kit as disclosed herein may contain printed or electronic instructions for performing an assay that employs the reagents contained in the kit. In one embodiment, the kit includes one or more PCR primers capable of amplifying and sequencing. Relevant primers include

Exon3F	TCCAGTTCCAACACCATCTTC
Exon 4F	TTTCTCTTTGGTTCTCTTGGTC
Exon 5-1F	CCCAACCCTCACCTCTCAAG
Exon 5-2F	CCAGTGGAACTGATGACCT
Exon 5-3F	CCATGCAGGAGGTCATGG
Exon 6-1F	CACTCATTCTCTTCTCTCTCCTCA
Exon6-2F	CCATTGTAGCCAGATTTGTCC
Exon 7F	CTTGGCTGTGTTTCCTTTGC
exon 8-1F	CTCTTCTCCTGGCCTGAGC
Exon 8-2F	CCCAGACCCATGAATACCAC
Exon 9-1F	TCACATGCCTCTTTCTCTACCA
Exon 9-2F	CAGTGCTACTTCCGCTCTGA
Exon 9-3F	CCCAGTGCTCGGTTTGTC
Exon 10F	GCTCTGACTCACCTTGTTTT
Exon 11-1F	CCTTCTCTCCCTGGTCACAG
Exon 11-2F	GGATCCTGATTGGCTGCTT
Exon 12-1F	TCTCCTTGCTCTTCTCTTCCA

Exon 12-2F	ACCGCTCCTCATCACCTAGT
exon 13-1F	CTCGTTGCCCTTGTCTTCC
Exon 13-2F	GAGGGGGTGCCCCACTAT
Exon 13-3F	AGTGCCTGCCGTCACCAT
exon 14-1F	TGATGCTGAGACTAGATGACTTTTG
Exon14-2F	GGAATGGAAAAATTCAAAGA
exon 15-1F	TTTATCTATGTCTGTATCCTCCCAAG
Exon 15-2F	CCATCTATTAGCTGTGTGTATCACTG
Exon 16-1F	CCTTCTGTCTTCTTGTCTATTTCTC
Exon 16-2F2	TCTCTTAATTTTGTTCACCGAGA
Exon 16-3F2	CTTTGGAATGAGCAGGAACC
Exon 17-1F	TGATTCCCATTCCTTTCTTTACTT
Exon 17-2F	TTTGTGGGAGACTTTCACCTTT
Exon 18-1F	TTTCCTTTATTTTGTTCCTCAAAG
Exon 18-2F	GCTGCTGGAGAAGAGATACGA
BRAF11-1F	TCTGTTTGGCTTGACTTGACTT
BRAF11-2F	GACGGGACTCGAGTGATGAT
Exon 12-1R	GCGATCGTAAGTCGAGTTGG
Exon 12-2R	CCCACCACATCATCCTCAC
exon 13-1R	TGTGTTGCCTCCTGTCACCTC
Exon 13-2R	TGGGGAACCTCCTCCACAG
Exon 13-3R	AAGGGAATCAAAGAATCAACTCA
exon 14-1R	GCTCGGAGCATTTTCACA
Exon14-2R	GGAAAATTCAAATGTAGACCACAG
exon 15-1R	CATGTATTCACTGATCATAACAGAGAGG
Exon 15-2R	AGAAGGAAGACCTGGCTTGTT
Exon 16-1R	TGTGTAGTTCTTACCCACTAAACAGT
Exon 16-2R2	GCCCTGGATCCGGTAATAGT
Exon 16-3R2	CAGGGCTTTAAATGCTGAGA
Exon 17-1R	TCTGACAGCTGGGAATAGGG
Exon 17-2R	CCATTCATCCCCAACAGTTC
Exon 18-1R	GCAGAAGGTGGATTTCTTGG
Exon 18-2R	AGGACCTGAGCCGTAGGAAC
BRAF11-1R	TCCAATTCTTTGTCCCACTG
BRAF11-2R	TGTCACAATGTACCACATTACA

BRAF15-1R	GACCCACTCCATCGAGATT
BRAF15-2R	TCAGTGGAAAAATAGCCTCAA

As used herein, a “primer” is an oligonucleotide that is complementary to a target nucleotide sequence and leads to addition of nucleotides to the 3’ end of the primer in the presence of a DNA or RNA polymerase. The 3’ nucleotide of the primer should generally be identical to the target sequence at a corresponding nucleotide position for optimal extension and/or amplification. The term “primer” includes all forms of primers that may be synthesized including peptide nucleic acid primers, locked nucleic acid primers, phosphorothioate modified primers, labeled primers, and the like. As used herein, a “forward primer” is a primer that is complementary to the anti-sense strand of DNA. A “reverse primer” is complementary to the sense-strand of DNA.

The kit may also include suitable buffers, reagents for isolating nucleic acid, and instructions for use. Kits may also include a microarray for measuring miRNA level.

The primers may be labeled with a detectable marker such as radioactive isotopes, or fluorescence markers. Instructions for using the kit or reagents contained therein are also included in the kit.

EXAMPLES

Example 1: Identification of novel DDR2 mutations in cancer

The following test was conducted, which reports a DETECTED/NOT DETECTED result for any mutation or indels found in the sixteen coding DDR2 exons and in BRAF exons 11 and 15, which are the sites of >99% of the known activating BRAF mutations in identified in melanoma.

