(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
11 March 2004 (11.03.2004)

PCT

(10) International Publication Number
WO 2004/020968 A2

(51) International Patent Classification[7]: G01N

(21) International Application Number:
PCT/US2003/023926

(22) International Filing Date: 30 July 2003 (30.07.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/407,391	30 August 2002 (30.08.2002)	US
10/356,736	30 January 2003 (30.01.2003)	US

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(81) Designated States *(national)*: AE, AG, AL, AM, AT (utility model), AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ (utility model), CZ, DE (utility model), DE, DK (utility model), DK, DM, DZ, EC, EE (utility model), EE, ES, FI (utility model), FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK (utility model), SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

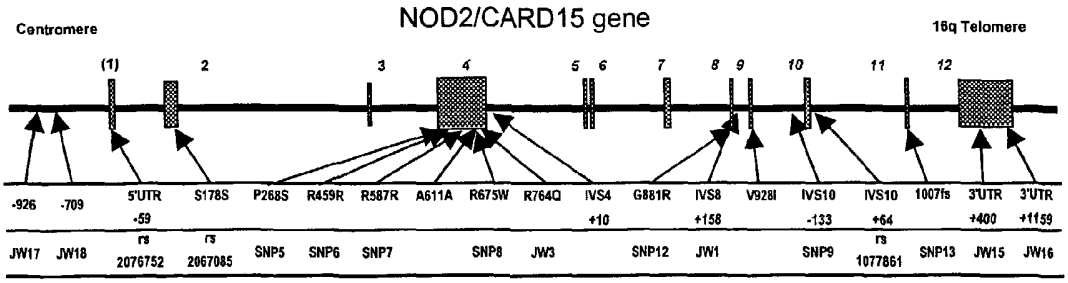
(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: MUTATIONS IN NOD2 ARE ASSOCIATED WITH FIBROSTENOSING DISEASE IN PATIENTS WITH CROHN'S DISEASE



(57) Abstract: The present invention provides a method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease by determining the presence or absence in an individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, where the presence of the fibrostenosis-predisposing allele is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease. In a method of the invention, the clinical subtype of Crohn's disease can be, for example, characterized by fibrostenosing disease independent of small bowel involvement. The invention also provides a method of optimizing therapy in an individual by determining the presence or absence in the individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, diagnosing individuals in which the fibrostenosis-predisposing allele is present as having a fibrostenosing subtype of Crohn's disease, and treating the individual having a fibrostenosing subtype of Crohn's disease based on the diagnosis.

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MUTATIONS IN NOD2 ARE ASSOCIATED WITH FIBROSTENOSING DISEASE IN PATIENTS WITH CROHN'S DISEASE

ACKNOWLEDGMENT

This work was supported by grant DK46763 and DK54967 awarded by NIDDK. The United States government has certain rights in this invention.

BACKGROUND OF THE INVENTION

FIELD OF THE INVENTION

The invention relates generally to the fields of genetics and autoimmune disease and, more specifically, to mutations linked to the NOD2/CARD15 gene and genetic methods for diagnosing clinical subtypes of Crohn's disease.

BACKGROUND INFORMATION

Inflammatory bowel disease (IBD) is the collective term used to describe two gastrointestinal disorders of unknown etiology: Crohn's disease (CD) and ulcerative colitis (UC). The course and prognosis of IBD, which occurs world-wide and is reported to afflict as many as two million people, varies widely. Onset of IBD is predominantly in young adulthood with diarrhea, abdominal pain, and fever the three most common presenting symptoms. The diarrhea may range from mild to severe, and anemia and weight loss are additional common signs of IBD. Of all patients with IBD, ten percent to fifteen percent will require surgery over a ten year period. In addition, patients with IBD are at increased risk for the development of intestinal cancer. Reports

of an increasing occurrence of psychological problems, including anxiety and depression, are perhaps not surprising symptoms of what is often a debilitating disease that strikes people in the prime of life.

Crohn's disease is a classification representing a number of heterogeneous disease subtypes that affect the gastrointestinal tract and produce similar symptoms. Both environmental and genetic factors likely contribute to the etiology of such disease subtypes. Patients with Crohn's disease can be classified, for example, into subtypes based on the presence of fibrostenosing disease, internal- perforating disease, perianal fistulizing disease or ulcerative colitis-like disease according to previously described criteria. The fibrostenosing disease subtype is characterized by documented persistent intestinal obstruction or intestinal resection for intestinal obstruction. The extensive and often protracted clinical testing required to diagnose Crohn's disease and disease subtypes may delay optimal treatment and involves invasive procedures such as endoscopy.

Identification of genetic markers which are closely associated with a clinical subtype of Crohn's disease would provide the basis for novel genetic tests and eliminate or reduce the need for the battery of laboratory, radiological, and endoscopic evaluations typically required to determine disease subtype. The availability of methods for diagnosing clinical subtypes of Crohn's disease would represent a major clinical advance that would aid in the therapeutic management of Crohn's disease and would further lay the groundwork for the design of treatment modalities which are specific to a particular disease subtype. Such methods can reduce

costs associated with treatment of unresponsive disease subtypes and eliminate the disappointment of those needlessly undergoing ineffective therapy. In particular, a reliable genetic test for the fibrostenosing subtype of Crohn's disease would be highly prized as a non-invasive method for the early diagnosis of this disease subtype and would also be useful for predicting susceptibility to the fibrostenosing subtype of Crohn's disease in asymptomatic individuals, making prophylactic therapy possible. The present invention satisfies this need and provides related advantages as well.

