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(54) Title: MEANS AND METHODS FOR IMPROVED TREATMENT OF CANCER BASED ON MDR1

(57) Abstract: The present invention relates to the use of irinotecan or a derivative thereof for the preparation of a pharmaceutical composition for treating colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer in a patient having a genotype with a variant allele which comprises a polynucleotide in accordance with the present invention. Preferably, a nucleotide deletion, addition and/or substitution comprised by said polynucleotide results in an altered expression of a variant allele compared to the corresponding wild type allele or an altered activity of the polypeptide encoded by the variant allele compared to the polypeptide encoded by the corresponding wild type allele. Finally, the present invention relates to a method for selecting a suitable therapy for a subject suffering from colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer.

Means and methods for improved treatment of cancer based on MDR1

The present invention relates to the use of camptothecin drugs, such as irinotecan (CPT-11) or a derivative thereof for the preparation of a pharmaceutical composition for treating colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer in a patient having a genotype with a variant allele which comprises a polynucleotide in accordance with the present invention. Preferably, a nucleotide deletion, addition and/or substitution comprised by said polynucleotide results in an altered expression of the variant allele compared to the corresponding wild type allele or an altered activity of the polypeptide encoded by the variant allele compared to the polypeptide encoded by the corresponding wild type allele. Finally, the present invention relates to a method for selecting a suitable therapy for a subject suffering from colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer or pancreatic cancer.

Irinotecan is a semisynthetic analog of the cytotoxic alkaloid camptothecin (CPT), which is obtained from the oriental tree, Camptotheca acuminata Camptothecins demonstrate anti-neoplastic activities by inhibiting specifically with the enzyme topoisomerase I which relieves torsional strain in DNA by inducing reversible single-strand breaks [D'Arpa, *et al.*, 1989, Biochim Biophys Acta 989:163-77, Horwitz, *et al.*, 1973, Cancer Res 33:2834-6]. Irinotecan and its active metabolite SN-38 bind to the topoisomerase I-DNA complex and prevent religation of these single-strand breaks [Kawato, *et al.*, 1991, Cancer Res 51:4187-91]. Irinotecan serves as a water-soluble prodrug of the lipophilic metabolite SN-38 (7-ethyl-10-hydroxycamptothecin) which is formed from irinotecan by carboxylesterase-mediated cleavage of the carbamate bond between the camptothecin moiety and the dipiperidino side chain [Tsuji, *et al.*, 1991, J Pharmacobiodyn 14:341-9].

Carboxylesterase-2 is the primary enzyme involved in this hydrolysis at at pharmacological concentrations [Humerickhouse, *et al.*, 2000, Cancer Res 60:1189-92]. Topoisomerase inhibition and irinotecan-related single strand breaks are caused primarily by SN-38 [Kawato, *et al.*, 1991, Cancer Res 51:4187-91]. Administration of irinotecan has resulted in antitumor activity in mice bearing cancers of rodent origin and in human carcinoma xenografts of various histological types [Furuta, *et al.*, 1988, Gan To Kagaku Ryoho 15:2757-60, Giovanella, *et al.*, 1989, Science 246:1046-8, Giovanella, *et al.*, 1991, Cancer Res 51:3052-5, Hawkins, 1992, Oncology (Huntingt) 6:17-23, Kunimoto, *et al.*, 1987, Cancer Res 47:5944-7].

Irinotecan is also oxidized by CYP3A4 and CYP3A5 [Haaz, *et al.*, 1998, Drug Metab Dispos 26:769-74, Kuhn, 1998, Oncology (Huntingt) 12:39-42, Santos, *et al.*, 2000, Clin Cancer Res 6:2012-20, Rivory, *et al.*, 1996, Cancer Res 56:3689-94]. The major elimination pathway of SN-38 is conjugation with glucuronic acid to form the corresponding glucuronide (SN-38G) [Atsumi, *et al.*, 1991, Xenobiotica 21:1159-69.]. SN-38G is reported to be deconjugated by the intestinal microflora to form SN-38 [Kaneda, *et al.*, 1990, Cancer Res 50:1715-20]. Glucuronidation of SN-38 is mediated by UGT1A1 and UGT1A7 [Lyer, *et al.*, 1998, J Clin Invest 101:847-54, Ciotti, *et al.*, 1999, Biochem Biophys Res Commun 260:199-202]. Mass balance studies have demonstrated that 64% of the total dose is excreted in the feces, confirming the important role of biliary excretion [Slatter, *et al.*, 2000, Drug Metab Dispos 28:423-33]. Studies suggest that the multidrug rsistance protein 1 (MRP1) is a major transporter of irinotecan and its metabolites [Kuhn, 1998, Oncology (Huntingt) 12:39-42, Chen, *et al.*, 1999, Mol Pharmacol 55:921-8, Chu, *et al.*, 1997, Cancer Res 57:1934-8, Chu, *et al.*, 1997, J Pharmacol Exp Ther 281:304-14] and facilitate their biliary excretion, where they cause side effects, although P-glycoprotein also participates in irinotecan excretion [Chu, *et al.*, 1998, Cancer Res 58:5137-43, Chu, *et al.*, 1999, Drug Metab Dispos 27:440-1, Chu, *et al.*, 1999, J Pharmacol Exp Ther 288:735-41, Mattern, *et al.*, 1993, Oncol Res 5:467-74, Hoki, *et al.*, 1997, Cancer Chemother Pharmacol 40:433-8, Sugiyama, *et al.*, 1998, Cancer Chemother Pharmacol 42:S44-9].

Cellular resistance to camptothecins and thus, therapeutic response of irinotecan has been related to intracellular carboxylesterase activity and cleavage activity of

topoisomerase I [van Ark-Otte, *et al.*, 1998, Br J Cancer 77:2171-6, Guichard, *et al.*, 1999, Br J Cancer 80:364-70].

The use of such camptothecin drugs, e.g. irinotecan, is limited by clearly dose-dependent myelosuppression and gastrointestinal toxicities, including nausea, vomiting, abdominal pain, and diarrhea which side effects can prove fatal. The major dose-limiting toxicity of irinotecan therapy is diarrhea, which occurs in up to 88% of patients and which depends on intestinal SN-38 accumulation [van Ark-Otte, *et al.*, 1998, Br J Cancer 77:2171-6, Guichard, *et al.*, 1999, Br J Cancer 80:364-70, Araki, *et al.*, 1993, Jpn J Cancer Res 84:697-702] secondary to the biliary excretion of SN-38, the extent of which is determined by SN-38 glucuronidation [Gupta, *et al.*, 1994, Cancer Res 54:3723-5, Gupta, *et al.*, 1997, J Clin Oncol 15:1502-10]. Myelosuppression has been correlated with the area under the concentration-time curve of both irinotecan and SN-38 [Sasaki, *et al.*, 1995, Jpn J Cancer Res 86:101-10].

Despite the approval of irinotecan for patients with metastatic colorectal cancer refractory to 5-fluorouracil therapy in 1997, the therapeutic benefit remains questionable. Recently two large clinical trials on colorectal cancer involving more than 2000 patients had to be canceled by the National Institute of Cancer (NCI) due to an almost 3-times increase of irinotecan toxicity-related mortality within the first 60 days of treatment. Causes of death were diarrhea- and vomiting-related dehydratation and neutropenia-related sepsis [2001, arznei-telegramm 32:58]. Although irinotecan was proven to be effective against thencancer itself, not all patients could benefit from longterm survival due to short term toxicity. Thus, it is highly desirable to identify those patients who will most likely suffer from irinotecan toxicity.

Currently, patients are treated according to most treatment schedules with a standard dose of initially 60 to 125 mg/m^2 irinotecan in combination with other anti-neoplastic drugs administered several courses of 3 to 4 weekly dosings, and subsequent doses are adjusted in 25 to 50 mg/m^2 increments based upon individual patient tolerance to treatment. Treatment may be delayed 1 to 2 weeks to allow for recovery from irinotecan-related toxicity and if the patient has not recovered, therapy has to be discontinued. Provided intolerable toxicity does not develop, treatment with additional courses are continued indefinitely as long as the

patient continues to experience clinical benefit. Response rates varies depending from tumor type from less than 10 % to almost 90 %. However, it takes at least 6 to 8 weeks to evaluate therapeutic response and to consider alternatives. Thus, finding the right dosage for the patient is tedious, time-consuming and takes the risk of lifethreatening adverse effects. Patients might be unnecessarily put to this risk who do not benefit from treatment and additionally, worthwhile time is wasted before these patients receive their suitable treatment.

Furthermore, as observed for many chemotherapeutic agents, the risk to develop cellular resistances against therapy is increased upon suboptimal exposure of cells to chemotherapeutic agents, such as irinotecan.

Pharmacokinetic modulation with inhibitors of biliary excretion (*e. g.,* MRP and P-glycoprotein) and inducers of UGT1A1 have been suggested as a tool to reduce camptothecin-related toxicity [Gupta, *et al.*, 1996, Cancer Res 56:1309-14, Gupta, *et al.*, 1997, Cancer Chemother Pharmacol 39:440-4]. Although preliminary data of a clinical study of irinotecan in combination with cyclosporine A, and phenobarbital show some promising results in respect to limit camptothecin-related diarrhea [Ratain, 2000, Clin Cancer Res 6:3393-4], cotreatment with drugs such as cyclosporine A, and phenobarbital takes the additional risk of adverse events and drug interactions.

Large interpatient variability exist for both SN-38 and SN-38G pharmacokinetics [Canal, *et al.*, 1996, J Clin Oncol 14:2688-95], which is likely to be due to interpatient differences in the metabolism pathways of irinotecan [Rivory, *et al.*, 1997, Clin Cancer Res 3:1261-6]. Furthermore, severe irinotecan toxicity has been reported in patients with Gilbert syndrome [Wasserman, *et al.*, 1997, Ann Oncol 8:1049-51]. Consequently, a genetic predisposition to the metabolism of irinotecan, that patients with low UGT1A1 activity are at increased risk for irinotecan toxicity has been suggested [Iyer, *et al.*, 1998, J Clin Invest 101:847-54, Ando, *et al.*, 1998, Ann Oncol 9:845-7]. A common polymorphism in the UGT1A1 promoter [Monaghan, *et al.*, 1996, Lancet 347:578-81] has been correlated with *in vitro* glucuronidation of SN-38 [Iyer, *et al.*, 1999, Clin Pharmacol Ther 65:576-82], and its possible clinical use has been suggested from a case control study [Ando, *et al.*, 2000, Cancer Res 60:6921-6]. However, irinotecan-related toxicity was predicted by UGT1A1 genotype only in the minority of affected patients (< 15 %).

In conclusion, it would be highly desirable to significantly improve therapeutic efficacy and safety of camptothecin-based therapies and to avoid therapy-caused fatalities, to avoid unnecessary development of resistances, and to reduce adverse events- and therapeutic delay-related hospitalization costs. However, no accepted mechanism for reducing irinotecan toxicity or to improve therapeutic efficacy are currently available.

Thus, the technical problem underlying the present invention is to provide improved means and methods for the efficient treatment of colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer, whereby the aforementioned undesirable side effects are to be avoided.
The technical problem underlying the present invention is solved by the embodiments characterized in the claims.

Accordingly, the present invention relates to the use of irinotecan or a derivative thereof for the preparation of a pharmaceutical composition for treating cancer, especially colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer in a subject having a genome with a variant allele which comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of any one of SEQ ID NOs: 337, 338, 341, 342, 345, 346, 349, 350, 353, 354, 357, 358, 361, 362, 365, 366, 369, 370, 373, 374, 377, 378, 381, 382, 385, 386, 389, 390, 393, 394, 397, 398, 401, 402, 405, 406, 409, 410, 413, 414, 417, 418, 421, 422, 425, 426, 429, 430, 433, 434, 437, 438, 441, 442, 445, 446, 449, 450, 453, 454, 457, 458, 461, 462, 465, 466, 469, 470, 473, 474, 477, 478, 481, 482, 485, 486, 489, 490, 493, 494, 497, 498, 501, 502, 505, 506, 509, 510, 513, 514, 517, 518, 521, 522, 525, 526 636, 637, 640 and/or 641;

(b) a polynucleotide encoding a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 606, 608, 610, 612, 618, 620, 622, 624, and/or 628;

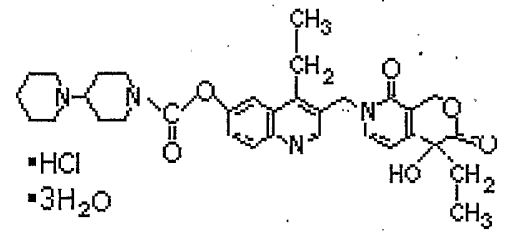
(c) a polynucleotide capable of hybridizing to a Multidrug Resistance 1 (MDR1) gene, wherein said polynucleotide is having at a position corresponding to positions 140837, 141529, 141590, 145984, 171404, 171456, 171466, 171511, 171512, 174901, 175068, 175074, 175142, 175180, 139015, 139064, 139119, 139177, 139276, 140118, 140216, 140490, 140568, 140576, 140595, 140727, 139479, 139619 of the MDR1 gene (Accession No: AC002457) and/or 84701, 83946, 83973, 84032, 84074, 84119, 77811, 78170, 73252, 70200, 70204, 70237, 70253, 70371, 65241, 50537, 43263, 43162 of the MDR1 gene (Accession No: AC005068) and/or 101, 308 of the MDR1 gene (Accession No: M29432) and/or 137, 176 of the MDR1 gene (Accession No: M29445), a substitution or deletion of at least one nucleotide;

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having at a position corresponding to position 83946, 70200, 70237, 65241 of the MDR1 gene (Accession No: AC005068) and/or 101 of the MDR1 gene (Accession No: M29432) and/or 141529, 174901, 139177, 140118, 140568, 140727, 139479 of the MDR1 gene (Accession No: AC002457) an A, at a position corresponding to position 308 of the MDR1 gene (Accession No: M29432) and/or 84701, 83973, 84074, 84119, 78170, 70204, 70253, 70371, 50537, 43162 of the MDR1 gene (Accession No: AC005068) and/or 137 or 176 of the MDR1 gene (Accession No: M29445) and/or 145984, 171466, 175068, 175074, 139064, 139276, 140576 of the MDR1 gene (Accession No: AC002457) a T, at a position corresponding to position 140837, 171404, 171456, 171511, 171512, 139119, 140490, 139619 of the MDR1 gene (Accession No: AC002457) and/or 43263 of the MDR1 gene (Accession No: AC005068) a C, at a position corresponding to position 84032, 77811, 73252 of the MDR1 gene (Accession No: AC005068) and/or 141590, 175142, 175180, 139015, 140216, 140595 of the MDR1 gene (Accession No: AC002457) a G;

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to positions 21, 103, 168, 400, 893, 999, 1001, 1107, and/or 1141 of the MDR1 polypeptide (Accession No: G2506118);

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution of Asn to Asp at a position corresponding to position 21 of the MDR1 polypeptide (Accession No: G2506118) or/and Phe to Leu at a position corresponding to position 103 of the MDR1 polypeptide (Accession No: G2506118) or/and Val to Ile at a position corresponding to position 168 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Asn at a position corresponding to position 400 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 999 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 1001 of the MDR1 polypeptide (Accession No: G2506118) or/and Gln to Pro at a position corresponding to position 1107 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Thr at a position corresponding to position 1141 of the MDR1 polypeptide (Accession No: G2506118).

The term "irinotecan or a derivative thereof" as used in accordance with the present invention preferably refers to a substance which is characterized by the general structural formula



$C_{33}H_{38}N_4O_6 \cdot HCl \cdot 3H_2O$

further described in US patents US05106742, US05340817, US05364858, US05401747, US05468754, US05559235 and US05663177. Moreover, also

comprised by the term "irinotecan or a derivative thereof" are analogues and derivatives of camptothecin. The types and ranges of camptothecin analogues available are well known to those of skill in the art and described in numerous texts, e.g. [Hawkins, 1992, Oncology (Huntingt) 6:17-23, Burris, *et al.*, 1994, Hematol Oncol Clin North Am 8:333-55, Slichenmyer, *et al.*, 1993, J Natl Cancer Inst 85:271-91, Slichenmyer, *et al.*, 1994, Cancer Chemother Pharmacol 34:S53-7]. Specific examples of active camptothecin analogues are hexacyclic camptothecin analogues, 9-nitro-camptothecin, camptothecin analogues with 20S configuration with 9- or 10-substituted amino, halogen, or hydroxyl groups, seven-substituted water-soluble camptothecins, 9-substituted camptothecins, E-ring-modified camptothecins such as (RS)-20-deoxyamino-7-ethyl-10-methoxycamptothecin, and 10-substituted camptothecin analogues [Emerson, *et al.*, 1995, Cancer Res 55:603-9, Ejima, *et al.*, 1992, Chem Pharm Bull (Tokyo) 40:683-8, Sugimori, *et al.*, 1994, J Med Chem 37:3033-9, Wall, *et al.*, 1993, J Med Chem 36:2689-700, Wani, *et al.*, 1980, J Med Chem 23:554-60, Kingsbury, *et al.*, 1991, J Med Chem 34:98-107]. Various other camptothecin analogues with similar therapeutic activity are described [Hawkins, 1992, Oncology (Huntingt) 6:17-23, Burris and Fields, 1994, Hematol Oncol Clin North Am 8:333-55, Slichenmyer, *et al.*, 1993, J Natl Cancer Inst 85:271-91, Slichenmyer, *et al.*, 1994, Cancer Chemother Pharmacol 34:S53-7]. Suitable methods for synthezising camptothecin analogues are described [Emerson, *et al.*, 1995, Cancer Res 55:603-9, Ejima, *et al.*, 1992, Chem Pharm Bull (Tokyo) 40:683-8, Sugimori, *et al.*, 1994, J Med Chem 37:3033-9, Wall, *et al.*, 1993, J Med Chem 36:2689-700, Wani, *et al.*, 1980, J Med Chem 23:554-60, Kingsbury, *et al.*, 1991, J Med Chem 34:98-107, Sugasawa, *et al.*, 1976, J Med Chem 19:675-9].

Said substances are known to be therapeutically useful as described, e.g., in colorectal cancer, non-small cell and small cell lung cancer, oesophageal cancer, renal cell carcinoma, ovarian cancer, breast cancer, pancreatic cancer, squamous cell cancer, leukemias and lymphomas [Kawato, *et al.*, 1991, Cancer Res 51:4187-91, Furuta, *et al.*, 1988, Gan To Kagaku Ryoho 15:2757-60, Hawkins, 1992, Oncology (Huntingt) 6:17-23, Slichenmyer, *et al.*, 1993, J Natl Cancer Inst 85:271-91, Slichenmyer, *et al.*, 1994, Cancer Chemother Pharmacol 34:S53-7, Tsuruo, *et al.*, 1988, Cancer Chemother Pharmacol 21:71-4, Wiseman, *et al.*, 1996, Drugs 52:606-23, Gottlieb, *et al.*, 1970, Cancer Chemother Rep 54:461-70, Negoro, *et al.*,

1991, J Natl Cancer Inst 83:1164-8, Rowinsky, *et al.*, 1994, Cancer Res 54:427-36]. Also encompassed by the use of the present invention are derivatives of those substances which are obtainable by way of any chemical modification, wherein said derivatives are equally well therapeutically suited for the use of the present invention. To determine whether a derivative of the substances of the invention is equally well therapeutically suited for the use of the invention biological assays well known in the art can be performed. Such assays are described , e.g., in [Kawato, *et al.*, 1991, Cancer Res 51:4187-91, Furuta, *et al.*, 1988, Gan To Kagaku Ryoho 15:2757-60, Giovanella, *et al.*, 1989, Science 246:1046-8, Giovanella, *et al.*, 1991, Cancer Res 51:3052-5, Kunimoto, *et al.*, 1987, Cancer Res 47:5944-7, Mattern, *et al.*, 1993, Oncol Res 5:467-74, Tsuruo, *et al.*, 1988, Cancer Chemother Pharmacol 21:71-4, Burris, *et al.*, 1992, J Natl Cancer Inst 84:1816-20, Friedman, *et al.*, 1994, Cancer Chemother Pharmacol 34:171-4].

It is contemplated that any of the compounds described in the above publications may be used in this invention.

It has been show that irinotecan is particularly well suited for the treatment of colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer. Thus, most preferably the substance used according to the present invention is irinotecan.

The term "pharmaceutical composition" as used herein comprises the substances of the present invention and optionally one or more pharmaceutically acceptable carrier. The substances of the present invention may be formulated as pharmaceutically acceptable salts. Acceptable salts comprise acetate, methylester, HCl, sulfate, chloride and the like. The pharmaceutical compositions can be conveniently administered by any of the routes conventionally used for drug administration, for instance, orally, topically, parenterally or by inhalation. The substances may be administered in conventional dosage forms prepared by combining the drugs with standard pharmaceutical carriers according to conventional procedures. These procedures may involve mixing, granulating and compressing or dissolving the ingredients as appropriate to the desired preparation. It will be appreciated that the form and character of the pharmaceutically acceptable character or diluent is dictated by the amount of active ingredient with which it is to be combined, the route of administration and other well-known

variables. The carrier(s) must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. The pharmaceutical carrier employed may be, for example, either a solid or liquid. Exemplary of solid carriers are lactose, terra alba, sucrose, talc, gelatin, agar, pectin, acacia, magnesium stearate, stearic acid and the like. Exemplary of liquid carriers are phosphate buffered saline solution, syrup, oil such as peanut oil and olive oil, water, emulsions, various types of wetting agents, sterile solutions and the like. Similarly, the carrier or diluent may include time delay material well known to the art, such as glyceryl mono-stearate or glyceryl distearate alone or with a wax. The substance according to the present invention can be administered in various manners to achieve the desired effect. Said substance can be administered either alone or in the formulated as pharmaceutical preparations to the subject being treated either orally, topically, parenterally or by inhalation. Moreover, the substance can be administered in combination with other substances either in a common pharmaceutical composition or as separated pharmaceutical compositions.

The diluent is selected so as not to affect the biological activity of the combination. Examples of such diluents are distilled water, physiological saline, Ringer's solutions, dextrose solution, and Hank's solution. In addition, the pharmaceutical composition or formulation may also include other carriers, adjuvants, or nontoxic, nontherapeutic, nonimmunogenic stabilizers and the like. A therapeutically effective dose refers to that amount of the substance according to the invention which ameliorate the symptoms or condition. Therapeutic efficacy and toxicity of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., ED50 (the dose therapeutically effective in 50% of the population) and LD50 (the dose lethal to 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic index, and it can be expressed as the ratio, LD50/ED50.

The dosage regimen will be determined by the attending physician and other clinical factors; preferably in accordance with any one of the above described methods. As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration,

general health, and other drugs being administered concurrently. Progress can be monitored by periodic assessment.

A typical dose can be, for example, in the range of 5 to 100 mg however, doses below or above this exemplary range are envisioned, especially considering the aforementioned factors. Generally, the regimen as a regular administration of the pharmaceutical composition should be in the range of 1 μg to 10 mg units per day. If the regimen is a continuous infusion, it should also be in the range of 1 μg to 10 mg units per kilogram of body weight per minute, respectively. Progress can be monitored by periodic assessment. However, depending on the subject and the mode of administration, the quantity of substance administration may vary over a wide range to provide from about 1 mg per m^2 body surface to about 500 mg per m^2 body surface, usually 20 to 200 mg per m^2 body surface.

The pharmaceutical compositions and formulations referred to herein are administered at least once in accordance with the use of the present invention. However, the said pharmaceutical compositions and formulations may be administered more than one time, for example once weekly every other week up to a non-limited number of weeks.

Specific formulations of the substance according to the invention are prepared in a manner well known in the pharmaceutical art and usually comprise at least one active substance referred to herein above in admixture or otherwise associated with a pharmaceutically acceptable carrier or diluent thereof. For making those formulations the active substance(s) will usually be mixed with a carrier or diluted by a diluent, or enclosed or encapsulated in a capsule, sachet, cachet, paper or other suitable containers or vehicles. A carrier may be solid, semisolid, gel-based or liquid material which serves as a vehicle, excipient or medium for the active ingredients. Said suitable carriers comprise those mentioned above and others well known in the art, see, e.g., Remington's Pharmaceutical Sciences, Mack Publishing Company, Easton, Pennsylvania. The formulations can be adopted to the mode of administration comprising the forms of tablets, capsules, suppositories, solutions, suspensions or the like.

The dosing recommendations will be indicated in product labeling by allowing the prescriber to anticipate dose adjustments depending on the considered patient group, with information that avoids prescribing the wrong drug to the wrong patients at the wrong dose.

The term "treating" means alleviation of he disease symptoms, i.e., regression of symptoms or inhibited progression of such symptoms, in subjects or disease populations which have been treated. Said alleviation off the diseases can be monitored by the degree of the clinical symptoms (e.g., tumor size) accompanied with the disease. While the invention may not be effective in 100% of patients treated, it is effective in treating a statistically significant (p value less than 0.05) number of patients. Whether said number of subjects is significant can be determined by statistical tests such as the Student's t-test, the chi^2-test, the U-test according to Mann and Whitney, the Kruskal-Wallis-test (H-test), Jonckheere-Terpstra-test or the Wilcoxon-test.

The present invention also encompasses all embodiments described in connection with pharmaceutical compositions in US patents US05106742, US05340817, US05364858, US05401747, US05468754, US05559235 and US05663177.

The terms "colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer" comprise diseases and dysregulations related to cancer. Preferred diseases encompassed by the use of the present invention are colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer. Said diseases and dysregulations are well known in the art and the accompanied symptoms are described, e.g., in standard text books such as Stedman.

The term "subject" as used in the sense of the present invention comprises animals, preferably those specified herein after, and humans.

The term " variant allele" as used herein refers to a polynucleotide comprising one or more of the polynucleotides described herein below corresponding to a MDR1 gene. Each individual subject carries at least two alleles of the MDR1 gene, wherein said alleles are distinguishable or identical. In accordance with the use of the present invention a variant allele comprises at least one or more of the polynucleotides specified herein below. Said polynucleotides may have a synergistic influence on the regulation or function of the variant allele. Preferably, a

variant allele in accordance with the use of the present invention comprises at least two of the polynucleotides specified herein.