Total nucleic acid was extracted from paraffin-embedded tissues in block forms or affixed to slides. For one detection method, thirty six pairs of primers were designed to amplify full coding DDR2 sequences and BRAF exon 11/15 which are located at chromosome 1 and 7 in a microfluidic device, 48.48 Access Array chip. All amplicons from each sample were harvested on the Access Array chip. The pooled amplicons were end-repaired and a unique barcoded A adaptor and a P1 adaptor were ligated onto both ends of amplicons for each sample. The resulting DNA amplicons were the “DNA sequencing library” with a unique barcode sequence for each sample. 12~16 DNA libraries were mixed

equally to make a 300 million DNA fragment pool. The emulsion PCR was performed by mixing 1 ml of PCR reaction mixture containing the library pool and Ion Sphere Particle (ISP) and 9 ml of oil. The ISP beads were recovered from emulsion PCR and the template-positive ISPs were enriched, the ISPs were loaded on to a chip for semiconductor sequencing analysis. Sequencing raw data were transferred to the Ion Torrent and processed into next-generation standard sequence formats. The sequence data were aligned and analyzed by Ion Suite Software, SeqNext or NEXTEGen software using GenBank accession number NM_006182 as reference. This semi-quantitative test reports a DETECTED/NOT DETECTED result for any mutation or indels found in the sixteen coding DDR2 exons and in BRAF exons 11 and 15, which are the sites of >99% of the known activating BRAF mutations identified in melanoma.

Table 1

Controls Used

Controls	Supplier and Catalog Number
No Primer control in Access Array PCR	
<i>DDR2</i> and BRAF positive heterozygous control serving as a PCR and Ion sequencing control	Previously tested <i>DDR2</i> and BRAF heterozygous patient samples if available. The Samples may also serve as an unmutated (negative) control in the other remaining exons.
<i>DDR2</i> I638F positive heterozygous control serving as a PCR and Ion sequencing control	ATCC cell line (NCI-H2286) with a known I638F mutation in exon 15. The DNA may also serve as an unmutated (negative) control for the other exons.
<i>DDR2</i> L239R and P815I positive heterozygous control serving as a PCR and Ion sequencing control	DSMZ cell line (HCC366) with a known L239R mutation in exon 8 and a novel P815I mutation in exon 18. The DNA may also serve as an unmutated (negative) control for the other exons.
<i>BRAF</i> V600E positive homozygous control a PCR and Ion sequencing control.	ATCC cell line (A375) with a known V600E mutation on exon 15. The DNA may also serve as an unmutated (negative) control for the other exons.

Example 2

Somatic mutations in *DDR2* were identified in melanomas that contained a BRAF V600 mutation. All mutations were detected by Ion Torrent advanced sequencing and then confirmed by bidirectional Sanger sequencing.

Table 2. Novel DDR2 Somatic Mutations Identified in Melanoma.

DDR2 Mutation Site	Domain location in DDR2	Conserved residue between DDR kinases	Biopsy Site	Lesion type	BRAF status
R105C	Extracellular DS, collagen-binding	Yes	Skin, thigh	2° nodule	BRAF V600E
P321L	Extracellular DS, collagen-binding	No	Skin, scalp	2° nodule	BRAF V600E BRAF G466V
I488S	Cytoplasmic	No	Breast	2° nodule	BRAF V600K
F574C	Kinase	Yes	Skin, abdomen	2° nodule	BRAF V600E
S667F	Kinase	Yes	Lymph node	EC Met	BRAF V600K
L701F	Kinase	Yes	Breast	2° nodule	BRAF V600E
DDR2 mutation arising in melanomas without BRAF exon 11 or 15 mutations					
S467F	Cytoplasmic	No	Skin, left wrist	nodule	None
P476S	Cytoplasmic	No	Skin, mid-chest	2° nodule	None
S674F	Kinase	Yes	Lung	EC Met	None
R680L	Kinase	No	Soft tissue, neck	2° nodule	None
R742Q	Kinase	Yes	Skin, thigh	nodule	None
T836A	Kinase	Yes	Lung	EC Met	None

Novel DDR2 mutations at conserved residues within DDR2 include R105C, P321L, R458H, F574C, S667F and L701F were identified in human malignant melanoma. Approximately 50% of the DDR2 mutations in melanoma were associated with concurrent mutations of the BRAF serine/threonine kinase at codon 600. Based on the mutation levels, DDR2 and BRAF mutations are predicted to be present in most, if not all, of the tumor cells.

These findings suggest that dysregulation by a DDR2 mutation plays a role in melanoma progression because, unlike BRAF mutations, we have not found DDR2 mutations in nevi. This finding is interesting in light of a previous study, which demonstrates that DDR2 downregulation in a melanoma cell line can modulate its metastatic potential (Oncol Rep 2011 Oct;26(4):971-8) and mediate cell cycle arrest and the adhesion phenotype of primary tumor cells (Frontiers in Bioscience 10, 2922-2931, September 1, 2005). This

finding may also be useful for distinguishing melanoma from nevi, which can be difficult to distinguish both clinically and histologically.

DDR2 mutations provide a targetable genetic feature in a group of melanomas for tyrosine kinase inhibitors such as imatinib, dasatinib and nilotinib. IC₅₀ for inhibition of wild-type DDR2 kinase activity is in the range of 600 nM for imatinib, 50 nM for nilotinib and 1.5 nM for dasatinib (Day E, et al. Inhibition of collagen-induced discoidin domain receptor 1 and 2 activation by imatinib, nilotinib and dasatinib. *Molec Cell Pharm* 2008;599:44-53), which are below the achievable plasma trough concentrations of the drugs in their current daily oral dosing (4 uM, 2 uM and 100nM respectively, see Bradcen et al. *Blood* 2006;108:2332-2338).

Therefore, melanoma may be treated by targeting DDR2 kinase activity along with targeting BRAF kinase activity. This discovery therefore opens up an additional therapeutic option for patients with melanoma.