In the context of the present invention the term "polynucleotides" or "polypeptides" refers to different variants of a polynucleotide or a polypeptide specified in accordance with the uses of the present invention. Said variants comprise a reference or wild type sequence of the polynucleotides or polypeptides specified herein as well as variants which differ therefrom in structure or composition. Reference or wild type sequences for the polynucleotides are Genbank accession No: GI:8850235, GI:11118740, GI:10281451, GI:11177452, GI:10281451, GI:6706037, U91318, GI:7209451, AC026452, AC003026, U91318, AF022830, GI:7209451, AC026452, AC003026, AC025277, AF022828, AF022829, AF022831, U07050, AC003026, AC002457, AC005068, M29432, M29445, and GI:11225259 or Accession No (Pid No): G8850236, G2828206, G2506118, and G12644118 for polypeptides. The differences in structure or composition usually occur by way of nucleotide or amino acid substitution(s), addition(s) and/or deletion(s).

Preferably, said nucleotide substitution(s), addition(s) or deletion(s) referred to in accordance with the use of the present invention result(s) in one or more changes of the corresponding amino acid(s) of the polypeptides. The variant polynucleotides also comprise fragments of said polynucleotides or polypeptides. The polynucleotides or polypeptides as well as the aforementioned fragments thereof are characterized as being associated with a MDR1 dysfunction or dysregulation comprising, e.g., insufficient and/or altered drug uptake.

The present invention also encompasses all embodiments described in connection with polynucleotides in WO9957322, WO0109183 or US5786344.

The term "hybridizing" as used herein refers to polynucleotides which are capable of hybridizing to the above polynucleotides or parts thereof which are associated with a MDR1 dysfunction or dysregulation. Thus, said hybridizing polynucleotides are also associated with said dysfunctions and dysregulations. Preferably, said polynucleotides capable of hybridizing to the aforementioned polynucleotides or parts thereof which are associated with MDR1 dysfunctions or dysregulations are at least 70%, at least 80%, at least 95% or at least 100% identical to the polynucleotides or parts thereof which are associated with MDR1 dysfunctions or dysregulations. Therefore, said polynucleotides may be useful as probes in

Northern or Southern Blot analysis of RNA or DNA preparations, respectively, or can be used as oligonucleotide primers in PCR analysis dependent on their respective size. Also comprised in accordance with the use of the invention are hybridizing polynucleotides which are useful for analyzing DNA-Protein interactions via, e.g., electrophoretic mobility shift analysis (EMSA). Preferably, said hybridizing polynucleotides comprise at least 10, more preferably at least 15 nucleotides in length while a hybridizing polynucleotide to be used as a probe preferably comprises at least 100, more preferably at least 200, or most preferably at least 500 nucleotides in length.

It is well known in the art how to perform hybridization experiments with nucleic acid molecules, i.e. the person skilled in the art knows what hybridization conditions s/he has to use in accordance with the present invention. Such hybridization conditions are referred to in standard text books, such as Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y. Preferred in accordance with the use of the present inventions are polynucleotides which are capable of hybridizing to the above polynucleotides or parts thereof which are associated with a MDR1 dysfunction or dysregulation under stringent hybridization conditions, i.e. which do not cross hybridize to unrelated polynucleotides such as polynucleotides encoding a polypeptide different from the MDR1 polypeptides of the invention.

Moreover, methods for determining whether a subject comprises a polynucleotide referred to herein above are well known in the art. To carry out said methods, it might be necessary to take a sample comprising biological material, such as isolated cells or tissue, from said subject. Further, the methods known in the art could comprise for example, PCR based techniques, RFLP-based techniques, DNA sequencing-based techniques, hybridization techniques, Single strand conformational polymorphism (SSCP), denaturating gradient gel electrophoresis (DGGE), mismatch cleavage detection, heteroduplex analysis, techniques based on mass spectroscopy, HPLC-based techniques, primer extension-based techniques, and 5'-nuclease assay-based techniques. A preferred and convenient method to be used in order to determine the presence or absence of one or more of the above specified polynucleotides is to isolate blood cells from a subject and to perform a PCR based assay on genomic DNA isolated from those blood cells, whereby the PCR is used to determine whether said polynucleotides specified herein above or

parts thereof are present or absent. Said method is described in more detail below and in the Examples.

The term "corresponding" as used herein means that a position is not only determined by the number of the preceding nucleotides and amino acids, respectively. The position of a given nucleotide or amino acid in accordance with the use of the present invention which may be deleted, substituted or comprise one or more additional nucleotide(s) may vary due to deletions or additional nucleotides or amino acids elsewhere in the gene or the polypeptide. Thus, under a "corresponding position" in accordance with the present invention it is to be understood that nucleotides or amino acids may differ in the indicated number but may still have similar neighboring nucleotides or amino acids. Said nucleotides or amino acids which may be exchanged, deleted or comprise additional nucleotides or amino acids are also comprised by the term "corresponding position". Said nucleotides or amino acids may for instance together with their neighbors form sequences which may be involved in the regulation of gene expression, stability of the corresponding RNA or RNA editing, as well as encode functional domains or motifs of the protein of the invention.

By, e.g., "position 17970 to 17970" it is meant that said polynucleotide comprises one or more deleted nucleotides which are deleted between positions 17970 and position 17970 of the corresponding wild type version of said polynucleotide. The same applies mutatis mutandis to all other position numbers referred to in the above embodiment which are drafted in the same format.

By, e.g., "position 1222/1223" it is meant that said polynucleotide comprises one or more additional nucleotide(s) which are inserted between positions 1222 and position 1223 of the corresponding wild type version of said polynucleotide. The same applies mutatis mutandis to all other position numbers referred to in the above embodiment which are drafted in the same format, i.e. two consecutive position numbers separated by a slash (/).

In accordance with the present invention, the mode and population distribution of genetic variations in the MDR1 gene - the different alleles of the MDR1 gene - have been analyzed by sequence analysis of relevant regions of the human said gene from many different individuals. It is a well known fact that genomic DNA of individuals, which harbor the individual genetic makeup of all genes, including the

MDR1 gene, can easily be purified from individual blood samples. These individual DNA samples are then used for the analysis of the sequence composition of the alleles of the MDR1 gene that are present in the individual which provided the blood sample. The sequence analysis was carried out by PCR amplification of relevant regions of said genes, subsequent purification of the PCR products, followed by automated DNA sequencing with established methods (e.g. ABI dyeterminator cycle sequencing).

One important parameter that has to be considered in the attempt to determine the individual genotypes and identify novel variants of the MDR1 gene by direct DNA-sequencing of PCR-products from human blood genomic DNA is the fact that each human harbors (usually, with very few abnormal exceptions) two gene copies of each autosomal gene (diploidy). Because of that, great care has to be taken in the evaluation of the sequences to be able to identify unambiguously not only homozygous sequence variations but also heterozygous variations. The details of the different steps in the identification and characterization of the polymorphisms in the MDR1 gene (homozygous and heterozygous) are described in the Examples below.

Over the past 20 years, genetic heterogeneity has been increasingly recognized as a significant source of variation in drug response. Many scientific communications (Meyer, Ann. Rev. Pharmacol. Toxicol. 37 (1997), 269-296 and West, J. Clin. Pharmacol. 37 (1997), 635-648) have clearly shown that some drugs work better in some patients than in others or may even be highly toxic and that such variations in patients' responses to drugs can be correlated to a molecular basis. This "pharmacogenomic" concept spots correlations between responses to drugs and genetic profiles of patient's (Marshall, Nature Biotechnology, 15 (1997), 954-957; Marshall, Nature Biotechnology, 15 (1997), 1249-1252). In this context of population variability with regard to drug therapy, pharmacogenomics has been proposed as a tool useful in the identification and selection of patients which can respond to a particular drug without side effects. This identification/selection can be based upon molecular diagnosis of genetic polymorphisms by genotyping DNA from leukocytes in the blood of a patient, for example, and characterization of disease (Bertz, Clin. Pharmacokinet. 32 (1997), 210-256; Engel, J. Chromatogra. B. Biomed. Appl. 678 (1996), 93-103). For the founders of health care, such as health maintenance organizations in the US and government public health services in

many European countries, this pharmacogenomics approach can represent a way of both improving health care and reducing costs related to health care caused by the development of unnecessary drugs, by ineffective drugs and by side effects due to drug administration.

The mutations in the variant genes of the invention sometimes result in amino acid deletion(s), insertion(s) and in particular in substitution(s) either alone or in combination. It is of course also possible to genetically engineer such mutations in wild type genes or other mutant forms. Methods for introducing such modifications in the DNA sequence of said genes are well known to the person skilled in the art; see, e.g., Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory (1989) N.Y.

For the investigation of the nature of the alterations in the amino acid sequence of the polypeptides of the invention may be used such as BRASMOL that are obtainable from the Internet. Furthermore, folding simulations and computer redesign of structural motifs can be performed using other appropriate computer programs (Olszewski, Proteins 25 (1996), 286-299; Hoffman, Comput. Appl. Biosci. 11 (1995), 675-679). Computers can be used for the conformational and energetic analysis of detailed protein models (Monge, J. Mol. Biol. 247 (1995), 995-1012; Renouf, Adv. Exp. Med. Biol. 376 (1995), 37-45). These analysis can be used for the identification of the influence of a particular mutation on metabolism, binding, inhibition, mediating of therapeutic action and/or transport of drugs. Moreover, based on the knowledge of the altered structure of the polypeptides which are encoded by the polynucleotides specified in the use of the present invention derivatives of the substances referred to above can be designed and synthesized which can be more efficiently metabolized, modified, transported, eliminated, and/or binded. Thereby, drugs or pro-drugs can be designed on the basis of the substances referred to herein which are more efficient in therapy of colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer in a subject having a genotype characterized by the presence of one or more polynucleotides of the invention.

Usually, said amino acid deletion, addition or substitution in the amino acid sequence of the protein encoded by the polynucleotide referred to in accordance with the use of the present invention is due to one or more nucleotide substitution,

insertion or deletion, or any combinations thereof. Preferably said nucleotide substitution, insertion or deletion may result in an amino acid substitution of Asn to Asp at a position corresponding to position 21 of the MDR1 polypeptide (Accession No: G2506118) or/and Phe to Leu at a position corresponding to position 103 of the MDR1 polypeptide (Accession No: G2506118) or/and Val to Ile at a position corresponding to position 168 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Asn at a position corresponding to position 400 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 999 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 1001 of the MDR1 polypeptide (Accession No: G2506118) or/and Gln to Pro at a position corresponding to position 1107 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Thr at a position corresponding to position 1141 of the MDR1 polypeptide (Accession No: G2506118). The polypeptides encoded by the polynucleotides referred to in accordance with the use described herein have altered biological properties due to the mutations referred to in accordance with the present invention. Examples for said altered properties are stability of the polypeptides or amount of the polypeptides which may be effected resulting in, e.g. an altered drug metabolism or an altered transport of drugs or an altered substrate specificity or an altered catalytic activity characterized by, e.g. insufficiencies in drug metabolism or a complete loss of the capability to metabolize drugs or an enhanced capacity to metabolize drugs or an altered transport activity characterized by, e.g., insufficiencies in drug transport or a complete loss of the capability of transporting drugs or an altered substrate binding characterized by, e.g. an altered drug action or an altered inhibition or induction of transport or an altered binding to receptors or other target molecules characterized by, e.g. an altered activation of signal transduction pathways or an altered protein or enzyme function. These altered properties result in an impaired pharmacological response to the substances referred to above of the subject to be treated in accordance with the use of the present invention. Moreover, due to said altered properties of the polypeptides encoded by the variant alleles specified herein the substances may be chemically modified in a way resulting in derivatives of the substances which are harmful or toxic for the subject or which cause undesirable side effects.

The mutations in the MDR1 gene detected in accordance with the present invention are listed in Tables 1 and 2. As is evident to the person skilled in the art, the genetic knowledge of the polynucleotides specified herein above can be used to exactly and reliably characterize the genotype of a patient.

Advantageously, therapeutical measures which are based on irinotecan or a derivative thereof can be more efficiently applied when taking into consideration said genetic knowledge. Undesirable side effects of said substances can be avoided and an effective but not harmful dosage can be calculated individually due the knowledge of the genetic makeup of the subject. Moreover in accordance with the foregoing, in cases where a given drug causes an unusual effect, a suitable individual therapy can be designed based on the knowledge of the individual genetic makeup of a subject. This tailored therapy will also be suitable to avoid the occurance of therapy resistances. Said resistances are one major problem in cancer chemotherapy with various chemotherapeutic agents, this fact being well known in the art. The use of the present invention, therefore, provides an improvement of the therapeutic applications which are based on the known therapeutically desirable effects of the substances referred to herein above since it is possible to individually treat the subject with an appropriate dosage and/or an appropriate derivative of said substances. Thereby, undesirable, harmful or toxic effects are efficiently avoided. Furthermore, the use of the present invention provides an improvement of the therapeutic applications which are based on the known therapeutically desirable effects of the substances referred to herein above since it is possible to identify those subject prior to onset of drug therapy and treat only those subjects with an appropriate dosage and/or an appropriate derivative of said substances who are most likely to benefit from therapy with said substances. Thereby, the unnecessary and potentially harmful treatment of those subjects who do not respond to the treatment with said substances (nonresponders), as well as the development of drug resistances due to suboptimal drug dosing can be avoided.

In a preferred embodiment of the use of the present invention said variant allele comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of any one of SEQ ID NO: 345, 417 or 636:

(b) a polynucleotid encoding a polypeptide having the amino acid sequence of SEQ ID NO: 612 or 618;

(c) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having a substitution at a position corresponding to position 101 of the MDR1 gene (Accession No: M29432), 176 of the MDR1 gene (Accession No: M29445), or 88883 of the MDR1 gene (Accession No: GI:10122135);

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having an A at a position corresponding to position 101 of the MDR1 gene (Accession No: M29432) or 88883 of the MDR1 gene (Accession No: GI:10122135), or a T at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445) or 88883 of the MDR1 gene (Accession No: GI:10122135);

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to position 400 or 893 of the MDR1 polypeptide (Accession No: G2506118); and

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution of Ser to Asn at a position corresponding to position 400 or Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118).

More preferably, said variant allele comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of SEQ ID NO: 417 or 636;

(b) a polynucleotid encoding a polypeptide having the amino acid sequence of SEQ ID NO: 618;

(c) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having a substitution at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445), 88883 of the MDR1 gene (Accession No: GI:10122135);

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having a T at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445) or 88883 of the MDR1 gene (Accession No: GI:10122135);

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118); and

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118).

Most preferably, said variant allele comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of SEQ ID NO: 417;

(b) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having a substitution at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445); and

(c) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having a T at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445).

In accordance with the present invention it has been surprisingly found that a variant allele corresponding to the MDR1 gene alters the pharmacological response of said subject to the administration of irinotecan or a derivative thereof. As has been found in accordance with he present invention, the pharmacokinetics of a drug which is based on irinotecan or a derivative thereof and the pharmacological response of a subject is mainly governed by the polypeptides encoded by the MDR1 genes. Therefore, in order to increase the predictability and/or efficiency of therapeutic measures applied in accordance with the present invention, the genetic constitution of a subject as regards the present or absence of the variant alleles referred to herein has to be determined and based on that knowledge an individual therapy can be developed which is therapeutically most effective and which avoids toxic or undesirable side effects caused by the substances according to the invention.

The present invention also relates to a method of treating colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer comprising:

(a) determining the presence or absence of a variant allele comprising a polynucleotide referred to herein; and

(b) administering to a subject a therapeutically effective dosage of irinotecan.

The definitions used in accordance with the use of the present invention apply mutatis mutandis to the above method. Further, all embodiments described in accordance with the use of the present invention can be applied mutatis mutandis to the method of the present invention. Moreover, also encompassed by the method of the present invention are any further developments of said method which the person skilled in the art can make without undue burden based on its knowledge and the prior art, such as those documents referred to throughout this specification.

In a preferred embodiment of the use of the present invention a nucleotide deletion, addition and/or substitution comprised by said polynucleotide results in an altered expression of the variant allele compared to the corresponding wild type allele.
As discussed above, the alleles referred to in accordance with the use of the present invention correspond to the MDR1 gene. It is well known in the art that genes comprise structural elements which encode an amino acid sequence as well as regulatory elements which are involved in the regulation of the expression of said genes. Structural elements are represented by exons which may either encode an amino acid sequence or which may code for RNA which is not encoding an amino acid sequence but is nevertheless involved in RNA function, e.g. by regulating the stability of the RNA or the nuclear export of the RNA.

Regulatory elements of a gene may comprise promoter elements or enhancer elements both of which could be involved in transcriptional control of gene expression. It is very well known in the art that a promoter is to be found upstream of the structural elements of a gene. Regulatory elements such as enhancer elements, however, can be found distributed over the entire locus of a gene. Said elements could reside, e.g., in introns, regions of genomic DNA which separate the exons of a gene. Promoter or enhancer elements correspond to polynucleotide fragments which are capable of attracting or binding polypeptides involved in the regulation of the gene comprising said promoter or enhancer elements. For example, polypeptides involved in regulation of said gene comprise the so called transcription factors.

Said introns may comprise further regulatory elements which are required for proper gene expression. Introns are usually transcribed together with the exons of a gene resulting in a nascent RNA transcript which contains both, exon and intron sequences. The intron encoded RNA sequences are usually removed by a process known as RNA splicing. However, said process also requires regulatory sequences present on a RNA transcript said regulatory sequences may be encoded by the introns.

In addition, besides their function in transcriptional control and control of proper RNA processing and/or stability, regulatory elements of a gene could be also involved in the control of genetic stability of a gene locus. Said elements control,

e.g., recombination events or serve to maintain a certain structure of the DNA or the arrangement of DNA in a chromosome.

Therefore, single nucleotide polymorphisms can occur in exons of an allele of a gene which encode an amino acid sequence as discussed supra as well as in regulatory regions which are involved in the above discussed process. The polymorphisms comprised by the polynucleotides referred to in accordance with the use of the present invention can influence the expression level of MDR1 protein via mechanisms involving enhanced or reduced transcription of the MDR1 gene, stabilization of the gene's RNA transcripts and alteration of the processing of the primary RNA transcripts.

Methods for the determination of an altered expression of a variant allele when compared to its wild type counterpart are well known in the art and comprise inter alia those referred to herein above, e.g., PCR based techniques, RFLP-based techniques, DNA sequencing-based techniques, hybridization techniques, Single strand conformational polymorphism (SSCP), denaturating gradient gel electrophoresis (DGGE), mismatch cleavage detection, heteroduplex analysis, techniques based on mass spectroscopy, HPLC-based techniques, primer extension-based techniques, and 5'-nuclease assay-based techniques. It might be necessary to obtain a sample comprising biological material, such as isolated cells or tissue from the subject prior to perform said methods for determination of the expression levels of the wild type and the variant alleles, respectively. An altered expression in accordance with the use of the present invention means that the expression of the wild type allele differs significantly from the expression of the variant allele. A significant difference can be determined by standard statistical methods, such as Student´s t-test, chi^2-test or the U-test according to Mann and Whitney. Moreover, the person skilled in the art can adopt these and other statistical method known in the art individually without an undue burden.

In a more preferred embodiment of the use of the invention said altered expression is decreased or increased expression.

To determine whether the expression of an allele referred to in accordance to the present invention is increased or decreased in comparison to the corresponding

wild type allele well known methods such as PCR based techniques, RFLP-based techniques, DNA sequencing-based techniques, hybridization techniques, Single strand conformational polymorphism (SSCP), denaturating gradient gel electrophoresis (DGGE), mismatch cleavage detection, heteroduplex analysis, techniques based on mass spectroscopy, HPLC-based techniques, primer extension-based techniques, and 5'-nuclease assay-based techniques can be applied. As discussed above, it might be necessary to obtain a sample comprising cells or tissue from the subject in order to determine the expression level of the variant allele referred to in the use of the invention. A decrease or increase of the expression is characterized by a significant difference in the expression level of the variant versus the wild type allele in those assays. Also encompassed by decreased expression is the absence detectable expression of a variant allele.

In a furthermore preferred embodiment of the use of the present invention a nucleotide deletion, addition and/or substitution comprised by said polynucleotide results in an altered activity of the polypeptide encoded by the variant allele compared to the polypeptide encoded by the corresponding wild type allele. As discussed supra, the variant alleles comprising those polynucleotides specified herein which correspond to coding regions of the MDR1 gene effect the amino acid sequences of the polypeptides encoded by said variant alleles. The variant polypeptides, therefore, exhibit altered biological and/or immunological properties when compared to their corresponding wild type counterpart. Preferred variant polypeptides in accordance with the use of the invention are those, which exhibit an altered biological activity, i.e. altered enzymatic function resulting in reduced, enhanced or complete loss of catalytic activity or altered transport function resulting in reduced, enhanced or complete loss of transport activity or altered binding to receptors or other drug targets resulting in altered activation of signal transduction pathways or altered inhibition of transporter or enzyme function. It might be necessary to obtain a sample comprising biological material such as isolated cells or tissue from the subject prior to perform said methods for determination of the activities of the wild type and the variant polypeptides, respectively. Whether a variant polypeptide has an altered activity or level of expression compared to its wild type corresponding counterpart can be determined by standard techniques well known in the art. Such standard techniques may comprise, e.g., ELISA based

assays, RIA based assays, HPLC-based assays, mass spectroscopy-based assays, western blot analysis or assays which are known in the art and described in [Hitzl, *et al.*, 2001, Pharmacogenetics 11:293-8]; Hoffmeyer, 2000 #77; van Helvoort, 1996 #115; Schumacher, 1997 #116; Cordon-Cardo, 1990 #117; Hafkemeyer, 1998 #118] for MDR1.

An altered activity in accordance with the use of the present invention means that the activity of the wild type polypeptide differs significantly from the variant polypeptide. A significant difference can be determined by standard statistical methods referred to herein above.

Most preferably, said altered activity is decreased or increased activity.
As discussed for the increase or decrease of expression, a decrease or increase of the activities is characterized by a significant difference in the activity of the variant versus the wild type polypeptide in the assays referred to herein. Also encompassed by decreased activity is the absence detectable activity of a variant allele.

Moreover, in a further preferred embodiment of the use of the present invention said subject is an animal.

As described supra, the subject in accordance with the use of the present invention encompasses animals. The term "animal" as used herein encompasses all animals, preferably animals belonging to the vertebrate family, more preferably mammals. Moreover, the animals can be genetically engineered by well known techniques comprising transgenesis and homologous recombination in order to incorporate one or more of the polynucleotides referred to supra into the genome of said animals. Said animals comprising the genetically engineered animals can be used to study the pharmacological effects of drugs or pro-drugs which are based on the substances or derivatives thereof referred to herein, preferably irinotecan.

In accordance with the foregoing, most preferably, said animal is a mouse or rat.

Said animals are particularly well suited for assaying the pharmacological properties of the substances or derivatives referred to in accordance with the use of the present invention as described in detail in Giovanella, *et al.*, 1991, Cancer Res 51:3052-5, Kunimoto, *et al.*, 1987, Cancer Res 47:5944-7, Kaneda, *et al.*, 1990, Cancer Res 50:1715-20.

Preferably, said mouse is lacking functional MDR1. It is well known in the art how said mice lacking functional MDR1 can be obtained. For instance said mice might be generated by homologous recombination as described for MDR1 in Schinkel, 1998, Int J Clin Pharmacol Ther 36:9-13, Schinkel, *et al.*, 2000, Pharmacogenetics 10:583-90.

Moreover, in another preferred embodiment of the use of the present invention said subject is a human.

In particular, the present invention is applicable to humans as is evident from the above. The use of the present invention is to be applied in order to treat or prevent side effects in patients which suffer from colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer. The pharmacological effects of the above substances or derivatives thereof are well described in humans. However, the conventional therapies do not take into account the individual genetic makeup of the patient. Ethnical populations have different genetic backgrounds, which can also influence the function or regulation of a variant allele and thereby alter the pharmacological response of a patient to a substance or derivative used as a basis for a drug or pro-drug in accordance with the invention.

In light of the foregoing, most carefully, said human is selected from the African population who shows compared to Caucasians or Japanese (approx. 50 %) a higher frequency (approx. 80%) of the MDR1 high expressor allele (nucleotide C at a position corresponding to position 137 of the MDR1 gene Acc. No. M29445) and are therefore more likely to suffer from irinotecan toxicity (population frequency data are from [Cascorbi, *et al.*, 2001, Clin Pharmacol Ther 69:169-74, Ameyaw, *et al.*, 2001, Pharmacogenetics 11:217-21, Ito, *et al.*, 2001, Pharmacogenetics 11:175-84]).

The present invention also relates to a method for selecting a suitable therapy for a subject suffering from cancer, especially colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer, wherein said method comprises:

(a) determining the presence or absence of a variant allele referred to above in the genome of a subject in a sample obtained from said subject; and

(b) selecting a suitable therapy for said subject based on the results obtained in (a).

The definitions and explanations of the terms made above apply mutatis mutandis to the above method.

The term "suitable therapy" as used herein means that a substance according to the invention is selected and said substance being administered in a certain dosage to a subject, wherein said substance and said dosage are selected based on the knowledge of the presence or absence of a variant allele referred to in accordance with the use of the invention. Said substance and said dosage of the substance are selected in a way that on one hand they are most effective in treating or preventing colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer on the other hand they do not cause toxic or undesirable side effects.

As is evident from the above, a prerequisite for selecting a suitable therapy is the knowledge of the presence or absence of a variant allele referred to in accordance with the use of the invention. Therefore, the method of the present invention encompasses the determination of the presence or absence of said variant alleles in a sample which has been obtained from said subject. The sample which is obtained by the subject comprises biological material which is suitable for the determination of the presence or absence of said variant alleles, such as isolated cells or tissue. Methods for the determination of the presence or absence of the variant alleles of the method of the invention comprise those methods referred to herein above.

Thanks to the method of the present invention, it is possible to efficiently select a suitable therapy for a subject, preferably a human, suffering from colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer Thereby, mistreatment of patients based on wrong medications and the results thereof, such as development of resistance towards cancer therapy, and subsequent increased costs in health care, can be efficiently avoided. Furthermore, patients that are at high risk can be excluded from therapy prior to the first dose and/or dosage can be adjusted according to the individual's genetic makeup prior to the onset of drug therapy. Also, inhibitors for the mentioned transporter gene (e.g. MDR1) can be applied in genetically defined patient subpopulations. Thus, adverse effects can be avoided and the optimal drug level can be reached faster without time-consuming and expensive drug monitoring-based dose finding. This can reduce costs of medical treatment and indirect costs of disease (e.g. shorter time and less frequent hospitalization of patients).

The following items are also encompassed by the present invention. The definitions and explanations made supra apply mutatis mutandis to the terms used to characterize the claims.

1. A method of using irinotecan to treat a patient suffering from cancer which comprises:

   (a) determining if the patient has one or more variant alleles of the MDR1 gene in the cancerous tissue;

   (b) in a patient having one or more of such variant alleles, administering to the patient an amount of irinotecan which is sufficient to treat a patient having such variant alleles which amount is increased or decreased in comparison to the amount that is administered without regard to the patient's alleles in the MDR1 gene.

2. The method of item 1 wherein the cancer is colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, or pancreatic cancer.

3. The method of item 2 in which:

   (a) the one or more variant alleles result in the patient expressing low amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is decreased to avoid toxicity; or

   (b) the one or more variant alleles result in the patient expressing high amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is increased to enhance efficacy.

4. The method of item 3 wherein the one or more variant alleles are in the promoter region of the MDR1 gene.

5. The method of item 3 wherein the one or more variant alleles are in the coding region of the MDR1 gene.

6. The method of item 3 wherein the one or more variant alleles are not in either the promoter region or the coding region of the MDR1 gene.

7. The method of item 3 wherein the one or more variant alleles are in both the promoter region and the coding region of the MDR1 gene.

8. The method of item 3 wherein the one or more variant alleles comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of any one of SEQ ID NOs: 337, 338, 341, 342, 345, 346, 349, 350, 353, 354, 357, 358, 361, 362, 365, 366, 369, 370, 373, 374, 377, 378, 381, 382, 385, 386, 389, 390, 393, 394, 397, 398, 401, 402, 405, 406, 409, 410, 413, 414, 417, 418, 421, 422, 425, 426, 429, 430, 433, 434, 437, 438, 441, 442, 445, 446, 449, 450, 453, 454, 457, 458, 461, 462, 465, 466, 469, 470, 473, 474, 477, 478, 481, 482, 485, 486, 489, 490, 493, 494, 497, 498, 501, 502, 505, 506, 509, 510, 513, 514, 517, 518, 521, 522, 525, 526 636, 637, 640 and/or 641;

(b) a polynucleotide encoding a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 606, 608, 610, 612, 618, 620, 622, 624, and/or 628;

(c) a polynucleotide capable of hybridizing to a Multidrug Resistance 1 (MDR1) gene, wherein said polynucleotide is having at a position corresponding to positions 140837, 141529, 141590, 145984, 171404, 171456, 171466, 171511, 171512, 174901, 175068, 175074, 175142, 175180, 139015, 139064, 139119, 139177, 139276, 140118, 140216, 140490, 140568, 140576, 140595, 140727, 139479, 139619 of the MDR1 gene (Accession No: AC002457) and/or 84701, 83946, 83973, 84032, 84074, 84119, 77811, 78170, 73252, 70200, 70204, 70237, 70253, 70371, 65241, 50537, 43263, 43162 of the MDR1 gene (Accession No: AC005068) and/or 101, 308 of the MDR1 gene (Accession No: M29432) and/or 137, 176 of the MDR1 gene (Accession No: M29445), a substitution or deletion of at least one nucleotide;

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having at a position corresponding to position 83946, 70200, 70237, 65241 of the MDR1 gene (Accession No: AC005068) and/or 101 of the MDR1 gene (Accession No: M29432) and/or 141529, 174901, 139177, 140118, 140568, 140727, 139479 of the MDR1 gene (Accession No: AC002457) an A, at a position corresponding to position 308 of the MDR1 gene (Accession No: M29432) and/or 84701, 83973, 84074, 84119, 78170, 70204, 70253, 70371, 50537, 43162 of the MDR1 gene (Accession No: AC005068) and/or 137 or 176 of the MDR1 gene

(Accession No: M29445) and/or 145984, 171466, 175068, 175074, 139064, 139276, 140576 of the MDR1 gene (Accession No: AC002457) a T, at a position corresponding to position 140837, 171404, 171456, 171511, 171512, 139119, 140490, 139619 of the MDR1 gene (Accession No: AC002457) and/or 43263 of the MDR1 gene (Accession No: AC005068) a C, at a position corresponding to position 84032, 77811, 73252 of the MDR1 gene (Accession No: AC005068) and/or 141590, 175142, 175180, 139015, 140216, 140595 of the MDR1 gene (Accession No: AC002457) a G;

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to positions 21, 103, 168, 400, 893, 999, 1001, 1107, and/or 1141 of the MDR1 polypeptide (Accession No: G2506118);

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution of Asn to Asp at a position corresponding to position 21 of the MDR1 polypeptide (Accession No: G2506118) or/and Phe to Leu at a position corresponding to position 103 of the MDR1 polypeptide (Accession No: G2506118) or/and Val to Ile at a position corresponding to position 168 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Asn at a position corresponding to position 400 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 999 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 1001 of the MDR1 polypeptide (Accession No: G2506118) or/and Gln to Pro at a position corresponding to position 1107 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Thr at a position corresponding to position 1141 of the MDR1 polypeptide (Accession No: G2506118).

9. The method of item 8 wherein the one or more variant alleles comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of any one of SEQ ID NO: 345, 417 or 636:

(b) a polynucleotide encoding a polypeptide having the amino acid sequence of SEQ ID NO: 612 or 618;

(c) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having a substitution at a position corresponding to position 101 of the MDR1 gene (Accession No: M29432), 176 of the MDR1 gene (Accession No: M29445), or 88883 of the MDR1 gene (Accession No: GI:10122135);

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having an A at a position corresponding to position 101 of the MDR1 gene (Accession No: M29432) or 88883 of the MDR1 gene (Accession No: GI:10122135), or a T at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445) or 88883 of the MDR1 gene (Accession No: GI:10122135);

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to position 400 or 893 of the MDR1 polypeptide (Accession No: G2506118); and

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution of Ser to Asn at a position corresponding to position 400 or Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118).

10. The method of item 8 in which the one or more variant alleles results in the patient expressing low amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is decreased.

11. The method of item 8 in which the one or more variant alleles results in the patient expressing high amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is increased.

12. The method of item 9 in which the one or more variant alleles results in the patient expressing low amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is decreased.

13. The method of item 9 in which the one or more variant alleles results in the patient expressing high amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is increased.

14. A method for determining whether a patient is at risk for a toxic reaction to treatment with irinotecan which comprises determining if the patient has one or more variant alleles of the MDR1 gene.

15. The method of item 14 which further comprises administering to the patient reduced amounts of irinotecan.

16. A method for determining the optimum treatment regimen for administering irinotecan to a patient suffering from cancer which comprises:

(a) determining if the patient has one or more variant alleles of the MDR1 gene;

(b) in a patient having one or more of such alleles altering the regimen to reduce peak amounts of irinotecan in the patient in comparison to the peak amount in the patient when irinotecan is administered without regard to the patient's alleles in the MDR1 gene.

17. A method of treating cancer in a patient having one or more variant alleles of the MDR1 gene such that expression levels of the MDR1 gene product are lower than in the general population and so indicates high sensitivity to irinotecan which comprises administering to the patient a decreased amount of irinotecan.

18. A method of treating cancer in a patient having one or more variant alleles of the MDR1 gene such that expression levels of the MDR1 gene product are higher than in the general population and so indicates resistance or predisposition to resistance to irinotecan which comprises administering to the patient an increased amount of irinotecan.

19. The method of item 18 in which patients that have a variant allele that indicates resistance or predisposition to resistance are treated with an MDR1 inhibitor.

20. The method of claim item 19 wherein the MDR1 inhibitor is selected from the group consisting of: GF120918, LY335979, XR 9576, XR 9051, flavonoids (e.g. apigenin, genistin, naringin, quercetin, flavone, flavonone, flavopiridol), bergamottin, Clarithromycin, Ketoconazole, Reserpine, 1,9-dideoxyforskolin, Azidopine, Dimethyl-b-cyclodextrin, Ivermectin, SDZ PSC 833, SDZ 280-446, B669, B-859-35 (R-enantiomere) and its major metabolite, MS-209 (quinolone derivative), PAK-104p, Amiloride, Amytriptyline, Atorvastatin, Aureobasidin & analogues, Berrylium fluoride (BeFx), Calmodulin inhibitors, Chloroquine, Chloropromazine, Clofazimine, Cremophor EL, Diltiazem, Verapamil, nifedipine, bepridil, nicardipine, niguldipine, nitrendipine, trifluoperazine, felodipine, Valinomycin, Dipyridamole, Erythromycine, Fluoroquinolones: fleroxacin, enoxacin, grepafloxacin, levofloxacin, norfloxacine, Glibenclamides & analogues, Gluconate salts, Gramicidin, Hydrocortisone, Itraconazole, Lidocaine, Phosphatidyl-choline, Pristinamycin Ia, Propafenone, Propranolol, Talinolol, Pyridine analogue, Quercetin 4'-b-glucoside, Quinine & quinidine,

quinacrine, cinchonine, Ritonavir , Saquinavir, Nelfinavir, Tamoxifen and metabolites, Taxoid (Tetracyclic taxopine C & derivatives), Terfenadine.

21. The method of item 17 which further comprises monitoring the patient during treatment by assaying for changes in expression levels of the MDR1 gene product in the cancerous cells whereby an increase in the expression level of the MDR1 gene product is compensated for by an increase in the amount of irinotecan administered to the patient.

22. A method of treating cancer in a patient which comprises internally administering to the patient an effective amount of irinotecan, wherein the treatment regimen is modified based upon the genotype of the patient's MDR1 gene.

23. A method of treating a population of patients suffering from cancer which comprises:

(a) determining, on a patient by patient basis, if the patient has one or more variant alleles of the MDR1 gene;

(b) in a patient having one or more of such variant alleles, administering to the patient an amount of irinotecan which is sufficient to treat a patient having such variant alleles which amount is increased or decreased in comparison to the amount that is administered without regard to the patient's alleles in the MDR1 gene.

24. A method for predicting sensitivity to irinotecan in a patient suffering from cancer which comprises determining if the patient has one or more variant alleles of the MDR1 gene, which alleles indicate that the cancerous cells express low or high amounts of the MDR1 protein, whereby low expression

indicates high sensitivity to irinotecan and high expression indicates resistance or predisposition to resistance to irinotecan.

25. The method of item 24 which further comprises administering to patients that have a genotype that indicates resistance or predisposition to resistance a MDR1 inhibitor.

26. The method of item 25 wherein the MDR1 inhibitor is selected from the group consisting of: GF120918, LY335979, XR 9576, XR 9051, flavonoids (e.g. apigenin, genistin, naringin, quercetin, flavone, flavonone, flavopiridol), bergamottin, Clarithromycin, Ketoconazole, Reserpine, 1,9-dideoxyforskolin, Azidopine, Dimethyl-b-cyclodextrin, Ivermectin, SDZ PSC 833, SDZ 280-446, B669, B-859-35 (R-enantiomere) and its major metabolite, MS-209 (quinolone derivative), PAK-104p, Amiloride, Amytriptyline, Atorvastatin, Aureobasidin & analogues, Berrylium fluoride (BeFx), Calmodulin inhibitors, Chloroquine, Chloropromazine, Clofazimine, Cremophor EL, Diltiazem, Verapamil, nifedipine, bepridil, nicardipine, niguldipine, nitrendipine, trifluoperazine, felodipine, Valinomycin, Dipyridamole, Erythromycine, Fluoroquinolones: fleroxacin, enoxacin, grepafloxacin, levofloxacin, norfloxacine, Glibenclamides & analogues, Gluconate salts, Gramicidin, Hydrocortisone, Itraconazole, Lidocaine, Phosphatidyl-choline, Pristinamycin Ia, Propafenone, Propranolol, Talinolol, Pyridine analogue, Quercetin 4'-b-glucoside, Quinine & quinidine, quinacrine, cinchonine, Ritonavir , Saquinavir, Nelfinavir, Tamoxifen and metabolites, Taxoid (Tetracyclic taxopine C & derivatives), Terfenadine.

27. The method of item 25 wherein the patients that have a genotype that indicates resistance or predisposition to resistance are monitored during treatment by assaying for changes of expression levels of the MDR1 gene product in the cancerous cells so that an updated prediction of sensitivity to irinotecan may be determined.

The decreased expression as referred to herein above includes in addition to a significantly decreased amount of transcripts encoding a functional gene product also a normal or even elevated amount of transcripts encoding a gene product which has no activity or a significantly decreased activity.

By "in comparison to the amount that is administered without regard to the patient's alleles in the MDR1 gene" a standard dose is meant which is routinely administered to patients in need thereof without regarding the genotype. Such a general population of patients is considered as having the normal genotype, i.e. wildtype genotype.

Further, the present invention encompasses a method for improving and/or modifying a therapy comprising determining the expression level of MDR1, hereinafter referred to as expression profile or the protein level of the MDR1 protein, hereinafter referred to as the protein profile, or the activity level of said protein, hereinafter referred to as the activity profile.

The term "expression level" as referred to in the context of the present invention means the detectable amount of transcripts of the MDR1 gene relative to the amount of transcripts for a housekeeping gene, such as PLA2. The amount of transcripts can be determined by standard molecular biology techniques including Northern analysis, RNAse protection assays, PCR based techniques encompassing Taq-Man analysis. Preferably, the determination can be carried out as described in the accompanied Examples 4 and 5. The term "expression profile" means that the expression level of a panel of the aforementioned gene is determined and the expression level are compared to a reference standard. As a reference standard, preferably transcripts are obtained from cells or tissues of a subject having the aforementioned wildtype alleles of the respective genes in their genomes.

The term "protein level" refers to the detectable amount of MDR1 relative to the amount of a protein encoded by a housekeeping gene, such as PLA2. The amount of proteins can be determined by standard biochemical techniques, such as Western analysis, ELISA, RIA or other antibody based techniques known in the art. The term "protein profile" means that the protein level of a panel of the aforementioned proteins is determined and the protein levels are compared to a reference standard. As a reference standard, preferably proteins are obtained from

cells or tissues of a subject having the aforementioned wildtype alleles of the respective genes in their genomes.

The term "activity level" means the detectable biological activity of MDR1 relative to the activity of a encoded by the allellic variants of these genes as disclosed in the present invention relative to the activity of the protein encoded by the corresponding wild-type allele of the gene. Biological assays for the aforementioned protein are well known in the art and described in Hitzl *et al.*, 2001, Pharmacogenetics 11:293-8. As a reference standard, preferable proteins are obtained from cells or tissues of a subject having the aforementioned wildtype alleles of the respective genes in their genomes.

The aforementioned methods, preferably, comprise the steps (i) obtaining a tumor sample from a patient during specific stages of a tumor therapy; and (ii) determining the expression profile, protein profile or activity profile for MDR1. Based on the expression profile, the protein profile compared to a suitable reference standard, a clinician can efficiently adapt the therapy. This comprises inter alia dosage adjustment and/or including administration of an MDR1 inhibitor. Preferably, said inhibitor is selected from the following group of MDR1 inhibitors: GF120918, LY335979, XR 9576, XR 9051, flavonoids (e.g. apigenin, genistin, naringin, quercetin, flavone, flavonone, flavopiridol), bergamottin, Clarithromycin, Ketoconazole, Reserpine, 1,9-dideoxyforskolin, Azidopine, Dimethyl-b-cyclodextrin, Ivermectin, SDZ PSC 833, SDZ 280-446, B669, B-859-35 (R-enantiomere) and its major metabolite, MS-209 (quinolone derivative), PAK-104p, Amiloride, Amytriptyline, Atorvastatin, Aureobasidin & analogues, Berrylium fluoride (BeFx), Calmodulin inhibitors, Chloroquine, Chloropromazine, Clofazimine, Cremophor EL, Diltiazem, Verapamil, Nifedipine, Bepridil, Nicardipine, Niguldipine, Nitrendipine, Trifluoperazine, Felodipine, Valinomycin, Dipyridamole, Erythromycine, Fluoroquinolones: Fleroxacin, Eenoxacin, Grepafloxacin, Levofloxacin, Norfloxacine, Glibenclamides & analogues, Gluconate salts, Gramicidin, Hydrocortisone, Itraconazole, Lidocaine, Phosphatidyl-choline, Pristinamycin Ia, Propafenone, Propranolol, Talinolol, Pyridine analogue, Quercetin 4'-b-glucoside, Quinine & quinidine, Quinacrine, Cinchonine, Ritonavir , Saquinavir, Nelfinavir, Tamoxifen and metabolites, Taxoid (Tetracyclic taxopine C & derivatives), Terfenadine (http://bigfoot.med.unc.edu/watkinsLab/intesinfo.htm, Paul Watkins, University of North Carolina).

The term inhibitor as used herein encompasses competitive and non-competitive inhibitors. Preferably competitive inhibitors are substrates such as (GF120918, LY335979, XR 9576, XR 9051, flavonoids). Preferably non-competitive inhibitors are substrates such as (SDZ PSC 833, SDZ 280-446, B669, B-859-35, Verapamil, MS-209, PAK-104p).

Finally, the present invention encompasses a method for determining whether a patient has developed a resistance against the drugs referred to in the context of the present invention. Said method comprising the steps of (i) obtaining a tumor sample from a patient during specific stages of a tumor therapy; and (ii) determining the expression levels of MDR1. The expression of the respective genes can be determined as described in Examples 4 and 5 or as described above. Based on the evaluation of said expression profile, a clinician can more efficiently adapt the therapy. This comprises inter alia dosage adjustment and/or including administration of an MDR1 inhibitor as defined supra.

Each of the documents cited herein (including any manufacturer's specifications, instructions, etc.) are hereby incorporated by reference.

The nucleic acid and amino acid sequences referred to in this application by sequence identification numbers (SEQ ID NOs.) are listed in the following Tables 1 and 2. For positions of polymorphic nucleotides, the following substitute letters are used in the nucleic acid sequences: R, G or A; Y, T or C; M, A or C; K, G or T; S, G or C; W, A or T.

Amino acid sequences are shown in the one letter code. The letter X at polymorphic amino acid positions represents the modified amino acid or its corresponding wild type amino acid (see accession numbers).

Moreover, all nucleic acid and amino acid sequences referred to herein by making reference to GenBank accession numbers are shown in Figures 4 to 29 below.

Table 1: The nucleic acid and amino acid sequences referred to in this application

Gene	Variation	SNP	Acc.no.	SEQ ID No	Sequence forward	SEQ ID NO	Sequence reverse	SEQ ID NO	Sequence wt>mut forward	SEQ ID NO	Sequence wt>mut reverse
UGT1A1	T>G	59	GI:8850235	001	GTCCTGGGCC**G** GCTGCTGTGT	002	ACACAGCAGC**C** GGCCCAGGAC	003	GTCCTGGGCC**K** GCTGCTGTGT	004	ACACAGCAGC**M** GGCCCAGGAC
UGT1A1	C>T	160	GI:8850235	005	GGCCATCCAG**T** AGCTGCAGCA	006	TGCTGCAGCT**A** CTGGATGGCC	007	GGCCATCCAG**Y** AGCTGCAGCA	008	TGCTGCAGCT**R** AGCTGCAGCA
UGT1A1	G>A	226	GI:8850235	009	CATCAGAGAC**A** GAGCATTTTA	010	TAAAATGCTC**T**G TCTCTGATG	011	CATCAGAGAC**R** GAGCATTTTA	012	TAAAATGCTC**Y**G TCTCTGATG
UGT1A1	T>A	539	GI:8850235	013	TTGCATGCAC**A** GCCATGCAGC	014	GCTGCATGGC**T** GTGCATGCAA	015	TTGCATGCAC**W** GCCATGCAGC	016	GCTGCATGGC**K** GTGCATGCAA
UGT1A1	T>C	544	GI:8850235	017	TGCACTGCCA**C** GCAGCCTGGA	018	TCCAGGCTGC**G** GTGCATGCAA	019	TGCACTGCCA**Y** GCAGCCTGGA	020	TCCAGGCTGC**R** GTGCATGCAA
UGT1A1	C>T	640	GI:8850235	021	CTTCCTGCAG**T** GGGTGAAGAA	022	TTCTTCACCC**A**C TGCAGGAAG	023	CTTCCTGCAG**Y** GGGTGAAGAA	024	TTCTTCACCC**R**C TGCAGGAAG

UGT1A1	C>A	701	GI:8850235	025	GTTTATTCCC**A**G	026	GGTTGCATAC**T**	027	GTTTATTCCC**M**	028	GGTTGCATAC**K**
					TATGCAACC		GGGAATAAAC		GTATGCAACC		GGGAATAAAC
UGT1A1	G>C	841	GI:8850235	029	GGTTTTTGTT**C**G	030	TTGATTCCAC**G**	031	GGTTTTTGTT**S**G	032	TTGATTCCAC**S**A
					TGGAATCAA		AACAAAAACC		TGGAATCAA		ACAAAAACC
UGT1A1	C>A	855	GI:8850235	033	GAATCAACTG**A**	034	TTTGGTGAAG**T**	035	GAATCAACTG**M**	036	TTTGGTGAAG**K**
					CTTCACCAAA		CAGTTGATTC		CTTCACCAAA		CAGTTGATTC
UGT1A1	C>T	890	GI:8850235	037	GAATTTGAAG**T**C	038	ATTAATGTAG**A**C	039	GAATTTGAAG**Y**	040	ATTAATGTAG**R**C
					TACATTAAT		TTCAAATTC		CTACATTAAT		TTCAAATTC
UGT1A1	G>A	938	GI:8850235	041	TTCTCTTTGG**A**A	042	GACCATTGAT**T**C	043	TTCTCTTTGG**R**A	044	GACCATTGAT**Y**
					TCAATGGTC		CAAAGAGAA		TCAATGGTC		CCAAAGAGAA
UGT1A1	C>T	1006	GI:8850235	045	CAAAATCCCT**T**A	046	AGGACTGTCT**A**	047	CAAAATCCCT**Y**A	048	AGGACTGTCT**R**
					GACAGTCCT		AGGGATTTTG		GACAGTCCT		AGGGATTTTG
UGT1A1	A>G	1007	GI:8850235	049	AAAATCCCTC**G**	050	CAGGACTGTC**C**	051	AAAATCCCTC**R**	052	CAGGACTGTC**Y**
					GACAGTCCTG		GAGGGATTTT		GACAGTCCTG		GAGGGATTTT
UGT1A1	G>A	1020	GI:8850235	053	CAGTCCTGTG**A**	054	CAGTGTACCG**T**	055	CAGTCCTGTG**R**	056	CAGTGTACCG**Y**
					CGGTACACTG		CACAGGACTG		CGGTACACTG		CACAGGACTG
UGT1A1	C>T	1084	GI:8850235	057	GTGGCTACCC**T**	058	AGATCGTTTT**A**G	059	GTGGCTACCC**Y**	060	AGATCGTTTT**R**
					AAACGATCT		GGTAGCCAC		AAACGATCT		GGGTAGCCAC

UGT1A1	A>G	1085	GI:8850235	061	TGGCTACCCC**G** AAACGATCTG	062	CAGATCGTTT**C** GGGGTAGCCA	063	TGGCTACCCC**R** AAACGATCTG	064	CAGATCGTTT**Y** GGGGTAGCCA
UGT1A1	C>G	1114	GI:8850235	065	CCCGATGACC**G** GTGCCTTTAT	066	ATAAAGGCAC**C** GGTCATCGGG	067	CCCGATGACC**S** GTGCCTTTAT	068	ATAAAGGCAC**S** GGTCATCGGG
UGT1A1	G>A	1117	GI:8850235	069	GATGACCCGT**A** CCTTTATCAC	070	GTGATAAAGG**T** ACGGGTCATC	071	GATGACCCGT**R** CCTTTATCAC	072	GTGATAAAGG**Y** ACGGGTCATC
UGT1A1	C>T	1139	GI:8850235	073	CATGCTGGTT**I** CCATGGTGTT	074	AACACCATGG**A** AACCAGCATG	075	CATGCTGGTT**Y** CCATGGTGTT	076	AACACCATGG**R** AACCAGCATG
UGT1A1	C>G	1158	GI:8850235	077	TTTATGAAAG**G**A TATGCAATG	078	CATTGCATAT**C**C TTTCATAAA	079	TTTATGAAAG**S**A TATGCAATG	080	CATTGCATAT**S**C TTTCATAAA
UGT1A1	CC> GT	1175 to 1176	GI:8850235	081	AATGGCGTTC**G** **T**ATGGTGATGA	082	TCATCACCAT**AC** GAACGCCATT	083	AATGGCGTTC**Y** ATGGTGATGA	084	TCATCACCAT**SR** GAACGCCATT
UGT1A1	G>C	1216	GI:8850235	085	GATGGACAAT**C** CAAAGCGCAT	086	ATGCGCTTTG**G** ATTGTCCATC	087	GATGGACAAT**S** CAAAGCGCAT	088	ATGCGCTTTG**S** ATTGTCCATC
UGT1A1	A>G	1297	GI:8850235	089	AAATGCTCTA**G**A AGCAGTCAT	090	ATGACTGCTT**C**T AGAGCATTT	091	AAATGCTCTA**R**A AGCAGTCAT	092	ATGACTGCTT**Y**T AGAGCATTT

UGT1A1	A>T	1324	GI:8850235	093	CAAAAGTTACTA GGAGAACAT	094	ATGTTCTCCTAG TAACTTTTG	095	CAAAAGTTACW AGGAGAACAT	096	ATGTTCTCCTW GTAACTTTTG
UGT1A1	T>G	1471	GI:8850235	097	CTGGTACCAGG ACCATTCCTT	098	AAGGAATGGTC CTGGTACCAG	099	CTGGTACCAGK ACCATTCCTT	100	AAGGAATGGTM CTGGTACCAG
UGT1A1	C>T	1478	GI:8850235	101	CAGTACCATTTC TTGGACGTG	102	CACGTCCAAGA AATGGTACTG	103	CAGTACCATTYC TTGGACGTG	104	CACGTCCAAGR AATGGTACTG
UGT1A1	*del*CT	372 to 373	GI:8850235	105	TAAAAAAGGAC TGCTATGCT	106	AGCATAGCAGT CCTTTTTTA	107	TAAAAAAGGAnC TGCTATGCT	108	AGCATAGCAGn TCCTTTTTTA
UGT1A1	*del*TT	523 to C 525	GI:8850235	109	GCCCACTGTAT TCTTGCATG	110	CATGCAAGAAT ACAGTGGGC	111	GCCCACTGTAn TTCTTGCATG	112	CATGCAAGAAnT ACAGTGGGC
UGT1A1	*del* TACA TTA ATGC TTC	892 to 905	GI:8850235	113	ATTTGAAGCCT GGAGAACAT	114	ATGTTCTCCAG GCTTCAAAT	115	ATTTGAAGCCnT GGAGAACAT	116	ATGTTCTCCAnG GCTTCAAAT
UGT1A1	*ins*T	470/ 471	GI:8850235	129	CTGACGGACCC TTTTCCTTCCTT	130	AAGGAAGGAAA TGGGTCCGTCA G	131	CTGACGGACCC nTTTCCTTCCTT	132	AAGGAAGGAAA nGGGTCCGTCA G