Example 3

Genomic DNA extracted from FFPE blocks or tissue sections in routine clinical tumor samples can be sequenced by standard PCR-based dideoxy chain termination sequencing ("Sanger" method). Relevant primers include:

Table 3. DDR2 PCR/ Sequencing Primers

DR3F	Tgt aaa acg acg gcc agt TGAGAATTGTACTCATTCATGTTGG
DR3R	cag gaa aca gct atg acc GTAGTCCCTCTTGGCAGCTT
DR4F	Tgt aaa acg acg gcc agt TCTTATTCCTTGTTCAATATTCAGTG
DR4R	cag gaa aca gct atg acc CCCCTAGGGTCAGGAATCTG
DR5F	Tgt aaa acg acg gcc agt CAGCTGCTTGCCTGTGAAC
DR5R	cag gaa aca gct atg acc CACACAGAAAACCTGTACCCTTC
DR6F	Tgt aaa acg acg gcc agt GTGGTGGGGTGAAGAAAAGT
DR6R	cag gaa aca gct atg acc TCCCTTTCTGATTTGATTGC
DR7F	Tgt aaa acg acg gcc agt CGCTGTGCAAGCTTATACCC
DR7R	cag gaa aca gct atg acc TTGATTGATTATTGATCCCAAGA

DR8F	Tgt aaa acg acg gcc agt GAGTGAAGATGCCGGGTAAA
DR8R	cag gaa aca gct atg acc TGAAGTGGCATCAGCCTAGA
DR9F	Tgt aaa acg acg gcc agt TACTGAGTTGGCTGGCACTG
DR9R	cag gaa aca gct atg acc TGAGAAGTTCTGGGCATGTG
DR10F	Tgt aaa acg acg gcc agt TCACTAAATTGATCTTGTAATGTGC
DR10R	cag gaa aca gct atg acc CCAGGGCTACTCTTCATCCA
DR11F	Tgt aaa acg acg gcc agt AGGAACAGGGTCTACCTCCA
DR11R	cag gaa aca gct atg acc AAATGTTTGCAATTTGCCTTTT
DR12F	Tgt aaa acg acg gcc agt TGGGAGAGCTGAGTTTAAGAAGA
DR12R	cag gaa aca gct atg acc GCAGAGACTAAAAATAGATGCAATGA
DR13F	Tgt aaa acg acg gcc agt GCCCTCCTCTCAGAGTTCCT
DR13R	cag gaa aca gct atg acc GTGAATCCACCTCTGGAAGG
DR14F	Tgt aaa acg acg gcc agt GGAAATGCCCAGCAAGAGTA
DR14R	cag gaa aca gct atg acc GCTCACTGACCTTCCCATCT
DR15F	Tgt aaa acg acg gcc agt ATAGGCCTTGGTGTGCATTC
DR15R	cag gaa aca gct atg acc ACTGACTTCCCCCACCATC
DR16F	Tgt aaa acg acg gcc agt GAATGTTGAGCTTTCAACCCTA
DR16R	cag gaa aca gct atg acc AGCCCACAAGCCAGTTGTTA
DR17F	Tgt aaa acg acg gcc agt AGAATTCCTTGCCTGTGGTG
DR17R	cag gaa aca gct atg acc AGTGACAAAGACTAACACCTGGA
DR18F	Tgt aaa acg acg gcc agt CAAATCAAACCATGATGCAAA
DR18R	cag gaa aca gct atg acc TGTCCAGATGGAGTGGCATA
M13-F	Tgt aaa acg acg gcc agt
M13-R	cag gaa aca gct atg acc
M13-F and M13-R are sequencing primers 100µM (for PCR reaction): For X mmol of the dry primer (provided by manufacturer), add 10 X µl of nuclease free distilled water.	

Example 4

To assess whether DDR2 is mutated or dysregulated in melanoma, we screened DNA extracted from a variety of different melanocytic lesions, focusing particularly on high-stage melanomas that would be candidates for kinase inhibitor therapy.

Mutations in the DDR2 kinase domain, F574C, S667F and L701F, were identified by Ion Torrent sequencing of genomic DNA extracted from macrodissected FFPE sections of primary melanomas. Normalized for pathologist estimates of tumor percentages in the macrodissected areas, all mutations were predicted to be present at heterozygous levels (percentages indicate unnormalized reads of mutant sequence compared to wild-type). Mutations were confirmed by bidirectional Sanger sequencing.

Ion sequencing was performed on the PGM platform on a 316 chip and the 200 base pair sequencing chemistry; emulsion PCR was performed on the OneTouch ES or 2 (all Life Technologies). To produce the library, singleplex PCR was performed on the Access Array system (Fluidigm, South San Francisco, CA) using custom-designed primers for 48 amplicons covering the entire coding region of *DDR2* and exons 11 and 15 of *BRAF*. Sequence analysis was performed on SequencePilot software (JSI Medical Systems, Costa Mesa, CA). Sanger sequencing was performed on a 3700 Genetic Analyzer, following standard PCR, cleanup and cycle sequencing methods using Big Dye v.3.1 reagents (Applied Biosystems, Foster City, CA).

Using a DNA-based Ion Torrent™ (Life Technologies, South San Francisco, CA) sequencing assay to assess the entire coding region of *DDR2* as well as exons 11 and 15 of *BRAF*, with confirmation by the Sanger sequencing method, we identified *DDR2* missense point mutations in 12/269 (4.5%) cases of melanoma. The mutation frequency did not differ markedly by BRAF V600 mutation status in that *DDR2* mutations were detected in 6/140 *BRAF*-mutated cases (V600E in 4, V600K in 2) and 7/129 without *BRAF* mutations. All but one of the *DDR2*-mutated melanomas were advanced stage: 3 were detected in extracutaneous metastases, and 7 in secondary skin or subcutaneous nodules, with no *DDR2* mutations identified in 31 early stage primary cutaneous melanomas screened. Also, no *DDR2* mutations were identified in 29 benign nevi, including blue nevi, typical dermal and compound nevi and dysplastic nevi.

In five cases, *DDR2* mutations involved highly evolutionarily conserved residues in the kinase domain (e.g., F574C, S667F, and L701F shown in **Figure 2**) suggesting hypofunctional effects on *DDR2* kinase activity. Mutations in the four other cases

were R458H, S467F, P476S and I488S, all located in the DDR2-specific region of the cytoplasmic domain. The clustering of mutations at highly conserved kinase domain residues in melanoma was different from previous findings in lung carcinomas, where mutations were more widely scattered and involved the discoidin and cytoplasmic domains and less conserved areas of the kinase domains.