UGT1A1	*ins*G	1222/ 1223	GI:8850235	133	CAATGCAAAG**C** **GG**CATGGAGAC T	134	AGTCTCCATG**C** **CG**CTTTGCATT G	135	CAATGCAAAGC nGCATGGAGAC T	136	AGTCTCCATGC nGCTTTGCATTG
Cyp3A5	T>C	47518	GI:10281451	137	AAGGA**C**TTCTA	138	TAGAA**G**TCCTT	139	AAGGA**Y**TTCTA	140	TAGAA**R**TCCTT
Cyp3A5	T>G	145601	GI:11177452	141	TGGGC**G**TGCAA	142	TTGCA**C**GCCCA	143	TGGGC**K**TGCAA	144	TTGCA**M**GCCCA
Cyp3A5	A>G	145929	GI:11177452	145	GCCCC**G**CCTCC	146	GGAGG**C**GGGG C	147	GCCCC**R**CCTCC	148	GGAGG**Y**GGGG C
Cyp3A5	A>G	9736	GI:10281451	149	CTCAC**G**CTGGG	150	CCCAG**C**GTGAG	151	CTCAC**R**CTGGG	152	CCCAG**Y**GTCTC
MRP1	G>A	21133	U91318	169	CCCAAAACAC**A** CACACCCTGC	170	GCAGGGTGTG**T** GTGTTTTGGG	171	CCCAAAACAC**R** CACACCCTGC	172	GCAGGGTGTG**Y** GTGTTTTGGG
MRP1	G>T	57998	GI:7209451	173	ACGCTCAGAG**T** TTCATGGACT	174	AGTCCATGAA**A** CTCTGAGCGT	175	ACGCTCAGAG**K** TTCATGGACT	176	AGTCCATGAA**M** CTCTGAGCGT
MRP1	C>T	137667	AC026452	177	GCAGGTGGCC**T** TGTGCACATT	178	AATGTGCAC**A** GGCCACCTGC	179	GCAGGTGGCC**Y** TGTGCACATT	180	AATGTGCAC**R** GGCCACCTGC
MRP1	C>T	137647	AC026452	181	TTGCCGTCTA**T** GTGACCATTG	182	CAATGGTCAC**A** TAGACGGCAA	183	TTGCCGTCTA**Y** GTGACCATTG	184	CAATGGTCAC**R** TAGACGGCAA
MRP1	G>A	27258	AC003026	185	GATTCTCTCC**A**A GAAAACATC	186	GATGTTTTCT**T**G GAGAGAATC	187	GATTCTCTCC**R**A GAAAACATC	188	GATGTTTTCT**Y**G GAGAGAATC

MRP1	G>A	14008	U91318	189	CTGGGAAGTC**A**/TCCCTGACCC	190	GGGTCAGGGA**T**/GACTTCCCAG	191	CTGGGAAGTC**R**/TCCCTGACCC	192 GGGTCAGGGA**Y**/GACTTCCCAG
MRP1	C>T	18067	U91318	193	CCACGGCAGC**T**/GTGGACCTGG	194	CCAGGTCCAC**A**/GCTGCCGTGG	195	CCACGGCAGC**Y**/GTGGACCTGG	196 CCAGGTCCAC**R**/GCTGCCGTGG
MRP1	G>A	79	AF022830	197	CCAGGCAGCC**A**/GTGAAGGTTG	198	CAACCTTCAC**T**/GGCTGCCTGG	199	CCAGGCAGCC**R**/GTGAAGGTTG	200 CAACCTTCAC**Y**/GGCTGCCTGG
MRP1	T>C	88	AF022830	201	CGGTGAAGGT**C**/GTGTACTCCT	202	AGGAGTACAC**G**/ACCTTCACCG	203	CGGTGAAGGT**Y**/GTGTACTCCT	204 AGGAGTACAC**R**/ACCTTCACCG
MRP1	T>G	249	AF022830	205	CTCATGAGCT**G**/CTTCTTCAAG	206	CTTGAAGAAG**C**/AGCTCATGAG	207	CTCATGAGCT**K**/CTTCTTCAAG	208 CTTGAAGAAG**M**/AGCTCATGAG
MRP1	T>C	95	AF022831	209	AGTTCGTGAA**C**/GACACGAAGG	210	CCTTCGTGTC**G**/TTCACGAACT	211	AGTTCGTGAA**Y**/GACACGAAGG	212 CCTTCGTGTC**R**/TTCACGAACT
MRP1	C>T	57853	GI:7209451	213	GGCAGTGGGC**T**/GAGGGAGTGG	214	CCACTCCCTC**A**/GCCCACTGCC	215	GGCAGTGGGC**Y**/GAGGGAGTGG	216 CCACTCCCTC**R**/GCCCACTGCC
MRP1	C>G	53282	GI:7209451	217	GCCAGTTGGA**G**/TCACTTGGGG	218	CCCCAAGTGA**C**/TCCAACTGGC	219	GCCAGTTGGA**S**/TCACTTGGGG	220 CCCCAAGTGA**S**/TCCAACTGGC
MRP1	A>G	137710	AC026452	221	ACTCTCACTC**G**/GGGCACAGCA	222	TGCTGTGCCC**C**/GAGTGAGAGT	223	ACTCTCACTC**R**/GGGCACAGCA	224 TGCTGTGCCC**Y**/GAGTGAGAGT

MRP1	G>C	27159	AC003026	225	TCGTTGATCA**C**A TCTGTCTGT	226	ACAGACAGAT**G** TGATCAACGA	227	TCGTTGATCA**S**A TCTGTCTGT	228	ACAGACAGAT**S** TGATCAACGA
MRP1	G>A	34218	AC003026	229	GTGCACTCAC**A** TGGCCGGGTG	230	CACCCGGCCA**T** GTGAGTGCAC	231	GTGCACTCAC**R** TGGCCGGGTG	232	CACCCGGCCA**Y** GTGAGTGCAC
MRP1	G>C	34215	AC003026	233	CATGTGCACT**C** ACGTGGCCGG	234	CCGGCCACGT**G** AGTGCACATG	235	CATGTGCACT**S** ACGTGGCCGG	236	CCGGCCACGT**S** AGTGCACATG
MRP1	G>A	39508	GI:7209451	237	GTTTCGTTGT**A** GGGGGTGGGA	238	TCCCACCCCC**T** ACAACGAAAC	239	GTTTCGTTGT**R** GGGGGTGGGA	240	TCCCACCCCC**Y** ACAACGAAAC
MRP1	T>C	55472	AC003026	241	TGTCTAATTA**C**A GAAATGGAT	242	ATCCATTTCT**G**T AATTAGACA	243	TGTCTAATTA**Y**A GAAATGGAT	244	ATCCATTTCT**R**T AATTAGACA
MRP1	G>A	150727	AC025277	245	CCATGTCAGC**A** TGACACAGGT	246	ACCTGTGTCA**T** GCTGACATGG	247	CCATGTCAGC**R** TGACACAGGT	248	ACCTGTGTCA**Y** GCTGACATGG
MRP1	*del*T	17970	U91318	249	CTGGTTTTT**TC**T TCCGGTCA	250	TGACCGGAA**GA** AAAAACCAG	251	CTGGTTTTTT**n**C TTCCGGTCA	252	TGACCGGAAG**n** AAAAAAACCAG
MRP1	C>T	17900	U91318	253	TGTCTCCTTT**T**G CTTCTCCCA	254	TGGGAGAAGC**A** AAAGGAGACA	255	TGTCTCCTTT**Y**G CTTCTCCCA	256	TGGGAGAAGC**R** AAAGGAGACA
MRP1	G>A	18195	U91318	257	CACTGGCACA**A** TGGCCTCTAG	258	CTAGAGGCCA**T** TGTGCCAGTG	259	CACTGGCACA**R** TGGCCTCTAG	260	CTAGAGGCCA**Y** TGTGCCAGTG

MRP1	G>A	33551	AC025277	261	TGTGACCACA**A** ATGAGTGTGT	262	ACACACTCAT**T**T GTGGTCACA	263	TGTGACCACA**R** ATGAGTGTGT	264	ACACACTCAT**Y**T GTGGTCACA
MRP1	C>T	174	AF022828	265	CCAGGCCCCC**T** AGACCTCAGG	266	CCTGAGGTCT**A** GGGGGCCTGG	267	CCAGGCCCCC**Y** AGACCTCAGG	268	CCTGAGGTCT**R** GGGGGCCTGG
MRP1	C>A	248	AF022829	269	CCTTTCCACT**A**C TGTGGCCTC	270	GAGGCCACAG**T** AGTGGAAAGG	271	CCTTTCCACT**M** CTGTGGCCTC	272	GAGGCCACAG**K** AGTGGAAAGG
MRP1	C>G	258	AF022829	273	CCTGTGGCCT**G** AATCCAGGAT	274	ATCCTGGATT**C** AGGCCACAGG	275	CCTGTGGCCT**S** AATCCAGGAT	276	ATCCTGGATT**S**A GGCCACAGG
MRP1	A>G	259	AF022831	277	AAGGTAGGGG**G** CGCTGTGCCA	278	TGGCACAGCG**C** CCCCTACCTT	279	AAGGTAGGGG**R** CGCTGTGCCA	280	TGGCACAGCG**Y** CCCCTACCTT
MRP1	T>C	124667	AC026452	281	GCGTGCCCAG**C** CCTGGGGTTT	282	AAACCCCAGG**G** CTGGGCACGC	283	GCGTGCCCAG**Y** CCTGGGGTTT	284	AAACCCCAGG**R** CTGGGCACGC
MRP1	G>A	1884	U07050	285	AGCCTTGGAG**A** ATCTGGGGTG	286	CACCCCAGAT**T** CTCCAAGGCT	287	AGCCTTGGAG**R** ATCTGGGGTG	288	CACCCCAGAT**Y** CTCCAAGGCT
MRP1	G>C	38646	AC026452	289	CCTTAAACAG**C** ATTTGAAAAG	290	CTTTTCAAAT**G**C TGTTTAAGG	291	CCTTAAACAG**S**A TTTGAAAAG	292	CTTTTCAAAT**S**C TGTTTAAGG
MRP1	C>A	1625	U07050	293	GGGAATCACT**A** AACCTCTCTG	294	CAGAGAGGTT**T** AGTGATTCCC	295	GGGAATCACT**M** AACCTCTCTG	296	CAGAGAGGTT**K** AGTGATTCCC

MRP1	C>T	1163	U07050	297	TGTGATCGGC**T**	298	AGCCGAGGCG**A**	299	TGTGATCGGC**Y**	300	AGCCGAGGCG**R**
					CGCCTCGGCT		GCCGATCACA		CGCCTCGGCT		GCCGATCACA
MRP1	A>G	381	U07050	301	TGGGGGACCC**G**	302	TTTATTGGCC**C**	303	TGGGGGACCC**R**	304	TTTATTGGCC**Y**
					GGCCAATAAA		GGGTCCCCCA		GGCCAATAAA		GGGTCCCCCA
MRP1	G>A	233	U07050	305	AAGAGTAGC**A**	306	CAAGATAAAA**T**T	307	AAGAGTAGC**R**	308	CAAGATAAAA**Y**T
					TTTTATCTTG		GCTACTCTT		TTTTATCTTG		GCTACTCTT
MRP1	C>A	189	U07050	309	AAAAAAATCC**A**A	310	TTTTTGGATT**T**G	311	AAAAAAATCC**M**	312	TTTTTGGATT**K**G
					ATCCAAAAA		GATTTTTTT		AATCCAAAAA		GATTTTTTT
MRP1	C>T	440	U07050	313	CTCCTTCCCT**T**G	314	AGGACCTAGC**A**	315	CTCCTTCCCT**Y**	316	AGGACCTAGC**R**
					CTAGGTCCT		AGGGAAGGAG		GCTAGGTCCT		AGGGAAGGAG
MRP1	*del*AT	34206 to 34207	AC003026	317	AGTCTCACA**CG**	318	GTGAGTGCA**CG**	319	AGTCTCACAC**n**	320	GTGAGTGCAC**n**
					TGCACTCAC		TGTGAGACT		GTGCACTCAC		GTGTGAGACT
MRP1	*del*GG	1720 to 1723	U07050	321	ACTCCAGGC**AG**	322	GAACGGAGC**CT**	323	ACTCCAGGCA**n**	324	GAACGGAGCC**n**
		TA			GCTCCGTTC		GCCTGGAGT		GGCTCCGTTC		TGCCTGGAGT
MRP1	*ins*T	926/ 927	U07050	325	TTAATTTTTTT**TT**	326	AAATAATAA**TAA**	327	TTAATTTTTTTT**n**	328	AAATAATAAT**n**A
					ATTATTATTT		AAAAAAATTAA		ATTATTATTT		AAAAAAATTAA

MRP1	*ins*TC	437/	U07050	329	TTCCTCCTTC**CT**	330	ACCTAGCGA**GG**	331	TTCCTCCTTCC**n**	332	ACCTAGCGAG**A**
	CTTC	438			**CCTTCCC**TCGC		**GAAGGAG**GAAG		CTCGCTAGGT		GGAAGGAGGAA
	C				TAGGT		GAGGAA				
MRP1	*ins*TG	55156/	AC003026	333	GGGGCTGGGG	334	CACGCACCCG**A**	335	GGGGCTGGGG	336	CACGCACCCG**n**
	GGG				**CTGGGGCT**GGG		**CCCCGA**CCCAG		C**n**TGGGTGCGT		ACCCAGCCCC
	C	55157			TGCGTG		CCCC		G		
MDR1	T>C	140837	AC002457	337	GCTCATTCGAG	338	AGAGCCGCT**G**C	339	CTCATTCGAG**Y**	340	AGAGCCGCT**R**C
					C**A**GCGGCTCT		TCGAATGAG		AGCGGCTCTT		TCGAATGAG
MDR1	G>A	84701	AC005068	341	AAAATTGCT**A**TC	342	AGATAGTGA**T**A	343	AAAATTGCT**R**TC	344	AGATAGTGA**Y**A
					ACTATCT		GCAATTTT		ACTATCT		GCAATTTT
MDR1	G>A	101	M29432	345	TTCACTTCA**A**TT	346	ATGGGTAA**T**TG	347	TCACTTCA**R**TTA	348	GATGGGTAA**Y**T
					ACCCATC		AAGTGAA		CCCATC		GAAGTGAA
MDR1	C>T	308	M29432	349	CTTGAAGGG**T**C	350	TCAGGTTCAG**A**	351	TCTTGAAGGG**Y**	352	TCAGGTTCAG**R**
					TGAACCTGA		CCCTTCAAGA		CTGAACCTG		CCCTTCAAGA
MDR1	C>T	83946	AC005068	353	TCAGCAGT**T**AC	354	TGCAATGT**A**ACT	355	CAGCAGT**Y**ACA	356	TGCAATGT**R**AC
					ATTGCA		GCTGA		TTGCAC		TGCTGA

MDR1	G>A	83973	AC005068	357	GACCCATGC**A**A GCTAGACC	358	GGTCTAGCT**T**G CATGGGTC	359	GACCCATGC**R**A GCTAGACC	360	GGTCTAGCT**Y**G CATGGGTC
MDR1	A>G	84032	AC005068	361	GAGCACAAC**G**G TCCAGCTG	362	CAGCTGGAC**C**G TTGTGCTC	363	GAGCACAAC**R**G TCCAGCTG	364	CAGCTGGAC**Y**G TTGTGCTC
MDR1	G>A	84074	AC005068	365	TGGGCAGAC**A**G TGGCCCTG	366	CAGGGCCAC**T**G TCTGCCCA	367	TGGGCAGAC**R**G TGGCCCTG	368	CAGGGCCAC**Y**G TCTGCCCA
MDR1	G>A	84119	AC005068	369	CTCGTCCTG**A**T AGATCTTG	370	CAAGATCTA**T**CA GGACGAG	371	CTCGTCCTG**R**T AGATCTTG	372	CAAGATCTA**Y**CA GGACGAG
MDR1	A>G	77811	AC005068	373	GGCTTGAAG**G**T GTAAGAAT	374	ATTCTTAC**C**CT TCAAGCC	375	GGCTTGAAG**R**T GTAAGAAT	376	ATTCTTAC**Y**CT TCAAGCC
MDR1	T>A	78170	AC005068	377	TATTCCTTTAC**A** AATTTTTG	378	CAAAAATT**T**GTA AAGGAATA	379	TATTCCTTTAC**W** AATTTTTG	380	ACAAAAATT**W**G TAAAGGAAT
MDR1	A>G	73252	AC005068	381	ACTTTGTCT**G**AT CTCCTGC	382	GCAGGAGAT**C**A GACAAAGT	383	ACTTTGTCT**R**AT CTCCTGC	384	GCAGGAGAT**Y**A GACAAAGT
MDR1	G>A	141529	AC002457	385	CTTCAGGTCGG **A**ATGGATCTTG	386	CAAGATCCAT**T**C CGACCTGA	387	CTTCAGGTCGG **R**ATGGATCTTG	388	CAAGATCCAT**Y** CCGACCTGAAG

MDR1	A>G	141590	AC002457	389	AAACTGAAC**G**A TAAAAGGTA	390	TACCTTTTAT**C**G TTCAGTTTAA	391	AAACTGAAC**R**AT AAAAGGTA	392	TACCTTTTAT**Y**G TTCAGTTTAA
MDR1	C>T	70200	AC005068	393	TTCTCCTTA**T**GG GTGTTAG	394	CTAACACCC**A**T AAGGAGAA	395	TTCTCCTTA**Y**GG GTGTTAG	396	CTAACACCC**R**T AAGGAGAA
MDR1	C>A	70204	AC005068	397	AATTTTCTC**A**TT ACGGGTG	398	CACCCGTAA**T**G AGAAAATT	399	AATTTTCTC**M**TT ACGGGTG	400	CACCCGTAA**K**G AGAAAATT
MDR1	C>T	70237	AC005068	401	TTAATTGGC**T**AT TTTGGAC	402	GTCCAAAAT**A**G CCAATTAA	403	TTAATTGGC**Y**AT TTTGGAC	404	GTCCAAAAT**R**G CCAATTAA
MDR1	G>A	70253	AC005068	405	TCTACTGGT**A**TT TGTCTTA	406	TAAGACAAA**T**AC CAGTAGA	407	TCTACTGGT**R**TT TGTCTTA	408	TAAGACAAA**Y**AC CAGTAGA
MDR1	C>A	70371	AC005068	409	AATCATTTT**A**TG TGCCACA	410	TGTGGCACA**T**A AAATGATT	411	AATCATTTT**M**TG TGCCACA	412	TGTGGCACA**K**A AAATGATT
MDR1	C>T	137	M29445	413	GAACATTGC**T**TA TGGAGAC	414	GTCTCCATA**A**G CAATGTTC	415	GAACATTGC**Y**TA TGGAGAC	416	GTCTCCATA**R**G CAATGTTC
MDR1	C>T	176	M29445	417	GAAGAGAT**T**GT GAGGG	418	CCCTCAC**A**ATC TCTTC	419	GAAGAGAT**Y**GT GAGGGC	420	CCCTCAC**R**ATC TCTTC
MDR1	A>C	43263	AC005068	421	TGAATGTTC**C**G	422	CGGAGCCAC**G**G	423	TGAATGTTC**M**G	424	CGGAGCCAC**K**G

				TGGCTCCG		AACATTCA		TGGCTCCG		AACATTCA
MDR1	T>A	43162	AC005068	425 CGGGTGGTGA**A**C ACAGGAAG	426	CTTCCTGTGT**T**CA CCACCCG	427	CGGGTGGTG**W** CACAGGAAG	428	CTTCCTGTG**W**C ACCACCCG
MDR1	C>T	145984	AC002457	429 AAAATACTT**T**GG AAATTTG	430	CAAATTTCC**A**AA GTATTTT	431	AAAATACTT**Y**GG AAATTTG	432	CAAATTTCC**R**AA GTATTTT
MDR1	T>C	171404	AC002457	433 ATCATTAAA**C**GA AATGAGT	434	ACTCATTTC**G**TT TAATGAT	435	ATCATTAAA**Y**GA AATGAGT	436	ACTCATTTC**R**TT TAATGAT
MDR1	G>C	171456	AC002457	437 GACTAAAG**A**CA CATAAATG	438	CATTTATGT**G**TC TTTAGTC	439	GACTAAAG**A**SA CATAAATG	440	CATTTATGT**S**TC TTTAGTC
MDR1	G>T	171466	AC002457	441 GACATAAATG**T**T ATGTTTGTTT	442	AAACAAACATA**A** CATTTATGTCT	443	AGACATAAATG **K**TATGTTTGT	444	AAACAAACATA **M**CATTTATGTC
MDR1	T>C	171511	AC002457	445 GATACAGGG**C**T CTTCATGA	446	TCATGAAGA**G**C CCTGTATC	447	GATACAGGG**Y**T CTTCATGA	448	TCATGAAGA**R**C CCTGTATC
MDR1	T>C	171512	AC002457	449 GATACAGGGT**C** CTTCATGAAT	450	ATTCATGAAG**G** ACCCTGTATC	451	GATACAGGGT**Y** CTTCATGAAT	452	ATTCATGAAG**R** ACCCTGTATC
MDR1	G>A	174901	AC002457	453 GTGCACGAT**A**T TGGGGAGC	454	GCTCCCCAA**T**A TCGTGCAC	455	GTGCACGAT**R**T TGGGGAGC	456	GCTCCCCAA**Y**A TCGTGCAC
MDR1	C>T	175068	AC002457	457 TAAGCAGCAA**T** 458		ACACGACATT**A**T	459	TAAGCAGCAA**Y** 460		ACACGACATT**R**T

					AATGTCGTGT GTGCATC		TGCTGCTTA CATTGTTG		AATGTCGTGT GTGCATC		TGCTGCTTA CATTGTTG	
MDR1	C>T	175074	AC002457	461	CAACAATGTTGT	462	GATGCACACAA	463	CAACAATGTYGT	464	GATGCACACRA	
MDR1	A>G	175142	AC002457	465	CATTAAATGGA GGACTGGG	466	CCCAGTCCTCC ATTTAATG	467	CATTAAATGRAG GACTGGG	468	CCCAGTCCTYC ATTTAATG	
MDR1	A>G	175180	AC002457	469	TCCTCTGAGGA TGTGCAGT	470	ACTGCACATCC TCAGAGGA	471	TCCTCTGAGRA TGTGCAGT	472	ACTGCACATYCT CAGAGGA	
MDR1	A>G	139015	AC002457	473	AACTTACTTGTA TCTTTGA	474	TCAAAGATACAA GTAAGTT	475	AACTTACTTRTA TCTTTGA	476	TCAAAGATAYAA GTAAGTT	
MDR1	A>T	139064	AC002457	477	AGAAATAGTTTA ATCAACA	478	TGTTGATTAAAC TATTTCT	479	AGAAATAGTWT AATCAACA	480	TGTTGATTAWA CTATTTCT	
MDR1	T>C	139119	AC002457	481	TAGGGAGGGCT TAAGGCCA	482	TGGCCTTAAGC CCTCCCTA	483	TAGGGAGGGYT TAAGGCCA	484	TGGCCTTAARC CCTCCCTA	
MDR1	G>A	139177	AC002457	485	GAAAGGTGAAA TAAAGCAA	486	TTGCTTTATTTC ACCTTTC	487	GAAAGGTGARA TAAAGCAA	488	TTGCTTTATYTC ACCTTTC	
MDR1	C>T	139276	AC002457	489	CATTTACCCTAG ATGGACC	490	GGTCCATCTAG GGTAAATG	491	CATTTACCCYAG ATGGACC	492	GGTCCATCTRG GGTAAATG	
MDR1	G>A	140118	AC002457	493	ATATGGAAGAA	494	TTGTAATTTTCT	495	ATATGGAAGRA	496	TTGTAATTTYCT	

				AATTACAA	TCCATAT	AATTACAA	TCCATAT		
MDR1	A>G	140216	AC002457	497 AACACGGGCGT	498 TCAGATCAACG	499 AACACGGGCRT	500 TCAGATCAAYG		
				TGATCTGA	CCCGTGTT	TGATCTGA	CCCGTGTT		
MDR1	T>C	140490	AC002457	501 TGTATTAAACGC	502 GGGATTCGCGT	503 TGTATTAAAYGC	504 GGGATTCGCRT		
				GAATCCC	TTAATACA	GAATCCC	TTAATACA		
MDR1	G>A	140568	AC002457	505 TTGAAAGACAT	506 ATGTAGACATG	507 TTGAAAGACRT	508 ATGTAGACAYG		
				GTCTACAT	TCTTTCAA	GTCTACAT	TCTTTCAA		
MDR1	A>T	140576	AC002457	509 CGTGTCTACTTA	510 TTCAACTTAAGT	511 CGTGTCTACWT	512 TTCAACTTAWG		
				AGTTGAA	AGACACG	AAGTTGAA	TAGACACG		
MDR1	A>G	140595	AC002457	513 ATGTCCCCAGT	514 GCTGAATCACT	515 ATGTCCCCART	516 GCTGAATCAYT		
				GATTCAGC	GGGGACAT	GATTCAGC	GGGGACAT		
MDR1	G>A	140727	AC002457	517 CCGGGCCGGAA	518 ATGACTGCTTC	519 CCGGGCCGGRA	520 ATGACTGCTYC		
				GCAGTCAT	CGGCCCGG	GCAGTCAT	CGGCCCGG		
MDR1	G>A	139479	AC002457	521 GAGGCGGGCA	522 CTCGTGATCTG	523 GAGGCGGGCR	524 CTCGTGATCYG		
				GATCACGAG	CCCGCCTC	GATCACGAG	CCCGCCTC		
MDR1	T>C	139619	AC002457	525 GGAGAATGGCG	526 CGGGTTCACGC	527 GGAGAATGGYG	528 CGGGTTCACRC		
				TGAACCCG	CATTCTCC	TGAACCCG	CATTCTCC		
MDR1	G>T	65241	AC005068	636 ACTAGAAGGTT	637 ACCTTCCCAGA	638 ACTAGAAGGTK	639 ACCTTCCCAGM		

					CTGGGAAGGT		ACCTTCTAGT		CTGGGAAGGT		ACCTTCTAGT	
MDR1	G>A	50537	AC005068	640	TCCTGACTATAC CAAAGCCAA	641	TTGGCTTTGGT ATAGTCAGGA	642	TCCTGACTATRC CAAAGCCAA	643	TTGGCTTTGGY ATAGTCAGGA	
TOP1	1334 G>T	133418 45	GI:11225259	529	ACTTTTCCGTTG CCGCGGCAACT	530	TTGCCGCGGCA ACGGAAAAGTT C	531	ACTTTTCCGTKG CCGCGGCAACT	532	TTGCCGCGGCM ACGGAAAAGTT C	
TOP1	1845 A>G	1845	GI:11225259	533	CTCGGGAAGGG CTCCATCAGA	534	TCTGATGGAGC CCTTCCCGAG	535	CTCGGGAAGGR CTCCATCAGA	536	TCTGATGGAGY CCTTCCCGAG	

Table 2: The nucleic acid and amino acid sequences referred to in this application

Gene	AS change	Protein Acc No	SEQ ID NO	**Protein**	SEQ ID N=	Protein wt>mut
UGT1A1	L15R	G8850236	538	PLVLGRLLCVL	539	PLVLGXLLCVL
UGT1A1	G71R	G8850236	540	LYIRDRAFYTL	541	LYIRDXAFYTL

UGT1A1	D119Dframeshift	G8850236	542	KKIKKD**CYAFC**	543	KKIKK**DX**
UGT1A1	P152Pframeshift	G8850236	544	VMLTDPF**PSLQ**	545	VMLTD**PX**
UGT1A1	F170del	G8850236	546	LSLPTV**FLHAL**	547	LSLPTV**FX**
UGT1A1	L175Q	G8850236	548	FFLHA**Q**PCSLE	549	FFLHA**X**PCSLE
UGT1A1	C177R	G8850236	550	LHALP**R**SLEFE	551	LHALP**X**SLEFE
UGT1A1	R209W	G8850236	552	MTFLQ**W**VKNML	553	MTFLQ**X**VKNML
UGT1A1	P229Q	G8850236	554	DVVYS**Q**YATLA	555	DVVYS**X**YATLA
UGT1A1	G276R	G8850236	556	NMVFV**R**GINCL	557	NMVFV**X**GINCL
UGT1A1	A292V	G8850236	558	SQEFE**V**YINAS	559	SQEFE**X**YINAS
UGT1A1	Y293Wframeshift	G8850236	560	QEFEA**W**RTWN	561	QEFEA**X**INASG
UGT1A1	G308E	G8850236	562	VVFSL**E**SMVSE	563	VVFSL**X**SMVSE
UGT1A1	Q331R	G8850236	564	LGKIP**R**TVLWR	565	LGKIP**X**TVLWR
UGT1A1	Q357R	G8850236	566	VKWLP**R**NDLLG	567	VKWLP**X**NDLLG

UGT1A1	R367G	G8850236	568	GHPMT**G**AFITH	569	GHPMT**X**AFITH
UGT1A1	A368T	G8850236	570	HPMTR**T**FITHA	571	HPMTR**X**FITHA
UGT1A1	P387R	G8850236	572	ICNGV**R**MVMMP	573	ICNGV**X**MVMMP
UGT1A1	S375F	G8850236	574	ITHAG**F**HGVYE	575	ITHAG**X**HGVYE
UGT1A1	S381R	G8850236	576	HGVYE**R**ICNGV	577	HGVYE**X**ICNGV
UGT1A1	A401P	G8850236	578	DQMDN**P**KRMET	579	DQMDN**X**KRMET
UGT1A1	R403Rframeshift	G8850236	580	MDNAK**RHGD.**	581	MDNAK**X**
UGT1A1	K428E	G8850236	582	LENAL**E**AVIND	583	LENAL**X**AVIND
UGT1A1	Y486D	G8850236	584	LTWYQ**D**HSLDV	585	LTWYQ**X**HSLDV
UGT1A1	S488F	G8850236	586	WYQYH**F**LDVIG	587	WYQYH**X**LDVIG
UGT1A1	Q49stop	G8850236	588	LGAIQ**.**	589	LGAIQ**.**
UGT1A1	C280stop	G8850236	590	VGGIN**.**	591	VGGIN**.**
UGT1A1	Q331stop	G8850236	592	LGKIP**.**	593	LGKIP**.**
UGT1A1	W335stop	G8850236	594	PQTVL**.**	595	PQTVL**.**

UGT1A1	Q357stop	G8850236	596	VKWLP.	597	VKWLP.
UGT1A1	K437stop	G8850236	598	NDKSY.	599	NDKSY.
MRP1	F329C	G2828206	600	YFLMS**C**FFKAI	601	YFLMS**X**FFKAI
MRP1	R433S	G2828206	602	SVDAQ**S**FMDLA	603	SVDAQ**X**FMDLA
MRP1	R723Q	G2828206	604	QNDSL**Q**ENILF	605	QNDSL**X**ENILF
MDR1	N21D	G2506118	606	FFKLN**D**KSEKD	607	FFKLN**X**KSEKD
MDR1	F103L	G2506118	608	INDTG**L**FMNLE	609	INDTG**X**FMNLE
MDR1	V168I	G2506118	610	FDVHD**I**GELNT	611	FDVHD**X**GELNT
MDR1	S400N	G2506118	612	RNVHF**N**YPSRK	613	RNVHF**X**YPSRK
MDR1	G412G	G2506118	614	VKILK**G**LNLKV	615	VKILK**X**LNLKV
MDR1	T436T	G2506118	616	CGKST**T**VQLMQ	617	CGKST**X**VQLMQ
MDR1	A893S	G2506118	618	KELEG**S**GKIAT	619	KELEG**X**GKIAT
MDR1	A999T	G2506118	620	FAPDY**T**KAKIS	621	FAPDY**X**KAKIS
MDR1	A1001T	G2506118	622	PDYAK**T**KISAA	623	PDYAK**X**KISAA

MDR1	Q1107P	G2506118	624	KRLNV**P**WLRAH	625	KRLNV**X**WLRAH
MDR1	A1132A	G2506118	626	IAEN**A**YGDNS	627	IAEN**X**YGDNS
MDR1	S1141T	G2506118	628	NSRVV**T**QEEIV	629	NSRVV**X**QEEIV
MDR1	I1145I	G2506118	630	VSQEE**I**VRAAK	631	VSQEE**X**VRAAK
TOP1	G363C	G12644118	632	PGLFR**C**RGNHP	633	PGLFR**X**RGNHP
TOP1	D533G	G12644118	634	DFLGK**G**SIRYY	635	DFLGK**X**SIRYY

The figure show:

Figure 1 shows the correlation of the exon 26 SNP with inestinal MDR1 expression in 21 volunteres determined by Western blot analyses. The box plot shows the distribution of MDR1 expression clustered according to the MDR1 3435C>T genotype at position corresponding to position 176 of the MDR1 gene (GenBank Acc. No. M29445). The T allele was associated with a lower expression of p-glycoprotein.

Figure 2 shows the correlation of MDR1 3435C>T genotype and digoxin uptake in 14 healthy volunteers who participated in a clinical study that addresses peak plama levels of digoxin at steady state [Johne et al., 1999, Clin. Pharmacol. Ther 66:338-345]. Maximum digoxin levels were statistically significantly different (p=0.006, Mann Whitney U test) between the two groups which were homozygous for the T and C allele, respectively.

Figure 3 represent the correlation of the genotype (wt/wt: 1; wt/mut and mut/mut:2) with MRP1 mRNA content in duodenal biopsies from healthy volunteers derived from two independent experiments, before and after application of rifampicin. Treatment with rifampicin had no effect on MRP1 mRNA expression ($p<0.001$, paired t-test). A strong trend of an association of MRP1 genotype with MRP1 mRNA levels was detected (p=0.086, Kruskal-Wallis test).

Figures 4 to 28 show the nucleic acid and amino acid sequences referred to herein.

Figure 29 shows the expression profile of genes relevant to Irinotecan metabolism in carcinoma cell lines. This semiquantitativ RT-PCR shows amounts of transcripts for the genes indicated right to the amplicons. PCR products were analyzed by agarose electrophoresis, stained with ethidium bromid. The respective fragment sizes are indicated on the left in basepaires (bp).

Figure 30 shows growth inhibition curves for CPT-11 (A) and SN-38 (B) with epithelial carcinoma cell lines LS174T (colon), KB 3-1 (cervix) and RT112 (bladder).

Concentrations of CPT-11 ranged from 0 to 200 µg/ml and of SN-38 from 0 to 200 ng/ml. Cells were treated for three days. The data for each concentration are mean values of at least three wells.

Figure 31 growth inhibition curves for CPT-11 (A) and SN-38 (B) with a epithelial cervix carcinoma cell line KB 3-1 and two subclones expressing high amounts of MDR1, KB 3-1 (MDR1) and KB 3-1 (MDR1, CYP3A5). Concentrations of CPT-11 ranged from 0 to 200 µg/ml and of SN-38 from 0 to 200 ng/ml. Cells were treated for three days. The data for each concentration are mean values and standard deviation of at least three wells.

Figure 32 shows growth inhibition curves for CPT-11 (A) and SN-38 (B) with the bladdercancer cell line RT112 and and its subclones RT112 (MDR1, UGT1A1) expressing MDR1 and higher amounts of UGT1A1. Concentrations of CPT-11 ranged from 0 to 200 µg/ml and of SN-38 from 0 to 200 ng/ml. Cells were treated for three days. The data for each concentration are mean values and standard deviation of at least three wells.

Figure 33 shows growth inhibition curves for CPT-11 (A) and SN-38 (B) with inhibition of MDR1 by R-Verapamil. The epithelial cervix carcinoma cell line KB 3-1 and the two subclones KB 3-1 (MDR1) and KB 3-1 (MDR1, CYP3A5), with high MDR1 expression, were tested for the influence of MDR1 inhibition by R-Verapamil on drug sensitivity. Concentrations of CPT-11 ranged from 0 to 200 µg/ml and of SN-38 from 0 to 200 ng/ml and R-Verapamil was added to 10 µg/ml final concentration(+V). Cells were treated for three days. The data for each concentration are mean values of two wells.

Figure 34 shows growth inhibition curves for CPT-11 (A) and SN-38 (B) with inhibition of MDR1 by R-Verapamil. To circumvent the MDR1 effect on drug resistance cells were treated in parallel with R-Verapamil. The KB 3-1 (MDR1) and KB 3-1 (MDR1, CYP3A5), which differ in their CYP3A5 expression, were tested for remaining resistance after inhibition of MDR1. Concentrations of CPT-11 ranged

from 0 to 200 µg/ml and of SN-38 from 0 to 200 ng/ml and R-Verapamil was added to 10 µg/ml final concentration(+V). Cells were treated for three days. The data for each concentration are mean values of two wells.

The present invention is illustrated by reference to the following biological Examples which are merely illustrative and are not to be constructed as a limitation of the scope of the present invention.

Example 1: Phenotypically impact of the C to T substitution at position corresponding to position 176 of the MDR1 gene (Acc. No. M29445).

To investigate the influence of the single nucleotide C to T substitution at position corresponding to position 176 of the MDR1 gene (Acc. No. M29445) also referred to as MDR1 exon 26 SNP C3435T on intestinal P-glycoprotein (PGP) expression, samples from biopsies and duodenal enterocyte preparations from 21 were investigated at the Dr. Margarete Fischer-Bosch-Institute for Clinical Pharmacology in Stuttgart by quantitative immunohistochemistry and Western blots. The results are shown in Figure 1. Homozygous carriers of the T allele (having at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445) a T) demonstrated significantly higher PGP levels compared to homozygous carriers of the C allele (having at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445) a C). Individuals with heterozygous genotype showed an intermediate level of PGP expression.

Furthermore, the influence of the MDR1 genotype on intestinal uptake-related pharmacokinetics of digoxin was investigated in a clinical study at the University Medical Center, Charite in Berlin. Maximal digoxin blood levels (Cmax) at steady state were correlated with the MDR1 3435C>T genotype 14 healthy volunteers after oral application of digoxin. Figure 2 shows, volunteers homozygous for the T allele show statistically significantly lower digoxin levels than volunteers with a C/C genotype. (p=0.006, Mann Whitney U test) and reflects the impact of this polymorphism on digoxin pharmacokinetics.

Example 2: Correlation of MRP1 polymorphisms with MRP1 expression and side effects during therapy with MRP1 substrates

Functional polymorphisms in the MRP1 gene affect the transport activity which in consequence modulates plasma levels and/or intracellular concentrations of MRP1 substrate drugs. Increased levels of such drugs can lead to side effects whereas decreased levels may result in subtherapeutical drug levels and therapy failure. MRP1 polymorphisms were correlated with the occurence of drug-related adverse effects and therapeutic efficacy in patients treated with MRP1 substrate drugs. In a case-control study, the frequency distribution of MRP1 SNPs was compared between a group of patients who suffered from cisplatin-related nephrotoxicity and a group of patients with nephro- and hepatotoxicities caused from anti-cancer drugs with a group of healthy controls. Furthermore, samples of known MRP1 mRNA levels were screened for MRP1 genotype. The results in the group of patients demonstrating nephro- and hepatotoxicity during anti-cancer treatment, are listed in the following table for one MRP1 SNP:

SNP	group	Allele frequency [%]		Genotype frequency [%]		
		G allele	A allele	*G/A	*A/A	*A/A expected[2]
150727G>A[1]	Controls	66.7	33.3	50	8.3	10.9
	Cases	50.0	50.0	14.3	42.9	25.0

[1]according to Acc. No. AC025277

[2] calculated according to Hardy-Weinberg

In contrast to control samples, the A allele (substitution of G to A at position according to position 150727 of the MRP1 gene, Acc. No. AC025277) was statistically significantly overrepresented in patients suffering from drug-related kidney- and liver side effects compared to healthy controls ($p=0.044$, Chi^2 test) and was thus predictive for these side effects.

Furthermore, an association of MRP1 genotype with mRNA expression before and after rifampicin application was detected for two MRP1 SNP's, 95T>C (SEQ. ID NOs. 209, 210, 211, and 212, nucleotide substitution of T to C at a position corresponding to position 95 of the MRP1 gene, Acc. No. AF022831) and 259A>G

(SEQ. ID NOs. 277, 278, 279, and 280, nucleotide substitution of A to G at a position corresponding to position 259 of the MRP1 gene, Acc. No. AF022831). These SNPs are linked and form one allele. The mutant allele (MRP1mut, C at position 95 and G at position 259 of the MRP1 gene, Acc. No. AF022831) is statistically significantly correlated with decreased MRP1 mRNA expression and the wildtype allele (MRP1wt, T at position 95 and A at position 259 of the MRP1 gene, Acc. No. AF022831) with increased MRP1 expression in two independent experiments (with and without rifampicin induction), as illustrated in figure 3.

The differences in the MRP1 mRNA content are based on MRP1 genotype-related interindividual differences and the analysis of these SNP's is of high diagnostic and prognostic value for MRP1 expression levels and to predict the therapeutic outcome and adverse effects of MRP1 substrate drugs.

Example 3: Dosage calculation

Therapeutic efficacy ans adverse effects of irinotecan depend on plasma levels and intracellular concentrations of the parent compound and the active metabolites (e.g. SN-38), processes which are controlled by CYP3A5- and UGT1A1-related metabolism and MRP1- and MDR1-related transport processes [Atsumi, *et al.*, 1991, Xenobiotica 21:1159-69, Iyer, *et al.*, 1998, J Clin Invest 101:847-54, Ciotti, *et al.*, 1999, Biochem Biophys Res Commun 260:199-202, Santos, *et al.*, 2000, Clin Cancer Res 6:2012-20, Kuhn, 1998, Oncology (Huntingt) 12:39-42, Chen, *et al.*, 1999, Mol Pharmacol 55:921-8, Chu, *et al.*, 1997, Cancer Res 57:1934-8, Chu, *et al.*, 1997, J Pharmacol Exp Ther 281:304-14; Chu, *et al.*, 1998, Cancer Res 58:5137-43, Chu, *et al.*, 1999, Drug Metab Dispos 27:440-1, Chu, *et al.*, 1999, J Pharmacol Exp Ther 288:735-41, Mattern, *et al.*, 1993, Oncol Res 5:467-74, Hoki, *et al.*, 1997, Cancer Chemother Pharmacol 40:433-8, Sugiyama, *et al.*, 1998, Cancer Chemother Pharmacol 42:S44-9]. For example, MRP1 works in close connection with glucuronosyltransferases as part of the cellular detoxification system and is known to transport glucuronosyl conjugates such as SN-38G [König et al., 1999, Biochim Biophys Acta 1461:377-394, Kerb et al., 2001, Pharmacogenomics 2:51-64]. For example, the extend to which SN-38G is exported from the cell into bile greatly influences the rate of its formation. For an efficient detoxification of SN-38 both processes are necessary, conjugation by UGT1A1 and export of the glucuronide.

The 47518T>C (SEQ. ID NOs.137, 138, 139, and 140) and 9736A>G (SEQ. ID NOs. 149, 150, 151, 152) nucleotide substitutions of the CYP3A5 gene (Acc. No. GI:10281451), and the 145601T>G (SEQ. ID NOs. 141, 142, 143, 144) and 145929A>G (SEQ. ID NOs. 145, 146, 147, and 148) nucleotide substitutions of the CYP3A5 gene (Acc. No. GI:11177452) form an high CYP3A5 expression-related allele and are therefore associated with a higher metabolic inactivation of irinotecan. Individuals with this allele are extensive metabolizers (EMs) and are therefore in contrast the reminder poor metabolizers (PMs) less likely to suffer from irinotecan toxicity. Those with one high expressor and one low expressor-related allele are regarded as intermediate metabolizers (IMs).

The 176C>T nucleotide substitution (SEQ. ID NOs. 217, 218, 219, and 220) of the MDR1 gene (Accession No: M29445) is associated with low PGP expression-related low drug efflux, and the 95T>C (SEQ. ID NOs. 209, 210, 211, and 212) and the 259A>G (SEQ. ID NOs. 277, 278, 279, and 280) nucleotide substitutions of the MRP1 gene (Acc. No. AF022831) are associated with low mRNA expression and the 150727G>A nucleotide substitution (SEQ. ID NOs. 217, 218, 219, and 220) of the MRP1 gene (Accession No: M29445) is associated with low PGP expression-related low drug efflux and the 150727G>A nucleotide substitution (SEQ. ID NOs. 217, 218, 219, and 220) of the MRP1 gene (Accession No: AC025277) is associated with adverse effects. Individuals carrying low transporter expression-related alleles are therefore less capable to clear cells from toxic compounds. Both, transport and metabolism are affected in a gene-dose dependant manner. According to the number of low expression-related alleles of the respective transport protein, individuals can be classified as having either extensive (ET), intermediate (IT) or poor transporter capacity (PT) of the respective gene.

By genetic testing prior to onset of treatment with irinotecan, the MDR1- and MRP1-related transport capacity of the patients can be predicted. The individual risk to adverse effects depends on the number of PM and/or PT alleles Individuals with PM-related alleles of CYP3A5 and UGT1A1 and PT-related alleles of MDR1 and MRP1 are at the highest risk to suffer from irinotecan toxicity.

Based on this knowledge, the initial dose can be adjusted prior to the first dose as shown by Brockmöller et al. (2000, Pharmacogenomics 1:125) for substrate drugs of CYP2D6, CYP2C9, and CYP2C19.

Dose adjustment can be achieved using a scoring system. For each PM- or PT-related allele a certain score is assigned e.g. a score of 2 is assigned to UGT1A1 PM alleles 226A, (SEQ. ID NOs 9, 10, 11, 12, 540, 541) and 701A (SEQ. ID NOs. 25, 26, 27, 28, 554, 555), and a score of 1 is assigned to the CYP3A5 PM-related alleles (47523T plus 35649A plus 145601T plus 145929A, 47523T plus 35649G plus 145601G plus 145929G, and 47523C plus 35649A plus 145601T plus 145929A), to the MDR1 low expression allele 176T (SEQ. ID NOs.: 417, 418, 419, and 420), to the MRP1 low expression alleles 150727A (SEQ. ID NOs. 217, 218, 219, and 220) and 259G (SEQ. ID NOs. 277, 278, 279, and 280), to the MRP1 150727A allele (SEQ. ID NOs. 217, 218, 219, and 220). After genotyping the scores are summarized and irinotecan dosage is adjusted according to the sum. Each single score corresponds to a dose reduction of 10%, i.e. a score of one corresponds to a 10% dose reduction, a score of two to 20%, a score of 3 to 30%, etc.

Example 4: Culture conditions and biological assays

The human epithelial cervical cancer cell line KB 3-1 with two subclones (KB 3-1 ($MDR1^{+++}$) and KB 3-1 ($MDR1^{+++}$, CYP3A5)) and the bladder cancer cell line RT112, also with subclone (RT112 ($MDR1^{+}$, UGT1A1)), were cultured in Dulbecco's Modified Eagle Medium (DMEM) including 3.7 g/l $NaHCO_3$, 4.5 g/l D-Glucose, 1.028 g/l N-Acetyl-L-Alanyl-L-glutamine and supplemented with 10% fetal bovine, 1 mM Na-pyruvate and 1% non-essential amino acids. The human colon cancer cell line LS174T was cultured in Dulbecco's modified Eagle medium containing L-glutamine, pyridoxine hydrochloride and 25 mM Hepes buffer without phenol red, supplemented with 10% fetal bovine, 1 mM Na-pyruvate and 1% non-essential amino acids. All cells were incubated at 37°C with 5% CO_2 in a humidified atmosphere.

Drugs

Irinotecan (CPT-11) and its active metabolite SN-38 were provided by Pharmacia. For preparation of stock solutions the substances were dissolved in methanol, 10 mg/ml for CPT-11 and 1 mg/ml for SN-38 and stored at 4°C protected from light. Lower concentrated dilutions were prepared in PBS and cell culture medium. R-Verapamil was applied from SIGMA, dissolved in DMSO to 50 mg/ml and further diluted in PBS.

Treatment of cells with drugs

Cells were seeded in 96-well culture plates 24 h prior to treatment. With respect to differential growth rates KB 3-1 and RT112 cells were seeded at 700 cells/well, RT112 ($MDR1^{+}$, UGT1A1) at 1000 cells/well and KB 3-1 ($MDR1^{+++}$) and KB 3-1 ($MDR1^{+++}$, CYP3A5) at 1200 cells/well. LS174T were seeded at 1.0×10^4 cells/well. Cells were treated with freshly prepared serial dilutions in culture medium, 0, 0.5, 1, 2.5, 5, 7.5, 10, 25, 50, 75, 100 and 200 µg/ml for CPT-11, and 0, 0.1, 0.25, 0.5, 1, 5, 10, 25, 50, 75, 100 and 200 ng/ml for SN-38. Four well were treated with the same drug dilution. Cells were incubated for 3 days at 37°C in a humidified 5% CO_2 atmosphere.

For MDR1 inhibition experiments R-Verapamil was added to 10 µg/ml final concentration in two wells of each drug dilution.

Cytotoxicity assay

A commercially available MTS assay system (Promega, Madison, USA) was used to determine growth inhibition and cell death according to the instructions of the manufacturer. Three days after adding the drugs, 20 µl of the combined MTS/PMS solution was added to each well of the 96-well culture plate. The plate was incubated for at least 45 min at 37°C in a humidified 5% CO_2 atmosphere and the absorbance at 492 nm was measured. The absorbance values of untreated control cells on each plate were set as 100% growth and used to calculate the remaining growth of drug treated cells. Untreated cells on the culture plates served as controls for unaffected growth and survival.

The drug concentration effecting a 50% inhibition of cell growth was defined as the IC_{50}.

RNA preparation and cDNA synthesis

From each cell batch used in these experiments messenger RNA was isolated from cell lysates by oligo-dT magnet beads (μMACS mRNA Isolation Kit; Miltenyi Biotech) following the instructions of the manufacturer. 250 ng mRNA of each cell line was applied in a 20 μl cDNA synthesis reaction with Superscript II reverse transcriptase (Gibco BRL). Dilutions of this cDNAs served as template in transcript specific amplification reactions.

PCR primers and reaction conditions

PCRs were set up in 25 μl reactions with 0.5 units Taq Polymerase (Qiagen), 200 μM nucleotide mix, 5 μl cDNA template dilution and 0.2 μM gene specific primers, as indicated in Table 3. All reactions were run under the same amplification conditions, differing only in number of cycles (table), 2 min pre-denaturation at 94°C, than for amplification: 45 sec denaturation at 94°C, 45 sec annealing at 62°C and 45 sec elongation at 72°C, except for UGT1A1 which needed longer elongation of 2 min.

Table 3: Sequences of gene specific primers and conditions for PCR reactions. F: forward primer; R: reverse primer for mRNA sequences.

Gene	Primer sequence (5'-3')	cDNA dilution	cycle number
MDR1	F: TGCCTTCATCGAGTCACTGCC R: TCACTGGCGCTTTGTTCCAGC	1:100	26
MRP1	F: TCTCCAAGGAGCTGGACACA R: CGTGGTGACCTGCAATGAGT	1:10	30
UGT1A	F: GATGATGCCCTTGTTTGGTG R: TGTTTTCAAGTTTGGAAATGACTAGGG	1:100	30

UGT1A1	F: AACCTCTGGCAGGAGCAAAGG R: TGTTTTCAAGTTTGGAAATGACTAGGG	1:10	34
CYP3A4	F: TCAGCCTGGTGCTCCTCTATCTAT R: AAGCCCTTATGGTAGGACAAAATATTT	1:10	34
CYP3A5	F: TTGTTGGGAAATGTTTTGTCCTATC R: ACAGGGAGTTGACCTTCATACGTT	1:10	34
PLA2 (house keeping gene)	F: GCTGGTTCAGAAGGCCAAAC R: GGGCCAGACCCAGTCTGATA	1:100	26

Example 5: Expression of genes involved in irinotecan metabolism

Messenger RNA was isolated from the human bladder cancer cell line RT112, its subclone RT112 (MDR1, UGT1A1), the human epithelial cervical cancer cell line KB 3-1 and two subclones KB 3-1 ($MDR1^{+++}$) and KB 3-1 ($MDR1^{+++}$, CYP3A5), and the colon carcinoma cell line LS174T (ATCC CL-188). These mRNAs were reverse transcribed into cDNA and applied as templates in transcript-specific amplification reactions to determine the expression levels of genes involved in irinotecan transport and metabolism (MDR1, MRP1, UGT1A, UGT1A1, CYP3A4, CYP3A5). Amplification of the house keeping gene phospholipase A2 (PLA2) was used as a control for comparable cDNA amounts in the reactions.