DDR2 transcript levels were assessed from total RNA extracted from FFPE sections of macrodissected human melanoma samples, using one-step reverse transcription/cDNA synthesis and real-time PCR with Gene Expression assay primer/probe sets for the *DDR1*, *DDR2* and *GAPDH* genes on the 7500 detection system (all Applied Biosystems). DDR2 transcript levels were normalized to GAPDH transcripts using the delta Ct method. Samples include advanced stage melanomas with *DDR2* mutation (n = 5), without *DDR2* or *BRAF* V600 mutation (wt, n = 17), and with *BRAF* V600 mutation but without *DDR2* mutation (n = 20).

Using reverse-transcription PCR on macrodissected FFPE melanoma samples, we noted that DDR2 was underexpressed in 4 of the 5 *DDR2*-mutated melanomas with available material as compared to only a small minority of advanced stage *DDR2/BRAF*-unmutated melanomas or *BRAF* V600-mutated cases that lacked *DDR2* mutations (**Figure 3**). *DDR2* mutations were seen in 4/10 cases with relative DDR2/GAPDH transcript levels below 0.025 compared to 1/32 cases with ratios above 0.025 (p = .008). *DDR1* transcript levels were more variable in the melanoma samples but also low in the *DDR2*-mutated subgroup (data not shown). This suggests that DDR2 expression can be used as a screening tool for *DDR2* mutations.

Downregulation of DDR2 has also been noted in lung carcinoma, with upregulation observed in some other tumor types. In the *DDR2*-mutated melanomas identified here, decreased DDR2 activity could be produced by a combination of inactivating or hypofunctional mutations in one allele and transcriptional downregulation of the other allele.

DDR2 kinase domain mutations occur in a subset of *BRAF*-mutated advanced-stage melanomas and likely produce hypofunctional kinases based on the codons affected. In many cases, the *DDR2*-mutated overlaps with the *BRAF*-mutated group of typical sun-exposed melanomas but, unlike *BRAF*, *DDR2* mutations have not yet been observed in nevi.

Example 5

Somatic DDR2 mutations were identified in basal cell carcinoma, including in the discoidin domain (N146K), the intracellular interacting domain (R399Q) and the kinase domain (S702F). See Figures 4 and 5. The frequency of DDR2 mutations in a small sampling of basal cell carcinomas was 32%.

It should be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification, improvement and variation of the inventions embodied therein herein disclosed may be resorted to by those skilled in the art, and that such modifications, improvements and variations are considered to be within the scope of this invention. The materials, methods, and examples provided here are representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention.

The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group.

In case of conflict, the present specification, including definitions, will control over references referred to herein.

The inventions illustratively described herein may suitably be practiced in the absence of any element or elements, limitation or limitations, not specifically disclosed herein. Thus, for example, the terms "comprising," "including," "containing," etc. shall be read expansively and without limitation. Additionally, the terms and expressions employed herein have been used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

Other embodiments are set forth within the following claims.

We Claim:

1. A method of diagnosing basal cell carcinoma (BCC) in an individual, comprising:
 - (a) analyzing a biological sample from the individual,
 - (b) detecting the presence of a nucleic acid encoding a discoidin domain receptor 2 (DDR2) protein having a mutation of N146K, R399Q, or S702F in the sample, and
 - (c) diagnosing the individual as having BCC when the mutation is detected, thereby indicating that the individual has BCC.

2. A method of diagnosing basal cell carcinoma (BCC) in an individual, comprising:
 - (a) analyzing a biological sample from the individual,
 - (b) detecting the presence of a discoidin domain receptor 2 (DDR2) protein having a mutation of N146K, R399Q, or S702F in the sample, and
 - (c) diagnosing the individual as having BCC when the mutation is detected, thereby indicating that the individual has BCC.

3. A method for determining likelihood of responding to treatment with a kinase inhibitor in an individual with basal cell carcinoma, comprising:
 - (a) analyzing a biological sample from the individual, wherein the biological sample comprises a discoidin domain receptor 2 (DDR2) protein or a DDR2 nucleic acid encoding the DDR2 protein in the sample;
 - (b) detecting the presence of a discoidin domain receptor 2 (DDR2) mutation that confers sensitivity to a kinase inhibitor in the DDR2 nucleic acid or DDR2 protein in the sample; and
 - (c) identifying the individual as likely to respond to treatment with a kinase inhibitor when one or more of the DDR2 mutations is detected, thereby indicating the individual is likely to respond to treatment with a kinase inhibitor, wherein the one or more DDR2 mutations are selected from the group consisting of N146K, R399Q, and S702F.

4. The method of claim 3, further comprising detecting the presence of a V600E or a V600K mutation in BRAF from the individual.
5. Use of therapeutically effective amount of a discoidin domain receptor 2 (DDR2) inhibitor for inhibiting DDR2 in an individual diagnosed with basal cell carcinoma and as having at least one DDR2 mutation of N146K, R399Q, or S702F.
6. The use of claim 5, wherein the DDR2 inhibitor is siRNA specific for DDR2 nucleic acid, shRNA specific for DDR2 nucleic acid, or an antibody that binds to DDR2 and inhibits DDR2 kinase activity.
7. The use of claim 5, wherein the DDR2 inhibitor is a kinase inhibitor.
8. The use of claim 7 wherein the kinase inhibitor is imatinib, nilotinib or dasatinib.
9. The use of claim 5, wherein the DDR2 inhibitor is for administration with a therapeutically effective amount of a BRAF inhibitor.
10. The use of claim 9, wherein the BRAF inhibitor is a serine/threonine kinase inhibitor.
11. The use of claim 9, wherein the BRAF kinase inhibitor is vemurafenib.
12. The use of claim 9, wherein the BRAF inhibitor is GDC-0879, PLX-4720, sorafenib tosylate, dabrafenib, or LGX818.
13. Use of a therapeutically effective amount of a discoidin domain receptor 2 (DDR2) inhibitor, for the preparation of a medicament for inhibiting DDR2 in an individual diagnosed as having basal cell carcinoma and as having one DDR2 mutation of N146K, R399Q, or S702F.

14. The use of claim 13, wherein the DDR2 inhibitor is siRNA specific for DDR2 nucleic acid, shRNA specific for DDR2 nucleic acid, or an antibody that binds to DDR2 and inhibits DDR2 kinase activity.
15. The use of claim 13, wherein the DDR2 inhibitor is a kinase inhibitor.
16. The use of claim 15 wherein the kinase inhibitor is imatinib, nilotinib or dasatinib.
17. The use of claim 13, wherein the DDR2 inhibitor is for administration with a therapeutically effective amount of a BRAF inhibitor.
18. The use of claim 17, wherein the BRAF inhibitor is a serine/threonine kinase inhibitor.
19. The use of claim 17, wherein the BRAF kinase inhibitor is vemurafenib.
20. The use of claim 17, wherein the BRAF inhibitor is GDC-0879, PLX-4720, sorafenib tosylate, dabrafenib, or LGX818.

Figure 1

DDR2 alignment (top lines) with DDR1 (bottom) showing conserved sequence between the two proteins at the sites of DDR2 mutations seen in extracellular-TM domains (amino acids 22-200) and the kinase domain (amino acids 550 to 851)

```

Query  22  KQVNPAPICRYPLGMSGGQIPDEDITASSQWSESTAACYGRLDSEEGDGAWCPEIPVEPD
81
      K  +PA CRY LGM      IPD DI+ASS WS+STAA++ RL+S +GDGAWCP  V P
Sbjct  23  KGHFDPACRYALGMQDRTIPDSIDASSWSDDSTAARHSRLESSDGDGAWCPAGSVFPK
82
                                R105C
Query  82  DLKEFLQIDLHTLHFITLVGTQGRHAGGHGIEFAPMYKINYSRDGTRWISWRNRHGKQVL
141
      + +E+LQ+DL  LH + LVGTQGRHAGG G EF+  Y++ YSRDG RW+ W++R G++V+
Sbjct  83  E-EEYLQVDLQRLHLVALVGTQGRHAGGLGKEFSRSYRLRYSRDGRRWGMWKDRWGQEV
141

Query  142 DGNSNPYDIFLKDLEPPIVARFVRFPVTDHSMNVCMRVELYGCVWLDGLVSYNAPAGQQ
201
      GN +P  + LKDL PP+VAR VRF P  D  M+VC+RVELYGC+W DGL+SY AP GQ
Sbjct  142 SGNEPPEGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVELYGCWLDGLSYTAPVGQT
201

Query  202 FVLPGGSIYYLNDSDYDG-AVGYSMTEGLGQLTDGVSGLDLDFDTQTHEYHVWPGYDYVGWR
260
      L      +YLNDSDYDG  VG      GLGQL DGV GLDDF ++ E  VWPGYDYVGW
Sbjct  202 MYL--SEAVYLNDSDYDGHTVGGLQYGGGLQADGVVGLDDFRKSQELRVWPGYDYVGWS
259

Query  261 NESATNGYIEIMFEFDRIRNFTTMKVHCNNMFAKGVKIFKEVQCYFR-SEASEWEPNAIS
319
      N S ++GY+E+ FEFDR+R F  M+VHCNNM  G ++  V+C FR  A WE  +
Sbjct  260 NHSFSSGYVEMEFEFDRIRAFQAMQVHCNNMHTLGARLPGGVECFRRGPAMAWEGEPMR
319

Query  320 FPLVLDDVNPSARFVTVPLHHRMASAIKCQYHFADTWMMFSEITFQSDAAMYNNSALPT
379
      L  +  +P AR V+VPL  R+A  ++C++ FA  W++FSEI+F SD  + N+S AL
Sbjct  320 HNLGGNLGDPRARAVSVPLGGRVARFLQCRFLFAGPWLLFSEISFISDV-VNNSSPALGG
378

Query  380 S-----PMAPTTYDPMLKVDDSNTRILIGCLVAIIFILLAIIVIIL
420
      +                                + P      P+ K + S T ILIGCLVAII +LL II ++L
Sbjct  379 TFPPAPWWPPGPPPTNFSSLELEPRGQPVAKAEGSPTAILIGCLVAIILLIILLIALLML
438

Query  421 WRQFWQKMLEKASRRMLDDEMTVSLSLPSDSSMFNNNRSSSPSEQGSNSTYDRIFPLRPD
480
      WR  W+++L  A RR+L++E+TV LS+P D+ + NN      P E              P
Sbjct  439 WRLHWRRL--SAERRVLEEELTVHLSVPGDTILINNRR--PGPREP-----PP
482
                                I488S
Query  481 YQEPSRLIRKLPEFAP----GEEESGCSGVVKPVQPSGP-----EGVPHYAEADIVNL
529
      YQEP R      P  AP      G  SG      ++P +P  P              VPHYAEADIV L