The amplification reactions in figure 29 show that the carcinoma cell lines RT112, KB 3-1, and LS174T have no or very low expression of MDR1, respectively. RT112 (MDR1, UGT1A1) is a subclone of RT112, which was selected for resistance to cytotoxic drugs as described in Seemann et al. (Urol Res 1995; 22:353-360), and is characterised by a moderately increased MDR1 expression. The drug resistant subclones KB 3-1 ($MDR1^{+++}$) and KB 3-1 ($MDR1^{+++}$, CYP3A5) were derived similarly from the original KB 3-1 cell line by exposure to MDR1 substrates. These subclones are characterized by highly increased MDR1 expression. They show >20-times more transcripts than the original KB 3-1 cells, implicating a very high MDR1 activity. MRP1 is expressed at the same level in all cell lines. Transcripts of UGT1A enzymes are present only in RT112, RT112 (MDR1, UGT1A1), and

LS174T cells. UGT1A1 is only weakly expressed in RT112, stronger expressed in RT112 (MDR1, UGT1A1) and shows highest expression in LS174T cells. CYP3A4 was solely detected in very small amounts in LS174T. RT112 cells, RT112 (MDR1, UGT1A1), and LS174T show a heterozygous expression of the functionally inactive splice variant and the functionally active transcript of CYP3A5. In contrast, KB 3-1 and KB 3-1 ($MDR1^{+++}$) cells have only the active CYP3A5 transcript and the KB 3-1 ($MDR1^{+++}$, CYP3A5) showed the highest expression of the active CYP3A5 transcript, implicating that the latter have the highest CYP3A5 activity.

Example 6: Colon and other epidermal cancer cell lines with no or low MDR1 and CYP3A5 activity are sensitive to CPT-11 and SN-38.

The colon cancer cell line LS174T, the cervical cancer cell line KB 3-1 and the bladder cancer cell line RT112 were seeded in 96-well culture plates 24 h prior to treatment. Four wells of each cell line were incubated with serial dilutions of CPT-11 and SN-38 and analysed as described above. Figure 30 shows that all three epidermal cancer cell lines stop proliferation and die upon treatment with CPT-11 and SN-38. The concentrations resulting in 50% inhibition (IC_{50}) for CPT-11 are 1.5 μg/ml for LS174T, 2.5 μg/ml for RT112 and 5 μg/ml for KB 3-1 cells. The active metabolite of CPT-11, SN-38 shows a 1000-fold higher efficacy than CPT-11, since 10^3-times lower concentrations cause the same degree of growth inhibition and cell death. The IC_{50} of SN-38 is 5 ng/ml for LS174T cells, 4 ng/ml for RT112 cells and 25 ng/ml for KB 3-1 cells.

These results show that all three epidermal cancer cell lines although derived from different tissues are similarly sensitive to CPT-11 and SN-38 treatment. This also indicates that cancer cells expressing no or only low levels of MDR1 (Figure 29) can be efficiently killed by CPT-11 and SN-38 (Figure 30).

Example 7: MDR1 activity correlates with resistance of cancer cells toward CPT-11 and SN-38

Cells of KB 3-1 and its strongly MDR1 expressing subclones KB 3-1 ($MDR1^{+++}$) and the KB 3-1 ($MDR1^{+++}$, CYP3A5) were seeded in 96-well culture 24 h prior to treatment. Four wells of each cell line were incubated with serial dilutions of CPT-11 and SN-38 and treated as described above. The inhibition curves (Figure 31) of the MDR1 high expresser KB 3-1 subclones (KB 3-1 ($MDR1^{+++}$) and KB 3-1 ($MDR1^{+++}$, CYP3A5)) (Figure 29) demonstrate a significant higher resistance to CPT-11 and SN-38 compared to the MDR1 low expresser KB 3-1 cell line (KB 3-1). The IC_{50} for CPT-11 increases 17 to 40 fold from 5 µg/ml in KB 3-1 to 85 µg/ml in KB 3-1 ($MDR1^{+++}$) and 200 µg/ml in KB 3-1 ($MDR1^{+++}$, CYP3A5) cells. The IC_{50} for SN-38 increases at least 8 times from 25 ng/ml in KB 3-1 to 200 ng/ml in KB 3-1 ($MDR1^{+++}$) and >200 ng/ml in KB 3-1($MDR1^{+++}$, CYP3A5).

CPT-11 and SN-38 are substrates of MDR1, and are therefore removed from the cells by MDR1 activity. The MDR1 expression level correlates inversely with the sensitivity of tumor cells towards CPT-11 and SN-38. Subsequently, the killing of cells with high MDR1 expresser phenotype requires much higher concentrations of CPT-11.

Example 8: UGT1A1 activity correlates with sensitivity towards SN-38 and not towards CPT-11

CPT-11 and SN-38 sensitivity was compared between RT112 cells and its subclone RT112 (MDR1, UGT1A1). Four wells of each cell line were incubated with serial dilutions of CPT-11 and SN-38 and treated as described above.
The difference in sensitivity against CPT-11 is only small as shown in Figure 32A. The IC_{50} of RT112(MDR1, UGT1A1) cells of 4 µg/ml CPT-11 is two-times higher compared to RT112 cells (IC_{50} of 2.5 µg/ml). In contrast to RT112 cells which express no MDR1, RT112 MDR1, UGT1A1) cells express an intermediate amount of MDR1 which can explain the small though significant increase of CPT-11 sensitivity. A much stronger difference exists between RT112 (IC_{50} of 4 ng/ml) and RT112 (MDR1, UGT1A1) cells (IC_{50} of 75 ng/ml) after treatment with SN-38 (Figure 32B). This 19-fold higher resistance of the RT112 (MDR1, UGT1A1) cell line can be explained by the additional detoxifying effect of UGT1A1 which is expressed at a higher level in RT112 (MDR1, UGT1A1) than in RT112 cells (Figure 29). In contrast to SN-38, CPT-11 is not metabolized by UGTs. Therefore, CPT-11-related toxicity

is not affected by UGT1A1 expression and the resistance-enhancing capabilitiy of UGTs in RT112(MDR1, UGT1A1) cells is only detected by application of SN-38.

Example 9: MDR1 inhibition serves as sensitizer towards CPT-11 and SN-38 in MDR1 high expressing but not low expressing cancer cells.

The sensitivity of KB 3-1 cells and its subclones KB 3-1 ($MDR1^{+++}$) and KB 3-1 ($MDR1^{+++}$, CYP3A5) against CPT-11 and SN-38 was assessed after blocking MDR1 function using the specific inhibitor R-Verapamil. Four wells of each cell line were incubated with serial dilutions of CPT-11, SN-38 and analysed as described above. Two wells were additionally treated with the MDR1 inhibitor R-Verapamil. Figure 33 shows that addition of R-Verapamil has only marginal effects on the CPT-11 and SN-38 sensitivity of MDR1 low expresser KB 3-1 cells (CPT-11 and SN-38 IC50s of 5 μg/ml and 25 ng/ml without R-Verapamil versus 4.5 μg/ml and 15 ng/m with R-Verapamil, respectively). In contrast, the sensitivity of the MDR1 expressing cells KB 3-1($MDR1^{+++}$) and KB 3-1($MDR1^{+++}$, CYP3A5) towards CPT-11 and SN-38 was 8-fold and 10-fold higher after inhibition of MDR1 transport function with R-Verapamil. The IC_{50} of KB 3-1($MDR1^{+++}$) cells for CPT-11 decreased from 85 μg/ml without to 10 μg/ml with R-Verapamil and from 200 μg/ml without to 25 μg/ml with R-Verapamil in KB 3-1 ($MDR1^{+++}$, CYP3A5) cells. The effect of MDR1 inhibition during SN-38 treatment is even stronger in these MDR1 high expresser cells, R-Verapamil blocked the MDR1 transport completely and they become as sensitive as KB 3-1 cells.

These results demonstrate that the MDR1 activity is relevant for resistance of cancer cells to CPT-11 and SN-38 and that inhibition of MDR1 sensitises the cells, so that they are more efficiently killed at lower drug concentrations.

Example 10: CYP3A5 activity influences resistance to CPT-11

KB 3-1 ($MDR1^{+++}$) and KB 3-1 ($MDR1^{+++}$, CYP3A5) cells which differ by their amounts of CYP3A5 (Figure 29). Four wells of each cell line were incubated with serial dilutions of CPT-11, SN-38 and analyzed as described above. Two wells were additionally treated with the MDR1 inhibitor R-Verapamil.

Because MDR1 activity is a major determinant of cellular sensitivity toward CPT11 and SN-38, the MDR1 activity in these MDR1 high expresser cell lines was completely blocked using an excess of the specific MDR1 inhibitor R-Verapamil to analyze the impact of CYP3A5 on CPT-11 and SN-38 sensitivity without interference of MDR1.

The high CYP3A5 expresser cell line KB 3-1 ($MDR1^{+++}$, CYP3A5) is with an IC_{50} of 25 μg/ml 2,5-times more resistant to CPT-11 than KB 3-1 ($MDR1^{+++}$) showing an IC_{50} of 10 μg/ml (Figure 34). No difference between these two cell lines can be observed regarding their sensitivity towards SN-38.

These experiments demonstrate a significant impact of CYP3A5 expression on the resistance to CPT-11 in contrast to SN-38. The fact that CYP3A5 activity had no influence on SN-38 toxicity further confirms the CYP3A5 effect, because CPT-11 but not SN-38 is metabolized by CYP3A5.

Example 11: MDR1 genotyping improves therapeutic efficacy of irinotecan by genotype-based prediction and monitoring of drug resistance.

Therapeutic efficacy and adverse effects of irinotecan depend on plasma levels and on intracellular tumor concentrations of the parent compound and the active metabolites (e.g. SN-38). The MDR1 gene controls the PGP-dependent penetration of irinotecan across membranes [Luo et al., Drug Metab Dispos 2002, 30:763-770; Jansen et al., Br J Cancer 1998, 77:359-65 Chu et al., J Pharmacol Exp Ther 1999; 288, 735-41; Sugiyama et al., Cancer Chemother Pharmacol 1998, 42 Suppl:S44-9] and is therefore an important determinant for its systemic availability and intracellular accumulation. The 176C>T nucleotide substitution (SEQ. ID NOs. 217, 218, 219, and 220) of the MDR1 gene (Accession No: M29445) is associated with low PGP expression-related low drug efflux and patient carrying this substitution are more likely to respond to irinotecan treatment for two reasons: 1) Due to the lower amount of PGP in enterocytes more irinotecan can enter the body across the intestinal barrier causing more irinotecan to reach its site of action, the tumor. 2) Due to the lower amount of PGP in the tumor cell membranes more irinotecan can penetrate into the tumor cells to deploy its cytotoxic effects. The currently used standard dose of irinotecan kills highly effective most tumor cells within the first cycles of chemotherapy with only very few surviving drug-resistant tumor cells and

tolerable adverse events. Independently from the mechanisms of drug resistance, in these patients, the number of surviving cells is to small to develop into a drug-resistant tumor which does not respond any longer to irinotecan therapy.

Patients with the high expresser MDR1 genotype (nucleotide C at position 176 of the MDR1 gene, Accession No: M29445) are less likely to respond to irinotecan treatment. Higher doses would be necessary to achieve a sufficiently efficient killing of tumor cells in order to prevent the development of a drug-resistant tumor. However, elevation of irinotecan dosage is limited due to the occurrence of intolerable adverse events (e.g. diarrhea, neutropenia, or thromboembolic complications). Alternatively, efficacy of irinotecan treatment can be improved by addition of a PGP inhibitor. A PGP inhibitor blocks efficiently the PGP function in MDR1 high expresser patients in such a way as to enable irinotecan to concentrate in the tumor cells for exerting its cytotoxicity as effective as in MDR1 low expresser patients. Consequently, genotypically MDR1 high expresser patients become phenotypically comparable to MDR1 low expressers.

According to the number of low or high expresser alleles of the MDR1 gene, individuals can be classified as having either extensive (ET, two high expresser alleles), intermediate (IT, one high expresser, one low expresser allele) or poor transport capacity (PT, two low expresser alleles). By genetic testing prior to onset of treatment with irinotecan, patients can be classified as ET, IT, or PT and the MDR1-related transport capacity of the patients can be predicted. The individual risk of an insufficient anticancer treatment increases with the number of MDR1 high expresser alleles. Individuals with ET genotype are at the highest risk to suffer from insufficient response to irinotecan and are at the highest risk to develop a drug resistant tumor. ET patients should be treated with a PGP-inhibitor in addition to irinotecan and more closely monitored for adverse events and for the development of chemotherapy-related drug-resistance. Furthermore, these patients, who are at high risk for developing a drug-resistant tumor, can particularly benefit from taking a tumor biopsy between each cycle of chemotherapy with subsequent individual profiling of tumor cells for drug resistance.

Claims

1. A method of using irinotecan to treat a patient suffering from cancer which comprises:

   (a) determining if the patient has one or more variant alleles of the MDR1 gene in the cancerous tissue;

   (b) in a patient having one or more of such variant alleles, administering to the patient an amount of irinotecan which is sufficient to treat a patient having such variant alleles which amount is increased or decreased in comparison to the amount that is administered without regard to the patient's alleles in the MDR1 gene.

2. The method of claim 1 wherein the cancer is colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, or pancreatic cancer.

3. The method of claim 2 in which:

   (a) the one or more variant alleles result in the patient expressing low amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is decreased to avoid toxicity; or

   (b) the one or more variant alleles result in the patient expressing high amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is increased to enhance efficacy.

4. The method of claim 3 wherein the one or more variant alleles are in the promoter region of the MDR1 gene.

5. The method of claim 3 wherein the one or more variant alleles are in the coding region of the MDR1 gene.

6. The method of claim 3 wherein the one or more variant alleles are not in either the promoter region or the coding region of the MDR1 gene.

7. The method of claim 3 wherein the one or more variant alleles are in both the promoter region and the coding region of the MDR1 gene.

8. The method of claim 3 wherein the one or more variant alleles comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of any one of SEQ ID NOs: 337, 338, 341, 342, 345, 346, 349, 350, 353, 354, 357, 358, 361, 362, 365, 366, 369, 370, 373, 374, 377, 378, 381, 382, 385, 386, 389, 390, 393, 394, 397, 398, 401, 402, 405, 406, 409, 410, 413, 414, 417, 418, 421, 422, 425, 426, 429, 430, 433, 434, 437, 438, 441, 442, 445, 446, 449, 450, 453, 454, 457, 458, 461, 462, 465, 466, 469, 470, 473, 474, 477, 478, 481, 482, 485, 486; 489, 490, 493, 494, 497, 498, 501, 502, 505, 506, 509, 510, 513, 514, 517, 518, 521, 522, 525, 526 636, 637, 640 and/or 641;

(b) a polynucleotide encoding a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 606, 608, 610, 612, 618, 620, 622, 624, and/or 628;

(c) a polynucleotide capable of hybridizing to a Multidrug Resistance 1 (MDR1) gene, wherein said polynucleotide is having at a position corresponding to positions 140837, 141529, 141590, 145984,

171404, 171456, 171466, 171511, 171512, 174901, 175068, 175074, 175142, 175180, 139015, 139064, 139119, 139177, 139276, 140118, 140216, 140490, 140568, 140576, 140595, 140727, 139479, 139619 of the MDR1 gene (Accession No: AC002457) and/or 84701, 83946, 83973, 84032, 84074, 84119, 77811, 78170, 73252, 70200, 70204, 70237, 70253, 70371, 65241, 50537, 43263, 43162 of the MDR1 gene (Accession No: AC005068) and/or 101, 308 of the MDR1 gene (Accession No: M29432) and/or 137, 176 of the MDR1 gene (Accession No: M29445), a substitution or deletion of at least one nucleotide;

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having at a position corresponding to position 83946, 70200, 70237, 65241 of the MDR1 gene (Accession No: AC005068) and/or 101 of the MDR1 gene (Accession No: M29432) and/or 141529, 174901, 139177, 140118, 140568, 140727, 139479 of the MDR1 gene (Accession No: AC002457) an A, at a position corresponding to position 308 of the MDR1 gene (Accession No: M29432) and/or 84701, 83973, 84074, 84119, 78170, 70204, 70253, 70371, 50537, 43162 of the MDR1 gene (Accession No: AC005068) and/or 137 or 176 of the MDR1 gene (Accession No: M29445) and/or 145984, 171466, 175068, 175074, 139064, 139276, 140576 of the MDR1 gene (Accession No: AC002457) a T, at a position corresponding to position 140837, 171404, 171456, 171511, 171512, 139119, 140490, 139619 of the MDR1 gene (Accession No: AC002457) and/or 43263 of the MDR1 gene (Accession No: AC005068) a C, at a position corresponding to position 84032, 77811, 73252 of the MDR1 gene (Accession No: AC005068) and/or 141590, 175142, 175180, 139015, 140216, 140595 of the MDR1 gene (Accession No: AC002457) a G;

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to positions 21, 103, 168, 400, 893, 999, 1001, 1107, and/or 1141 of the MDR1 polypeptide (Accession No: G2506118);

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution of Asn to Asp at a position corresponding to position 21 of the MDR1 polypeptide (Accession No: G2506118) or/and Phe to Leu at a position corresponding to position 103 of the MDR1 polypeptide (Accession No: G2506118) or/and Val to Ile at a position corresponding to position 168 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Asn at a position corresponding to position 400 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 999 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 1001 of the MDR1 polypeptide (Accession No: G2506118) or/and Gln to Pro at a position corresponding to position 1107 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Thr at a position corresponding to position 1141 of the MDR1 polypeptide (Accession No: G2506118).

9. The method of claim 8 wherein the one or more variant alleles comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of any one of SEQ ID NO: 345, 417 or 636:

(b) a polynucleotid encoding a polypeptide having the amino acid sequence of SEQ ID NO: 612 or 618;

(c) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having a substitution at a position corresponding to position 101 of the MDR1 gene (Accession No: M29432), 176 of the MDR1 gene (Accession No: M29445), or 88883 of the MDR1 gene (Accession No: GI:10122135);

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having an A at a position corresponding to position

101 of the MDR1 gene (Accession No: M29432) or 88883 of the MDR1 gene (Accession No: GI:10122135), or a T at a position corresponding to position 176 of the MDR1 gene (Accession No: M29445) or 88883 of the MDR1 gene (Accession No: GI:10122135);

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to position 400 or 893 of the MDR1 polypeptide (Accession No: G2506118); and

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution of Ser to Asn at a position corresponding to position 400 or Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118).

10. The method of claim 8 in which the one or more variant alleles results in the patient expressing low amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is decreased.

11. The method of claim 8 in which the one or more variant alleles results in the patient expressing high amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is increased.

12. The method of claim 9 in which the one or more variant alleles results in the patient expressing low amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is decreased.

13. The method of claim 9 in which the one or more variant alleles results in the patient expressing high amounts of the MDR1 gene product, whereby the amount of irinotecan administered to the patient is increased.

14. A method for determining whether a patient is at risk for a toxic reaction to treatment with irinotecan which comprises determining if the patient has one or more variant alleles of the MDR1 gene.

15. The method of claim 14 which further comprises administering to the patient reduced amounts of irinotecan.

16. A method for determining the optimum treatment regimen for administering irinotecan to a patient suffering from cancer which comprises:

(a) determining if the patient has one or more variant alleles of the MDR1 gene;

(b) in a patient having one or more of such alleles altering the regimen to reduce peak amounts of irinotecan in the patient in comparison to the peak amount in the patient when irinotecan is administered without regard to the patient's alleles in the MDR1 gene.

17. A method of treating cancer in a patient having one or more variant alleles of the MDR1 gene such that expression levels of the MDR1 gene product are lower than in the general population and so indicates high sensitivity to irinotecan which comprises administering to the patient a decreased amount of irinotecan.

18. A method of treating cancer in a patient having one or more variant alleles of the MDR1 gene such that expression levels of the MDR1 gene product are higher than in the general population and so indicates resistance or predisposition to resistance to irinotecan which comprises administering to the patient an increased amount of irinotecan.

19. The method of claim 18 in which patients that have a variant allele that indicates resistance or predisposition to resistance are treated with an MDR1 inhibitor.

20. The method of claim 19 wherein the MDR1 inhibitor is selected from the group consisting of: GF120918, LY335979, XR 9576, XR 9051, flavonoids (e.g. apigenin, genistin, naringin, quercetin, flavone, flavonone, flavopiridol), bergamottin, Clarithromycin, Ketoconazole, Reserpine, 1,9-dideoxyforskolin, Azidopine, Dimethyl-b-cyclodextrin, Ivermectin, SDZ PSC 833, SDZ 280-446, B669, B-859-35 (R-enantiomere) and its major metabolite, MS-209 (quinolone derivative), PAK-104p, Amiloride, Amytriptyline, Atorvastatin, Aureobasidin & analogues, Berrylium fluoride (BeFx), Calmodulin inhibitors, Chloroquine, Chloropromazine, Clofazimine, Cremophor EL, Diltiazem, Verapamil, nifedipine, bepridil, nicardipine, niguldipine, nitrendipine, trifluoperazine, felodipine, Valinomycin, Dipyridamole, Erythromycine, Fluoroquinolones: fleroxacin, enoxacin, grepafloxacin, levofloxacin, norfloxacine, Glibenclamides & analogues, Gluconate salts, Gramicidin, Hydrocortisone, Itraconazole, Lidocaine, Phosphatidyl-choline, Pristinamycin Ia, Propafenone, Propranolol, Talinolol, Pyridine analogue, Quercetin 4'-b-glucoside, Quinine & quinidine, quinacrine, cinchonine, Ritonavir , Saquinavir, Nelfinavir, Tamoxifen and metabolites, Taxoid (Tetracyclic taxopine C & derivatives), Terfenadine.

21. The method of claim 17 which further comprises monitoring the patient during treatment by assaying for changes in expression levels of the MDR1 gene product in the cancerous cells whereby an increase in the expression level of the MDR1 gene product is compensated for by an increase in the amount of irinotecan administered to the patient.

22. A method of treating cancer in a patient which comprises internally administering to the patient an effective amount of irinotecan, wherein the

treatment regimen is modified based upon the genotype of the patient's MDR1 gene.

23. A method of treating a population of patients suffering from cancer which comprises:

(a) determining, on a patient by patient basis, if the patient has one or more variant alleles of the MDR1 gene;

(b) in a patient having one or more of such variant alleles, administering to the patient an amount of irinotecan which is sufficient to treat a patient having such variant alleles which amount is increased or decreased in comparison to the amount that is administered without regard to the patient's alleles in the MDR1 gene.

24. A method for predicting sensitivity to irinotecan in a patient suffering from cancer which comprises determining if the patient has one or more variant alleles of the MDR1 gene, which alleles indicate that the cancerous cells express low or high amounts of the MDR1 protein, whereby low expression indicates high sensitivity to irinotecan and high expression indicates resistance or predisposition to resistance to irinotecan.

25. The method of claim 24 which further comprises administering to patients that have a genotype that indicates resistance or predisposition to resistance a MDR1 inhibitor.

26. The method of claim 25 wherein the MDR1 inhibitor is selected from the group consisting of: GF120918, LY335979, XR 9576, XR 9051, flavonoids (e.g. apigenin, genistin, naringin, quercetin, flavone, flavonone, flavopiridol), bergamottin, Clarithromycin, Ketoconazole, Reserpine, 1,9-dideoxyforskolin, Azidopine, Dimethyl-b-cyclodextrin, Ivermectin, SDZ PSC 833, SDZ 280-446,

B669, B-859-35 (R-enantiomere) and its major metabolite, MS-209 (quinolone derivative), PAK-104p, Amiloride, Amytriptyline, Atorvastatin, Aureobasidin & analogues, Berrylium fluoride (BeFx), Calmodulin inhibitors, Chloroquine, Chloropromazine, Clofazimine, Cremophor EL, Diltiazem, Verapamil, nifedipine, bepridil, nicardipine, niguldipine, nitrendipine, trifluoperazine, felodipine, Valinomycin, Dipyridamole, Erythromycine, Fluoroquinolones: fleroxacin, enoxacin, grepafloxacin, levofloxacin, norfloxacine, Glibenclamides & analogues, Gluconate salts, Gramicidin, Hydrocortisone, Itraconazole, Lidocaine, Phosphatidyl-choline, Pristinamycin Ia, Propafenone, Propranolol, Talinolol, Pyridine analogue, Quercetin 4'-b-glucoside, Quinine & quinidine, quinacrine, cinchonine, Ritonavir , Saquinavir, Nelfinavir, Tamoxifen and metabolites, Taxoid (Tetracyclic taxopine C & derivatives), Terfenadine.

27. The method of claim 25 wherein the patients that have a genotype that indicates resistance or predisposition to resistance are monitored during treatment by assaying for changes of expression levels of the MDR1 gene product in the cancerous cells so that an updated prediction of sensitivity to irinotecan may be determined.

28. Use of irinotecan or a derivative thereof for the preparation of a pharmaceutical composition for treating colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer in a subject having a genome with a first variant allele which comprises a polynucleotide selected from the group consisting of:

(a) a polynucleotide having the nucleic acid sequence of any one of SEQ ID NOs: 337, 338, 341, 342, 345, 346, 349, 350, 353, 354, 357, 358, 361, 362, 365, 366, 369, 370, 373, 374, 377, 378, 381, 382, 385, 386, 389, 390, 393, 394, 397, 398, 401, 402, 405, 406, 409, 410, 413, 414, 417, 418, 421, 422, 425, 426, 429, 430, 433, 434, 437, 438, 441, 442, 445, 446, 449, 450, 453, 454, 457, 458, 461, 462, 465, 466, 469, 470, 473, 474, 477, 478, 481, 482, 485, 486, 489, 490, 493, 494, 497, 498,

501, 502, 505, 506, 509, 510, 513, 514, 517, 518, 521, 522, 525 and/or 526;

(b) a polynucleotide encoding a polypeptide having the amino acid sequence of any one of SEQ ID NOs: 606, 608, 610, 612, 618, 620, 622, 624, and/or 628;

(c) a polynucleotide capable of hybridizing to a Multidrug Resistance 1 (MDR1) gene, wherein said polynucleotide is having at a position corresponding to positions 140837, 141529, 141590, 145984, 171404, 171456, 171466, 171511, 171512, 174901, 175068, 175074, 175142, 175180, 139015, 139064, 139119, 139177, 139276, 140118, 140216, 140490, 140568, 140576, 140595, 140727, 139479, 139619 of the MDR1 gene (Accession No: AC002457) and/or 84701, 83946, 83973, 84032, 84074, 84119, 77811, 78170, 73252, 70200, 70204, 70237, 70253, 70371, 43263, 43162 of the MDR1 gene (Accession No: AC005068) and/or 101, 308 of the MDR1 gene (Accession No: M29432) and/or 137, 176 of the MDR1 gene (Accession No: M29445), a substitution or deletion of at least one nucleotide;

(d) a polynucleotide capable of hybridizing to a MDR1 gene, wherein said polynucleotide is having at a position corresponding to position 83946, 70200, 70237of the MDR1 gene (Accession No: AC005068) and/or 101 of the MDR1 gene (Accession No: M29432) and/or 141530, 174901, 139177, 140118, 140568, 140727, 139479 of the MDR1 gene (Accession No: AC002457) an A, at a position corresponding to position 308 of the MDR1 gene (Accession No: M29432) and/or 84701, 83973, 84074, 84119, 78170, 70204, 70253, 70371, 43162 of the MDR1 gene (Accession No: AC005068) and/or 137 or 176 of the MDR1 gene (Accession No: M29445) and/or 145984, 171466, 175068, 175074, 139064, 139276, 140576 of the MDR1 gene (Accession No: AC002457) a T, at a position corresponding to position 140827, 171404, 171456, 171511, 171512, 139119, 140490, 139619 of the MDR1 gene (Accession No: AC002457) and/or 84032, 77811, 73252 of the MDR1 gene (Accession No: AC005068) a C, at a position corresponding to position 43263 of the MDR1 gene

(Accession No: AC005068) and/or 141590, 175142, 175180, 139015, 140216, 140595 of the MDR1 gene (Accession No: AC002457) a G;

(e) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution at a position corresponding to positions 21, 103, 168, 400, 893, 999, 1001, 1107, and/or 1141 of the MDR1 polypeptide (Accession No: G2506118);

(f) a polynucleotide encoding an MDR1 polypeptide or fragment thereof, wherein said polypeptide comprises an amino acid substitution of Asn to Asp at a position corresponding to position 21 of the MDR1 polypeptide (Accession No: G2506118) or/and Phe to Leu at a position corresponding to position 103 of the MDR1 polypeptide (Accession No: G2506118) or/and Val to Ile at a position corresponding to position 168 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Asn at a position corresponding to position 400 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Ser at a position corresponding to position 893 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 999 of the MDR1 polypeptide (Accession No: G2506118) or/and Ala to Thr at a position corresponding to position 1001 of the MDR1 polypeptide (Accession No: G2506118) or/and Gln to Pro at a position corresponding to position 1107 of the MDR1 polypeptide (Accession No: G2506118) or/and Ser to Thr at a position corresponding to position 1141 of the MDR1 polypeptide (Accession No: G2506118).

29. The use of any one of claim 28, wherein a nucleotide deletion, addition and/or substitution comprised by said polynucleotide results in an altered expression of the variant allele compared to the corresponding wild type alleles.

30. The use of claim 29, wherein said altered expression is decreased or increased expression.

31. The use of any one of claims 28 to 30, wherein a nucleotide deletion, addition and/or substitution comprised by said polynucleotide results in an altered activity of the polypeptide encoded by the variant allele compared to the polypeptide encoded by the corresponding wild type allele.

32. The use of claim 31, wherein said altered activity is decreased or increased activity.

33. The use of any one of claim 28 to 32, wherein said subject is an animal.

34. The use of claim 33, wherein said subject is a mouse.

35. The use of any one of claims 28 to 32, wherein said subject is a human.

36. The use of claim 35, wherein said human is African or Asian.

37. A method for selecting a suitable therapy for a subject suffering from colorectal cancer, cervical cancer, gastric cancer, lung cancer, malignant glioma, ovarian cancer, and pancreatic cancer, wherein said method comprises:

(a) determining the presence or absence of a variant allele as specified in any one of items 1 to 5 in the genome of a subject in a sample obtained from said subject; and

(b) selecting a suitable therapy for said subject based on the results obtained in (a).

Figure 1

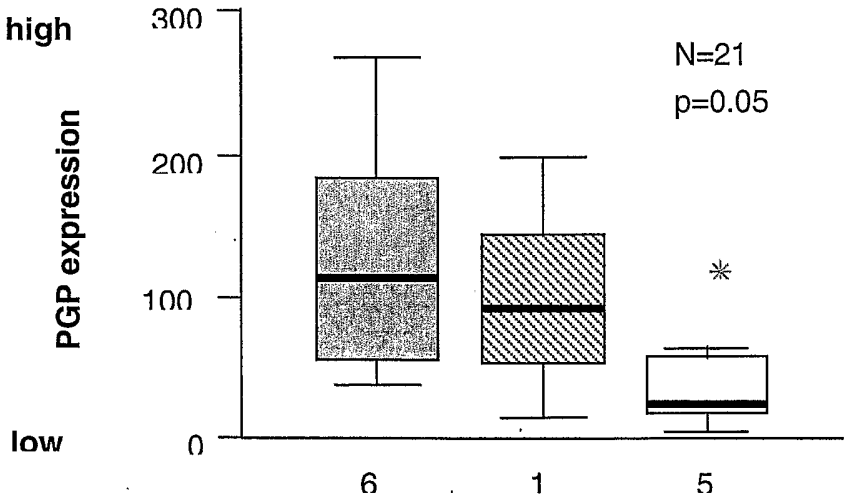

high
PGP expression
low
300
200
100
0
N=21
p=0.05
*
6
1
5
MDR1 3435C>T genotype: C C
C T
T T

Figure 2

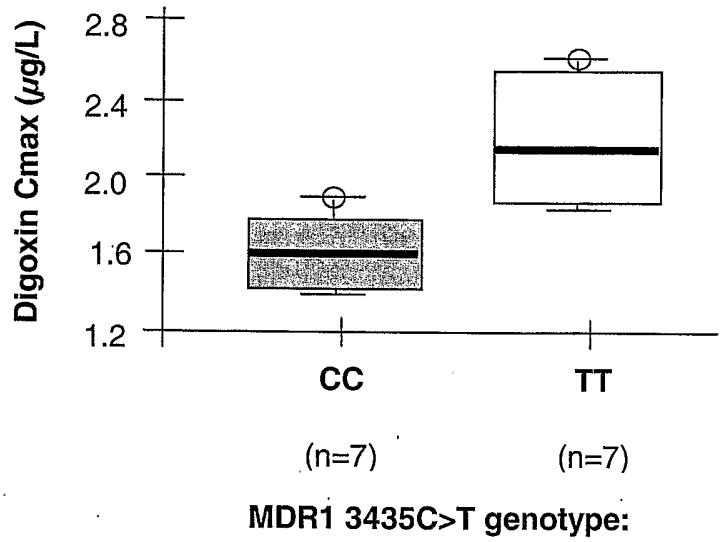

Digoxin Cmax (µg/L)
2.8
2.4
2.0
1.6
1.2
CC
TT
(n=7)
(n=7)
MDR1 3435C>T genotype:

Figure 3

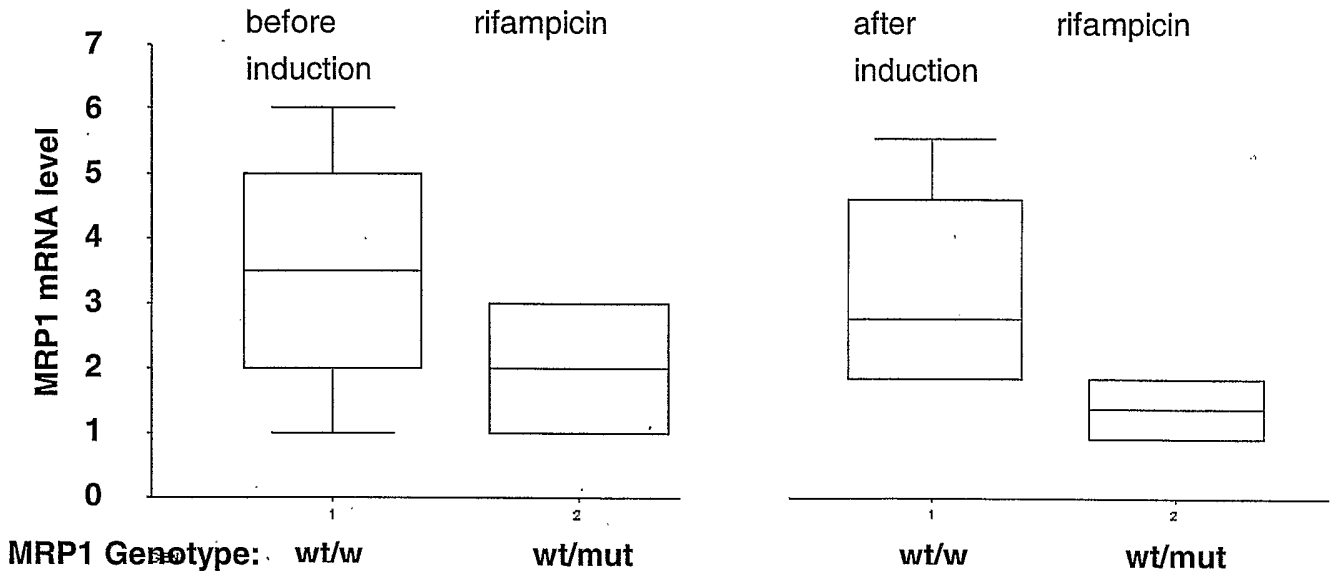

before induction
rifampicin
after induction
rifampicin
MRP1 mRNA level
0
1
2
3
4
5
6
7
MRP1 Genotype:
wt/w
wt/mut
wt/w
wt/mut

Figure 1

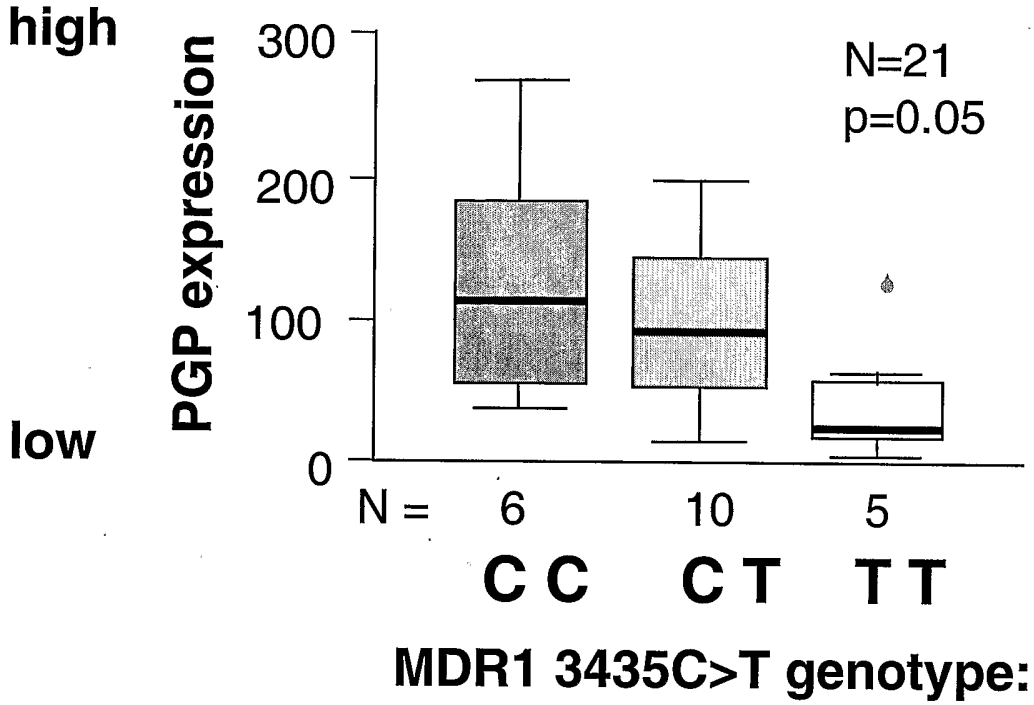
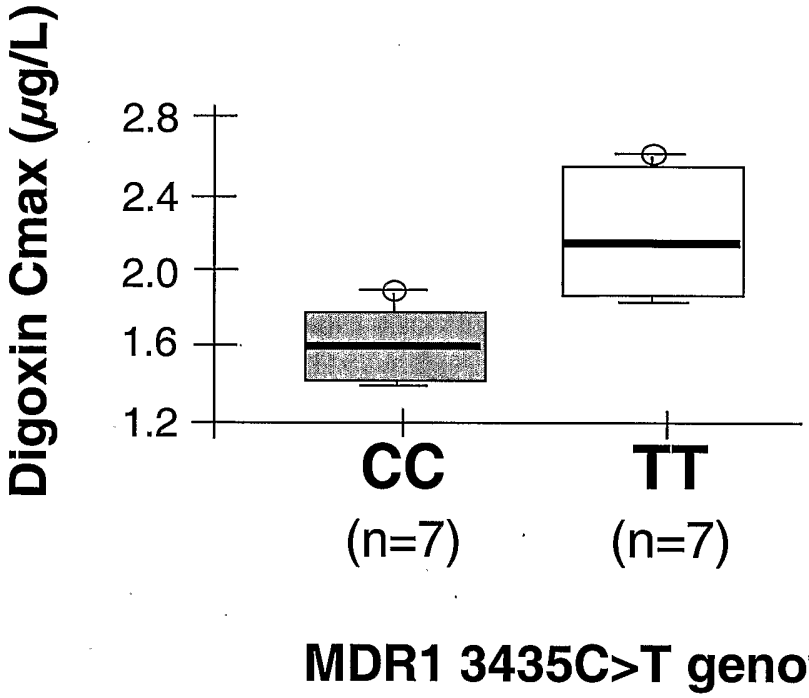

high
low
PGP expression
300
200
100
0
N=21
p=0.05
N = 6 10 5
C C C T T T
MDR1 3435C>T genotype:

Figure 2


Digoxin Cmax (µg/L)
2.8
2.4
2.0
1.6
1.2
CC
(n=7)
TT
(n=7)
MDR1 3435C>T genotype:

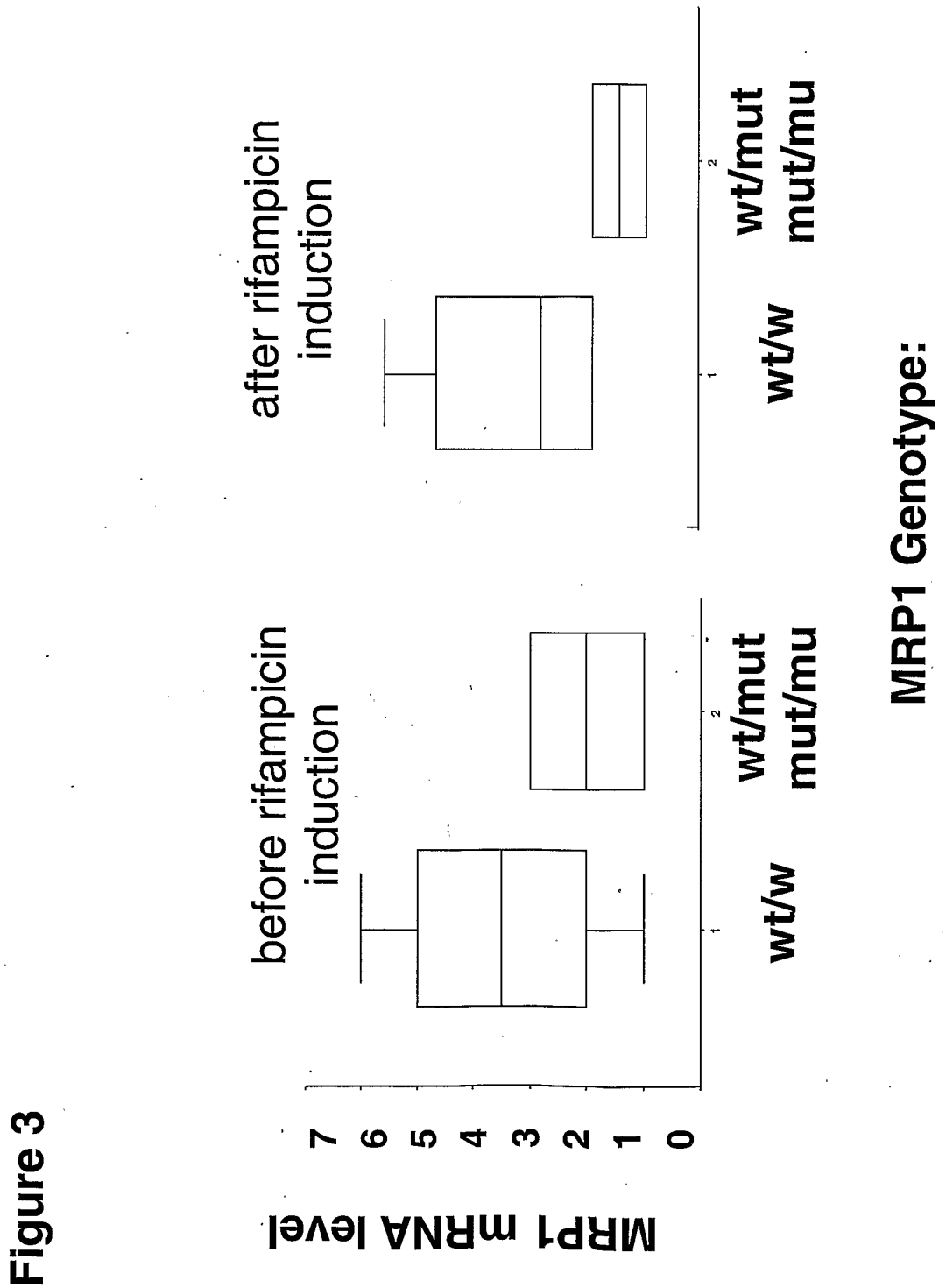

MRP1 mRNA level
7
6
5
4
3
2
1
0
before rifampicin induction
after rifampicin induction
wt/w
wt/mut
mut/mu
MRP1 Genotype:

Figure 3

Figure 29

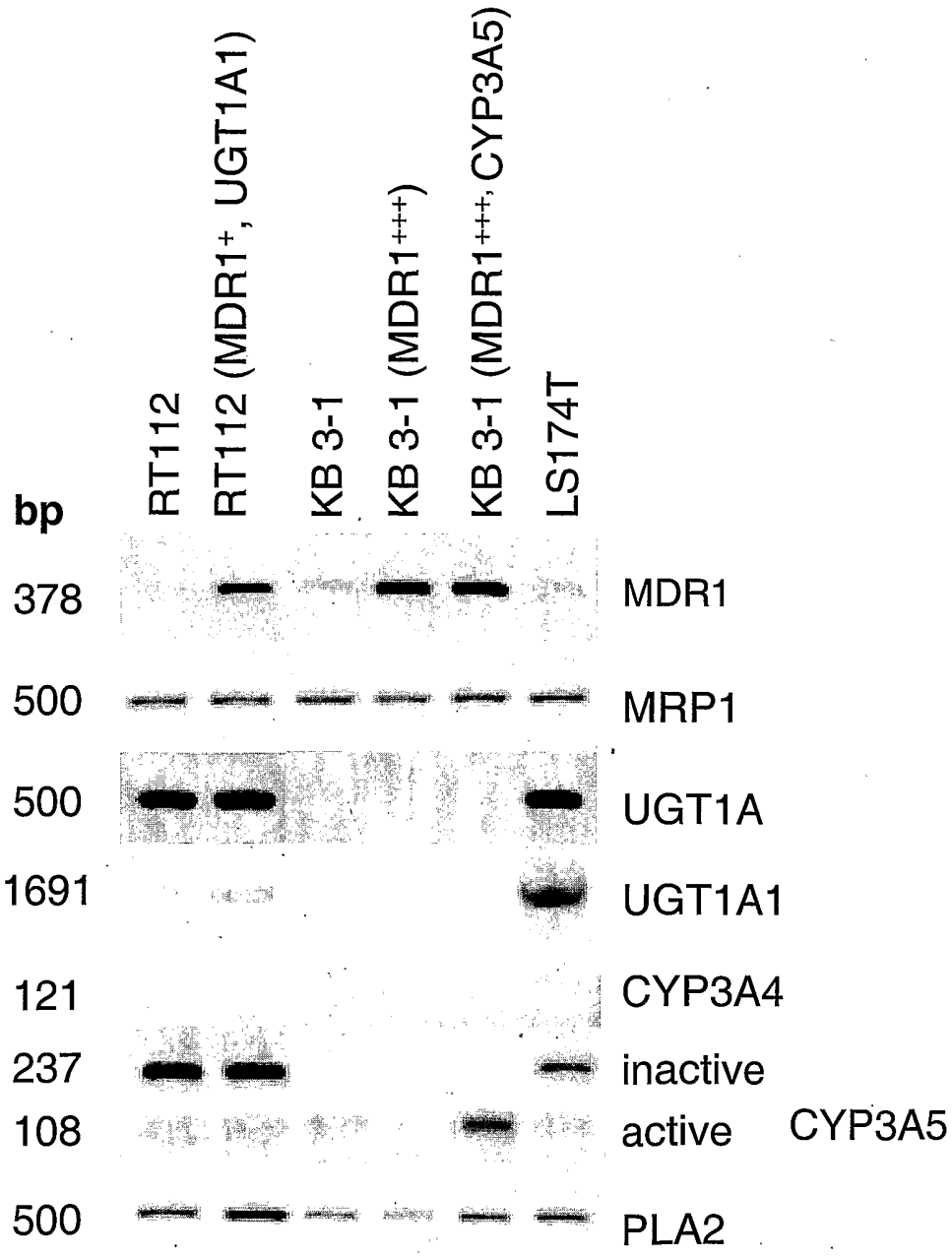
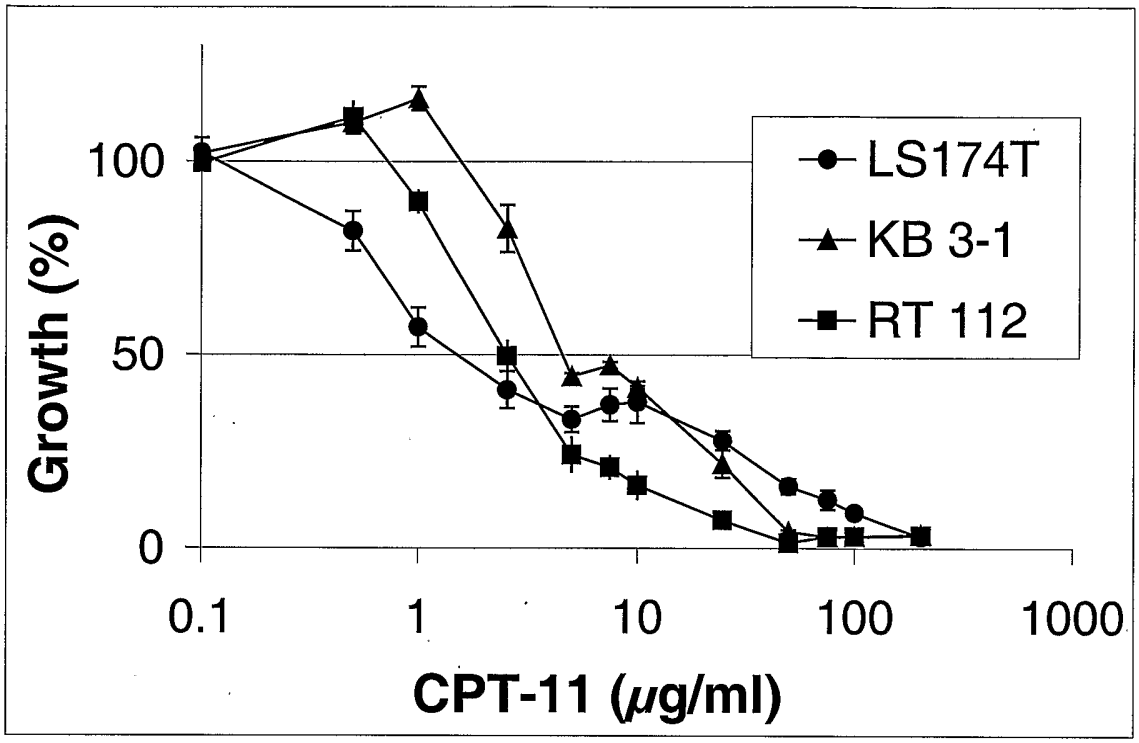

bp
RT112
RT112 (MDR1+, UGT1A1)
KB 3-1
KB 3-1 (MDR1+++)
KB 3-1 (MDR1+++, CYP3A5)
LS174T
378
MDR1
500
MRP1
500
UGT1A
1691
UGT1A1
121
CYP3A4
237
inactive
108
active
CYP3A5
500
PLA2