```

Figure 1 (Cont.)

```

Sbjct  483  YQEP-RPRGNPPHSAPCVPNGSAYSG--DYMEPEKPGAPLLPPPPQNSVPHYAEADIVTL
539
                                         F574C
Query  530  QGVTGGNTYSVPAVTMDLLSGKDVAVEEFPRKLLTFKEKLGEQFGEVHLCEVEGMEKFK
589
      QGVTGGNTY+VPA+      + G      +FPR L FKEKLGEQFGEVHLCEV+ +
Sbjct  540  QGVTGGNTYAVPALPPGAV-GDGPVRVDFPRSRLRFKEKLGEQFGEVHLCEVDSPQDLV
598

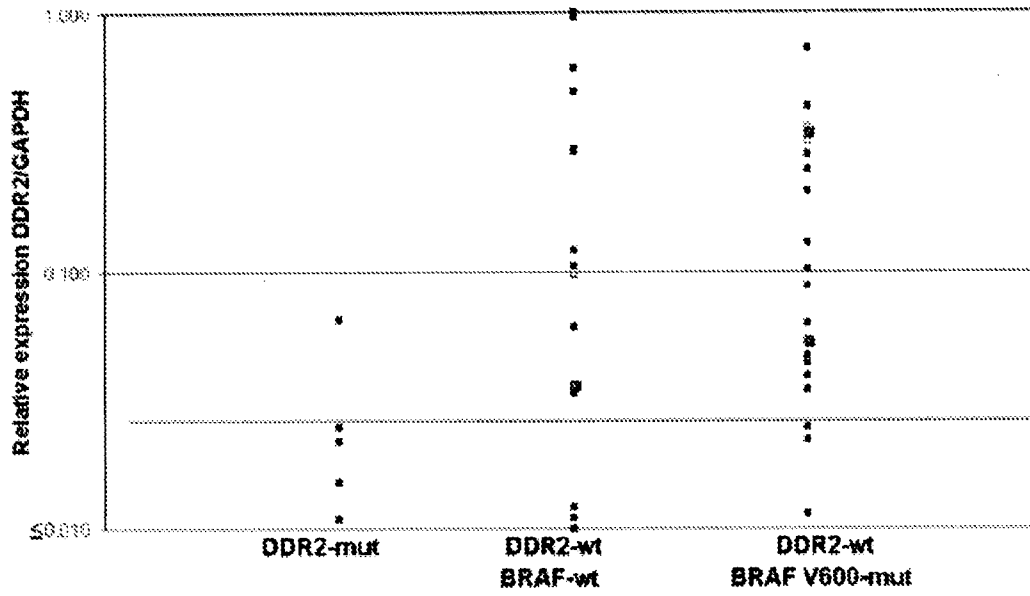
Query  590  DKDFALDVSANQPVLVAVKMLRADANKNARNDFLKEIKIMSRLKDPNIIHLLSVCITDDP
649
      DF L+V      P+LVAVK+LR DA KNARNDFLKE+KIMSRLKDPNII LL VC+ DDP
Sbjct  599  SLDFFPLNVRKGHPLLVAVKILRPDATKNARNDFLKEVKIMSRLKDPNIIIRLLGVCVQDDP
658
                                         S667F
Query  650  LCMITEYMENGDLNQFLSRHE-----PPNSSSDVVRTVSYTNLKFMATQIASGMKY
700
      LCMIT+YMENGDLNQFLS H+      P + ++ T+SY L +A QIASGM+Y
Sbjct  659  LCMITDYMENGDLNQFLSAHQLEDKAAEGAPGDGQAAQGPTISYPMLLHVAAQIASGMRY
718
      L701F
Query  701  LSSLNFBVHRDLATRNLVGNKNTIKIADFGMSRNLYSGDYRIQGRAVLPIRWMWSWESIL
760
      L++LNFVHRDLATRNLVGN+N+TIKIADFGMSRNLY+GDYYR+QGRAVLPIRWM+WE IL
Sbjct  719  LATLNFVHRDLATRNLVGENFTIKIADFGMSRNLYAGDYRVQGRAVLPIRWMWECIL
778

Query  761  LGKFTTASDVWAFGVTLWETFTFCQEQPYSQLSDEQVIENTGEFFRDQGRQTYLPQPAIC
820
      +GKFTTASDVWAFGVTLWE      C+ QP+ QL+DEQVIEN GEFFRDQGRQ YL +P C
Sbjct  779  MGKFTTASDVWAFGVTLWEVLMLCRAQPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPAC
838

Query  821  PDSVYKLMLSCWRRDTKNRPSFQEIHLLLLQ 851
      P +Y+LML CW R+++ RP F ++H L +
Sbjct  839  PQGLYELMLRCWSRESEQRPPFSQLHRFLAE 869

```


Figure 3



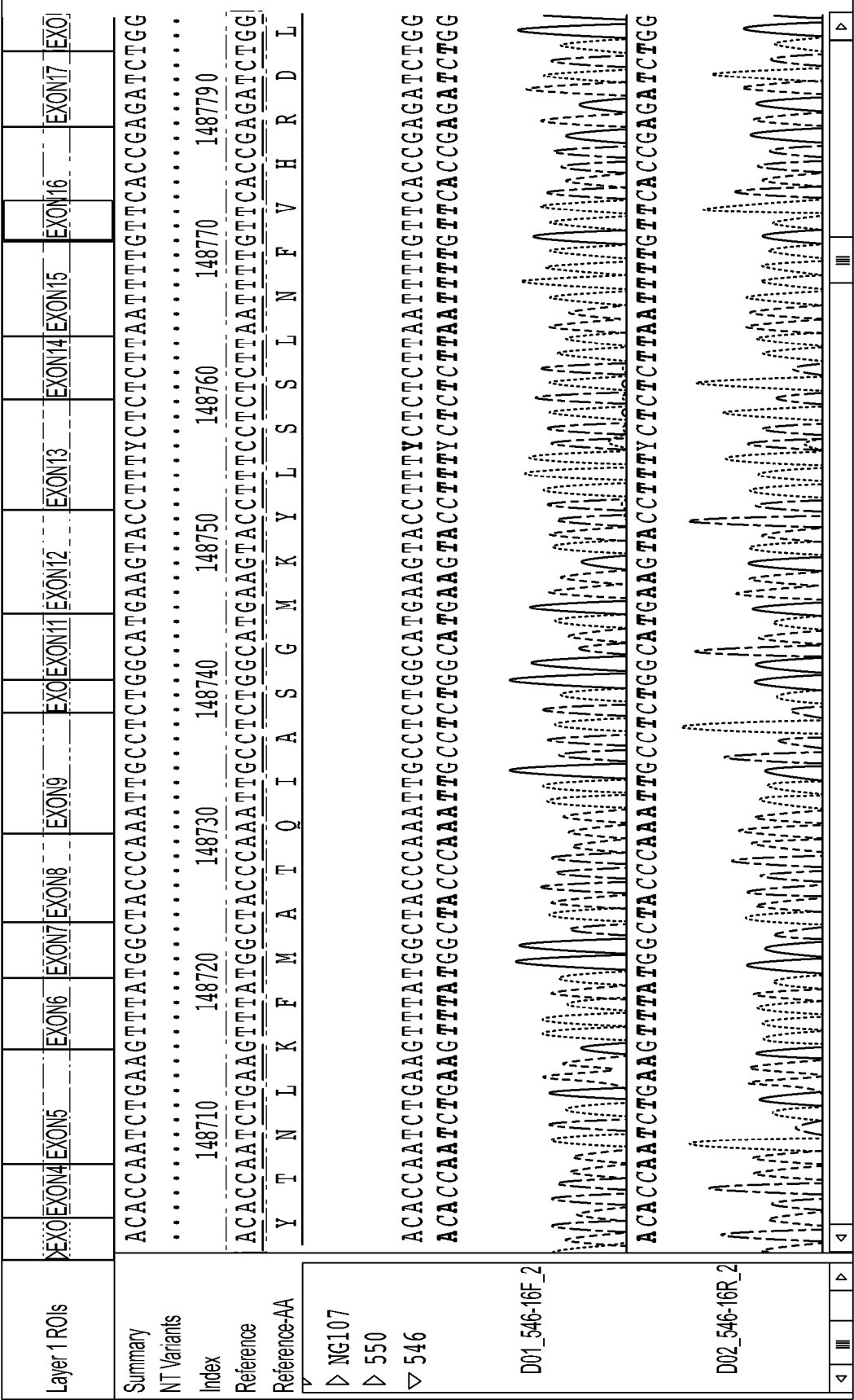


FIG. 4

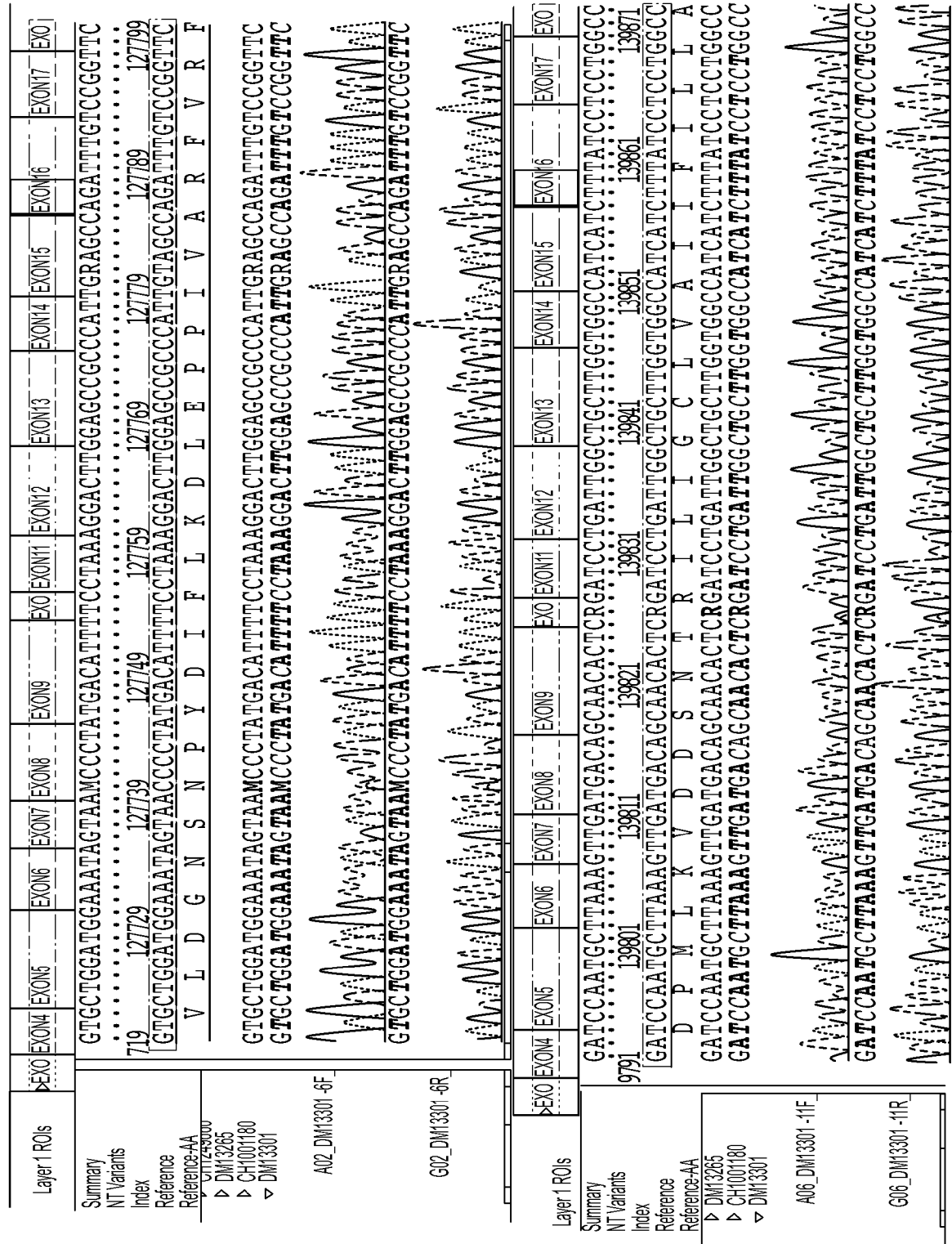


FIG. 5

DDR2 alignment (top lines) with DDR1 (bottom) showing conserved sequence between the two proteins at the sites of DDR2 mutations seen in extracellular-TM domains (amino acids 22-200) and the kinase domain (amino acids 550 to 851)

```

Query 22  KAGVNAEACRYELGSGGGQIPDEDITASSQWSESAAKYGRDSEEDGAMCEPVEPDE
61      K  +EA CHY LGM  IPD DI+ASS NS+STAA++ RL+S +GDGAMCP  V P
Sbjct 23  KGHFDPAKRYALGMQDRTIPSEDIASSGWSOSTAAHRSLESSDGDGAMCPAGSVEFK
62      K105C
Query 82  DLKEFLQIDLHLEHTLVTGQRHAGCHIEFAPIKYNKYNSKGTNRWISNRHRHGKVL
141      + +E+LQ+DL  LH + LVSTGQRHAGG G EF+ Y++ YSRDG RM+ W++R C++V+
Sbjct 83  E-EEYLVQDLQLRLHVALVVTGQRKAGSLGKEFRSRYALRYSDGRRRWGMKDRWGCEVI
141
Query 142  DGNENPYDI FLKDLSPPIVARFVRFPVTDHSMNVCMRVLYGCVMLDGLVSYNAPGQQ
201      GN +P + LKDL PP+VAR VRF P D HAVC+RVLYGCV+M DCL+SY AP CQ
Sbjct 142  SGHEDPGYGVVLDKLGFPFVARLVRFPPRADRVHSGVRLVLYGCVLRDGLSYTAPGQPT
201
Query 202  FVLEGGSIYVLDNSVYDG-AVGYSNTEGLGLQIDTGVSGLDQDTQTTHETHVWFGYDYVGR
260      L  +VLNDS YDG VG  GLCQL DGV GLDDF ++ E  VWPGDYDVGR
Sbjct 202  MYL--SEAVYLDNSTYDGHVYVGLQYSGLGQLADGVVGLDDFVKSQELRVWPGDYDVVGS
259
Query 261  NESATNGYIEIMFEDRIRNFTTMKVHCMMFAKGVKIEFVQCIFR-SEASQNSPNAIS
319      N S ++GY+E+ FEEDR+R F M+VHOMM  G ++ V+C FR  A NE  +
Sbjct 260  NSEFESGYVMEFEFDALRAFQAMQVCHNRHRTLGARLEGGVCEFRPGVANAHEGEWNR
319
Query 320  FPLVLDDVWPSARFVTVPLAHNRKASAIKQCYHFDATYMWSESIITQSDAAMYNNSCALPT
379      L  +  +P AR V-VPL  R+A  ++C++ EA  M++FSEI+P SD  + N+S AL
Sbjct 320  HNLGCHLGDPARAVSVPLGCRVARPLQCRFLFAGQMLLFSEISPTSDV-VNMSPPALGG
379
Query 380  S-----PMAPTTYQEMLEVDSDNRILIGCLWAIIFILLAIIVILL
420      +          + F  P+ K + S T ILIGCLWAI I +LL II ++L