Figure 30


Growth (%)
100
50
0
0.1
1
10
100
1000
CPT-11 (µg/ml)
LS174T
KB 3-1
RT 112

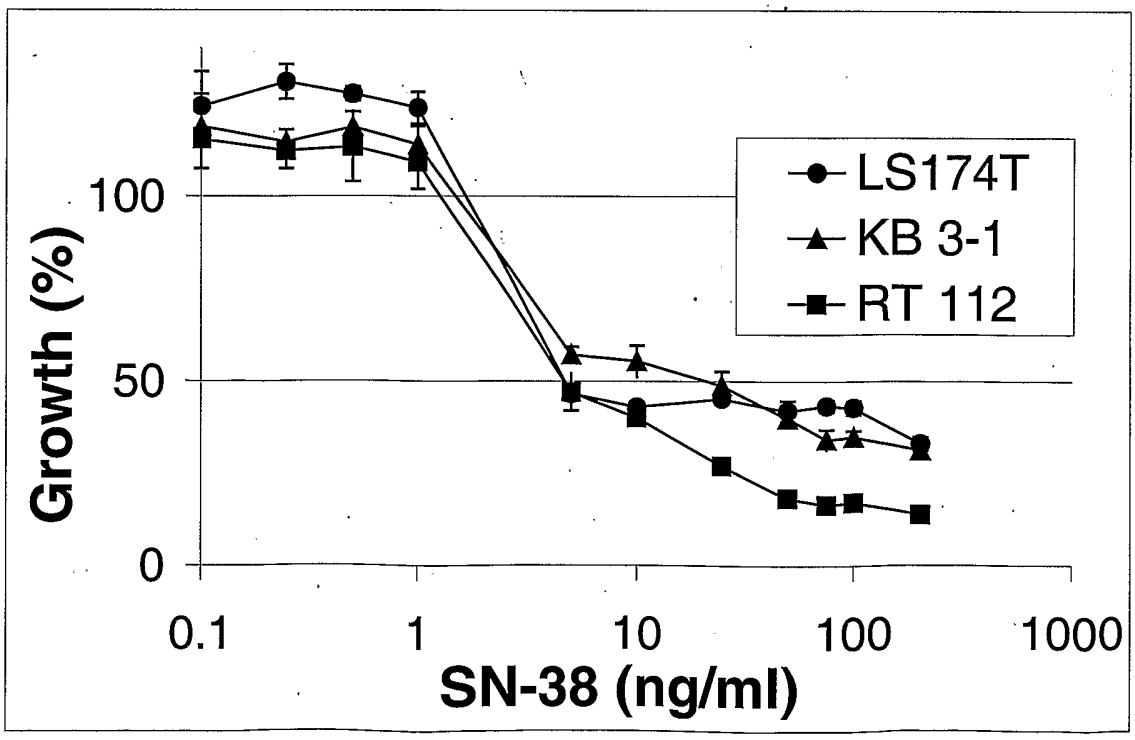
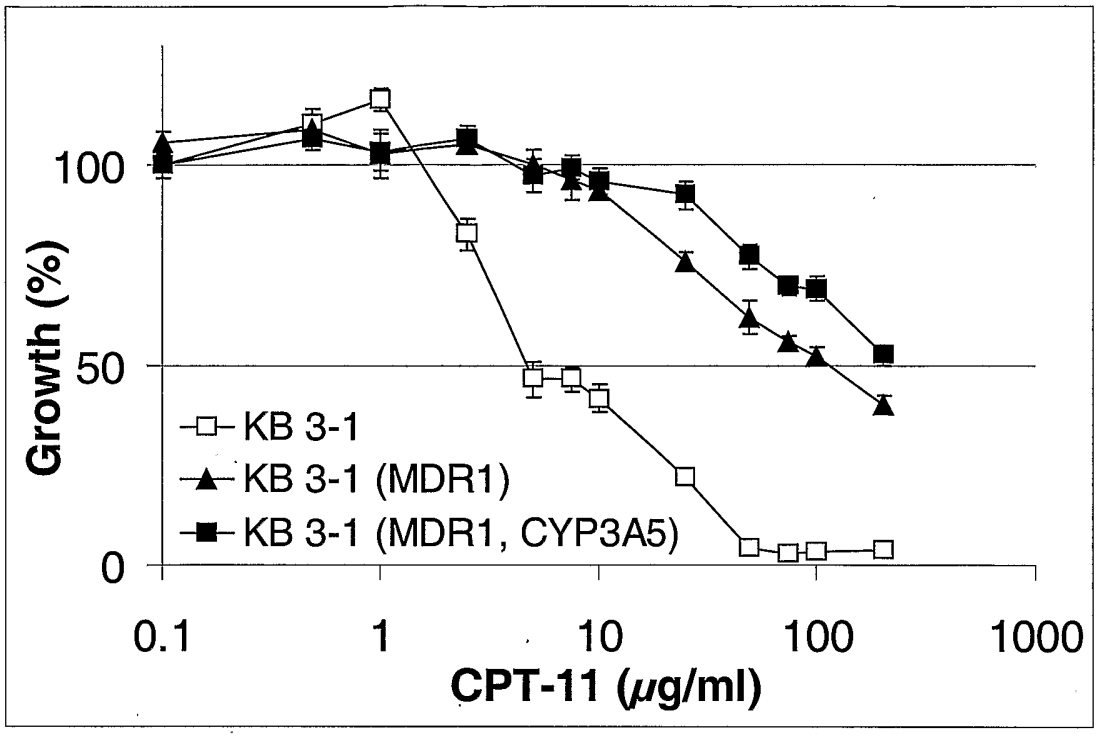

Growth (%)
100
50
0
0.1
1
10
100
1000
SN-38 (ng/ml)
LS174T
KB 3-1
RT 112

Figure 31


100
50
0
Growth (%)
KB 3-1
KB 3-1 (MDR1)
KB 3-1 (MDR1, CYP3A5)
0.1
1
10
100
1000
CPT-11 (µg/ml)

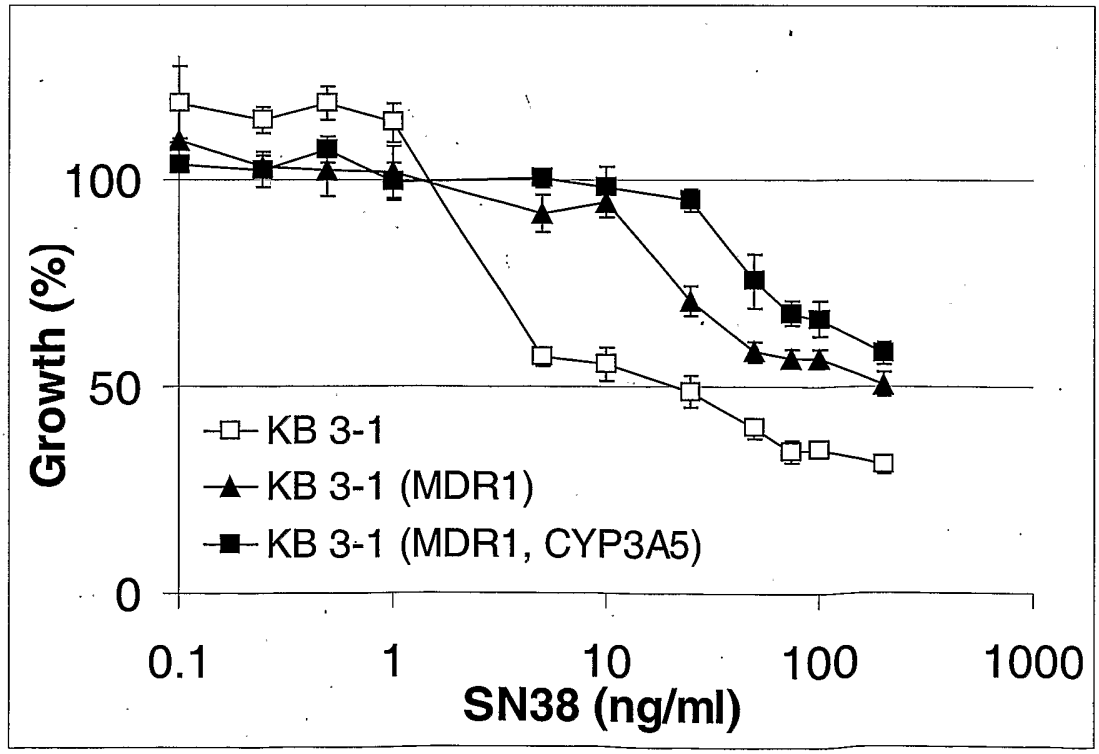
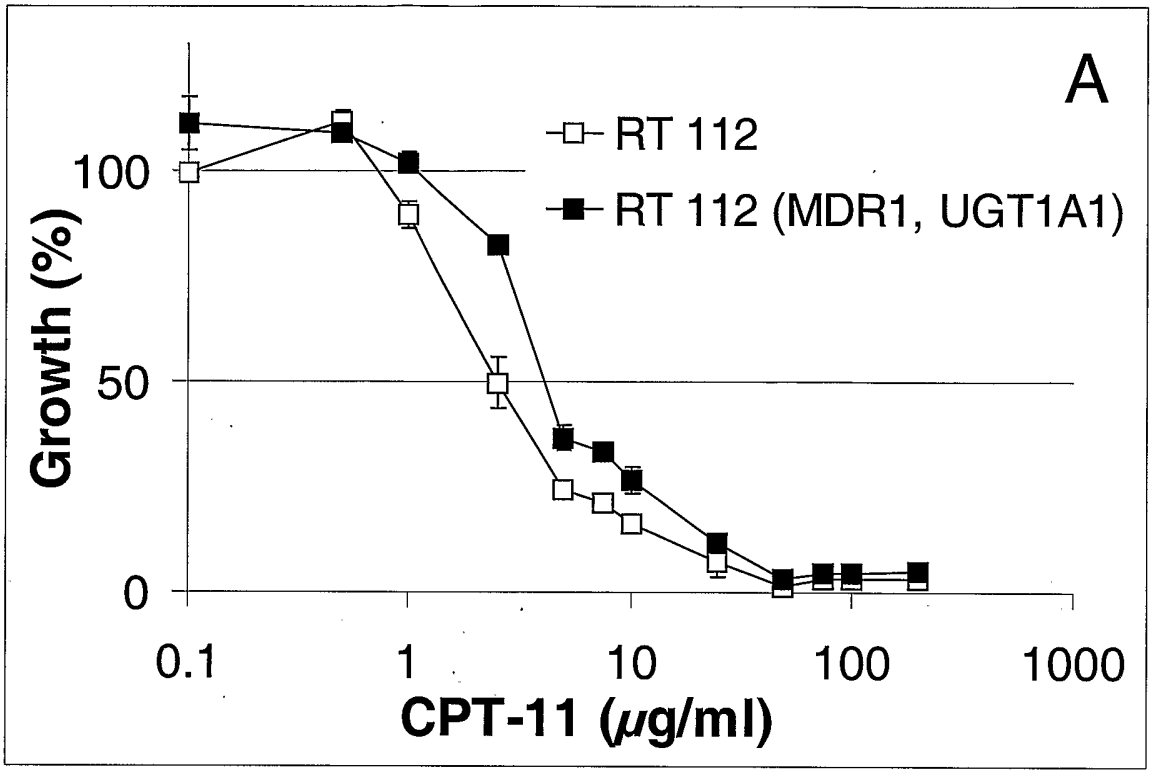

100
50
0
Growth (%)
KB 3-1
KB 3-1 (MDR1)
KB 3-1 (MDR1, CYP3A5)
0.1
1
10
100
1000
SN38 (ng/ml)

Figure 32


A
RT 112
RT 112 (MDR1, UGT1A1)
Growth (%)
100
50
0
0.1
1
10
100
1000
CPT-11 (µg/ml)

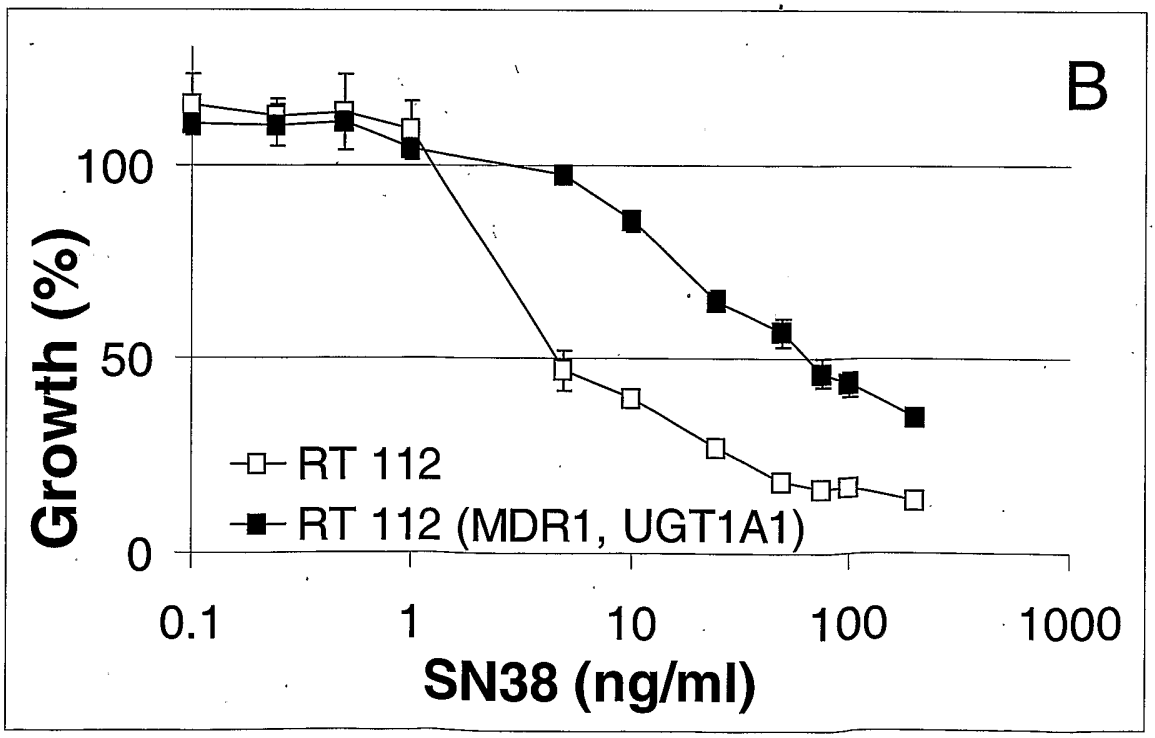
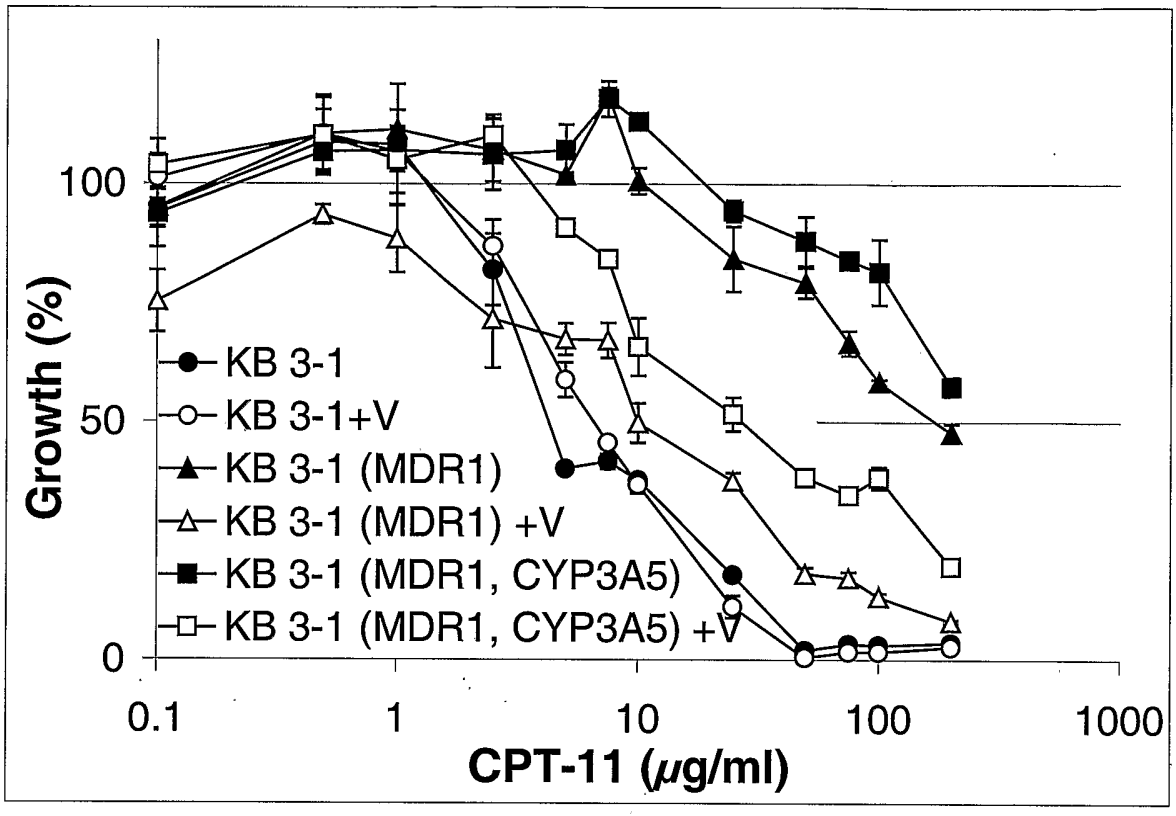

B
Growth (%)
100
50
0
RT 112
RT 112 (MDR1, UGT1A1)
0.1
1
10
100
1000
SN38 (ng/ml)

Figure 33


100
50
0
Growth (%)
KB 3-1
KB 3-1+V
KB 3-1 (MDR1)
KB 3-1 (MDR1) +V
KB 3-1 (MDR1, CYP3A5)
KB 3-1 (MDR1, CYP3A5) +V
0.1
1
10
100
1000
CPT-11 (µg/ml)

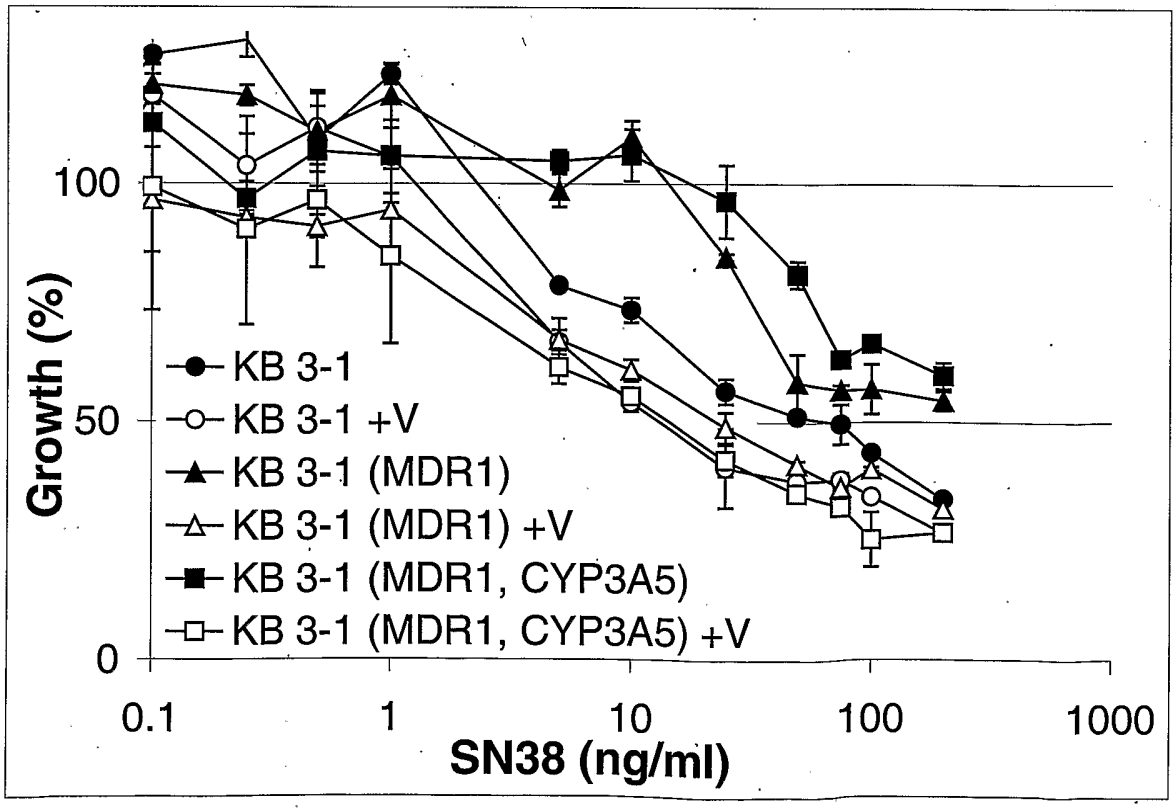
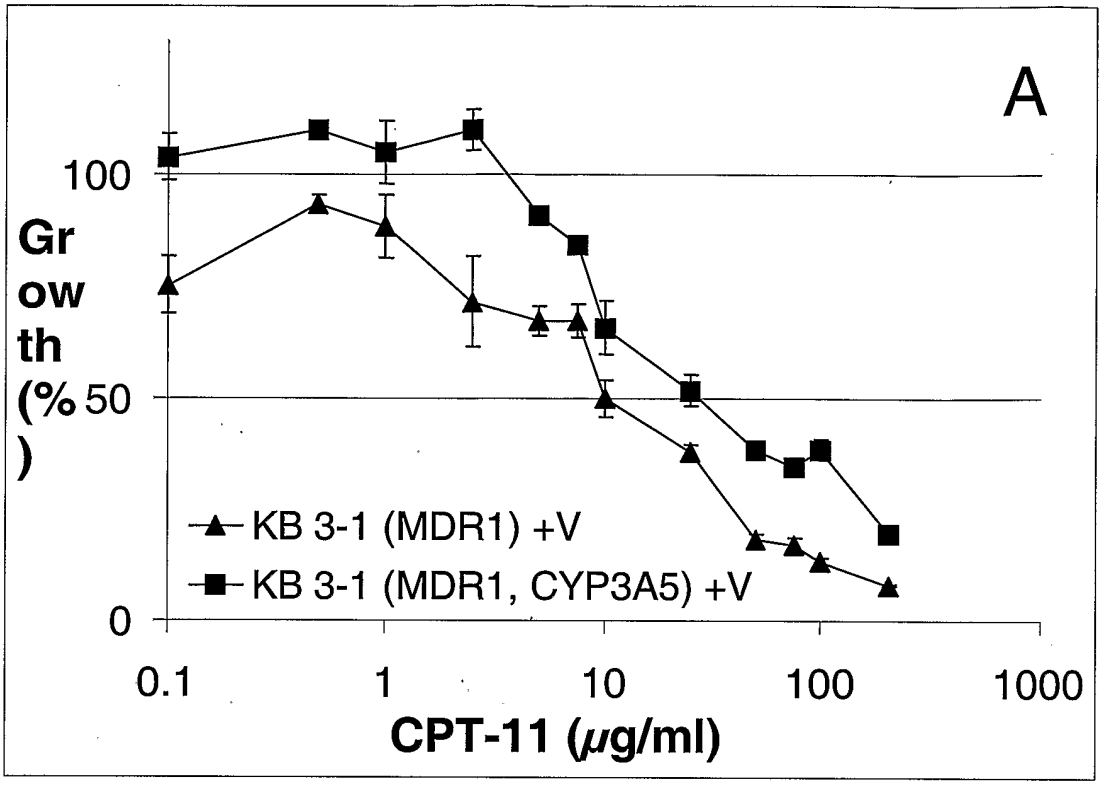
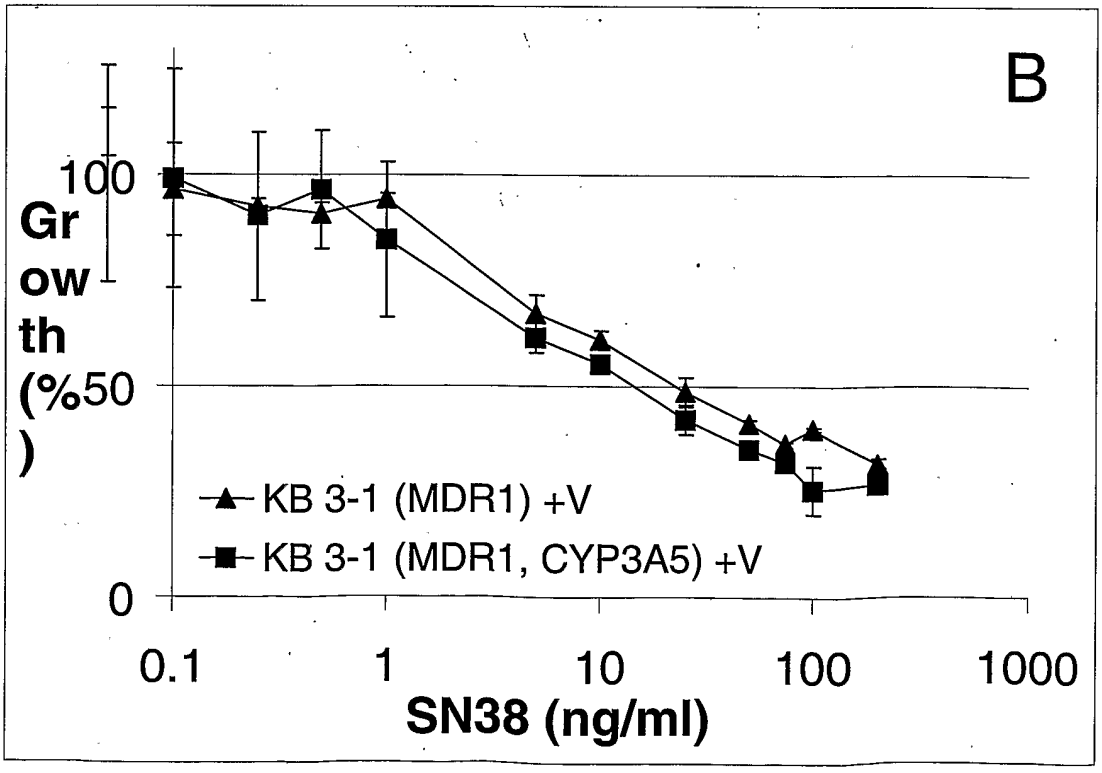

100
50
0
Growth (%)
KB 3-1
KB 3-1 +V
KB 3-1 (MDR1)
KB 3-1 (MDR1) +V
KB 3-1 (MDR1, CYP3A5)
KB 3-1 (MDR1, CYP3A5) +V
0.1
1
10
100
1000
SN38 (ng/ml)

Figure 34


A
100
Gr
ow
th
(%
)
50
0
KB 3-1 (MDR1) +V
KB 3-1 (MDR1, CYP3A5) +V
0.1
1
10
100
1000
CPT-11 (µg/ml)


B
100
Gr
ow
th
(%50
)
0
KB 3-1 (MDR1) +V
KB 3-1 (MDR1, CYP3A5) +V
0.1
1
10
100
1000
SN38 (ng/ml)