Sbjct 379  VFPAPWVFPQFPPTNFSLELRPGQDPVAKAEGSPTAILIGCLWAIILLILLIAILNL
438
Query 421  WRQVQWMLKASRNLDDGMTVLSLSPSSSHFNWNRSSPSSEQGSNSTYDIRFPLAPD
480      WR W++L A RR+L++E+TV LS+P D+ + NH  P E  P
Sbjct 439  WRLLWRLL-SAEKRVLEELIVHLSVPGDTILINRR--PGPREP-----PP
482      I489S
Query 481  YQEPERLIKKLEFAP----GEESSGCGSVKVPQPSGF-----EGVHYAZADIVNL
529      YQEP R  P  AP  G  SG  ++P +P  F  VHYAZADIV L

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Sbjct 483  YQEP-RPRGNFWNSARCVFNGSAYSQ---DYMEPEKPGAPLLFPFQNSVPHYAEADIVTL
539      F574C
Query 530  QGVVGGNTYVPAVTMDLLSGDKDVAVEEFPKLLTTEKLEGGQFGEVLCEVGEKFK
589      QGVVGGNTY+VPA+  + G  +FFR L TEKLEGGQFGEVHLCEV+  +
Sbjct 540  QGVVGGNTYAVPALPGAV-GGGPRVDFVFRSLRFKEKLEGGQFGEVHLCEVDSFDLV
598
Query 590  DKDFALQVSAQNPVLVAHKLADAMNARNRNDPLKEIKINSLKDKFNIIILSVCIITDDP
649      DF L+V  P+LVAVK+LR DA RNARNDFLKE+RNHSLKNDENII LL VC+ DDP
Sbjct 599  SLDFPLNVRKGHPLLVAHKLADATNRARNDFLKEVHMSLNDENIIIRLLZVCVQDDP
658      S667F
Query 650  LCNITETYMENGDLAQFLSPAE-----PPNSSSSDVRVTSYTNLKTATQIASGMKY
700      LCNIT+YMEGDLAQFLS H+  P + ++ T+SY L +A QIASGM+Y
Sbjct 659  LCNITDYMEGDLAQFLSAHQHEDKAAEGAPGDQQAACQPTISYTNLLHVAQAQIASGMKY
718      L701F
Query 701  LSSINPVHRLATRNCLNGENTIKIADFGMSRNLYSGDYTRQGFVLPKRWNSWESIL
760      L++LNFVHRDLATRNCLNG+M+TIKIADFGMSRNLY+GDYTR+QGFVLPKRW+WE IL
Sbjct 719  LATLNFVHRDLATRNCLNGENTIKIADFGMSRNLYAGDYTRVQGFVLPKRWNAECIL
778
Query 761  LGRPTASDVNAFQVTLWEFTFCQEQPYSQLSDEQVIENTGEFFEDQSGRTLEPQPAIC
820      +GKPTASDVNAFQVTLWE  C+ QP+ QI+DEQVIENTGEFFEDQSGRYL +P C
Sbjct 779  NGRPTASDVNAFQVTLWEVLMLCRAQFPQQLTDEQVIENTAGEFFEDQSGRYLSPPAC
836
Query 821  PDSYKMLKSLKFPADINKNRFSQIIEHLLLQ 851
851      P +Y+MLL CW R+++ RP F +H L +
Sbjct 839  PQGLYELMLRCWSRESEQRPFPFSQLRFLAE 859

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