SUMMARY OF THE INVENTION

The present invention provides a method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease by determining the presence or absence in an individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, where the presence of the fibrostenosis-predisposing allele is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease. In a method of the invention, the clinical subtype of Crohn's disease can be, for example, characterized by fibrostenosing disease independent of small bowel involvement.

The invention also provides a method of optimizing therapy in an individual by determining the presence or absence in the individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, diagnosing individuals in which the fibrostenosis-predisposing allele is present as having a

fibrostenosing subtype of Crohn's disease, and treating the individual having a fibrostenosing subtype of Crohn's disease based on the diagnosis.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the NOD2/CARD15 locus intron and exon structure with the location of SNP 8, SNP 12, SNP 13, and JW1 as well as other markers.

Figure 2 shows the frequency of NOD2 variant carriers having at least one of the three NOD2/CARD15 rare variant alleles (a "2" allele at SNP 8, SNP 12 or SNP 13) in Cohort 1 ("CD1"), Cohort 2 ("CD2") or a combination of Cohort 1 and Cohort 2 ("Combined CD"). The striped bars indicate Crohn's disease patients with fibrostenosing disease and the solid bars indicate Crohn's disease patients who did not have the fibrostenosing subtype of disease.

Figure 3 shows the frequency of fibrostenosing complications in patients relative to the number of NOD2/CARD15 rare variant alleles at SNP 8, SNP 12 or SNP 13. Based on genotyping at SNP 8, SNP 12 and SNP 13, patients were described as carrying 0, 1, or 2 rare variant alleles (x axis, number of mutant NOD2 alleles). The left y axis shows the frequency of fibrostenosing complications as filled circles. The right y axis shows the odds ratio as a filled diamond with 95% confidence intervals in parentheses. The * indicates a p value = 0.008 and ** indicates a p value of 0.004 compared with 0 alleles.

Figure 4 shows a comparison of NOD2/CARD15 variant allelic frequencies in patients with

fibrostenosing disease compared with perforating disease. Patients were separated by the presence of fibrostenosing disease with perforating complications ("Fib + perf") or fibrostenosing disease without perforating complications ("Fib only") compared with patients with perforating complications and without evidence of fibrostenosis ("Perf only").

Figure 5 shows the nucleotide sequence of NOD2/CARD15 surrounding SNP 8. The top strand is labeled as SEQ ID NO:1 and the bottom strand is labeled as SEQ ID NO:2. Nucleotide sequences which can be used as primers for PCR amplification are indicated. In addition, the position of a nucleotide sequence which can be used as a probe in an allelic discrimination assay is indicated, in this figure, by a box and lower-case letters. The underlined nucleotide indicates the position of the polymorphic site.

Figure 6 shows the nucleotide sequence of NOD2/CARD15 surrounding SNP 12. The top strand is labeled as SEQ ID NO:3 and the bottom strand is labeled as SEQ ID NO:4. Nucleotide sequences which can be used as primers for PCR amplification are indicated. In addition, the position of a nucleotide sequence which can be used as a probe in an allelic discrimination assay is indicated, in this figure, by a box and lower case letters. The underlined nucleotide indicates the position of the polymorphic site.

Figure 7 shows the nucleotide sequence of NOD2/CARD15 surrounding SNP 13. The top strand is labeled as SEQ ID NO:5 and the bottom strand is labeled as SEQ ID NO:6. Nucleotide sequences which can be used as primers for PCR amplification are indicated. In

addition, the position of a nucleotide sequence which can be used as a probe in an allelic discrimination assay is indicated, in this figure, by a box and lower case letters. The underlined nucleotide indicates the position of the polymorphic site.

Figure 8 shows the nucleotide sequence of NOD2/CARD15 surrounding SNP 5. The top strand is labeled as SEQ ID NO:7 and the bottom strand is labeled as SEQ ID NO:8. Nucleotide sequences which can be used as primers for PCR amplification are indicated. In addition, the position of a nucleotide sequence which can be used as a probe in an allelic discrimination assay is indicated, in this figure, by a box and lower case letters. The underlined nucleotide indicates the position of the polymorphic site.

Figure 9 shows the nucleotide sequence of NOD2/CARD15 surrounding the JW1 variant sequence. The top strand is labeled as SEQ ID NO:9 and the bottom strand is labeled as SEQ ID NO:10. Nucleotide sequences which can be used as primers for PCR amplification are indicated. In addition, the position of a nucleotide sequence which can be used as a probe in an allelic discrimination assay is indicated, in this figure, by a box and lower case letters. The underlined nucleotide indicates the position of the polymorphic site.

Figure 10 shows the nucleotide sequence of the 5' untranslated region of NOD2/CARD15 in 12 individuals (SEQ ID NOS:12-23) compared to the wild-type NOD2/CARD15 sequence (SEQ ID NO:11). Areas of sequence identity are shaded. The location of two polymorphic sites, JW18 and JW17, are indicated.

Figure 11 shows the nucleotide sequence of the 3' untranslated region of NOD2/CARD15 in 12 individuals. Areas of sequence identity are shaded. The location of two polymorphic sites, JW15 and JW16, are indicated. Figure 11 A shows the nucleotide sequence of the 3' untranslated region of NOD2/CARD15 in 12 individuals (SEQ ID NOS:25-36) compared to the wild-type NOD2/CARD15 sequence (SEQ ID NO:24) and the location of JW16. Figure 11 B shows the nucleotide sequence of the 3' untranslated region of NOD2/CARD15 in 12 individuals (SEQ ID NOS:56-67) compared to the wild-type NOD2/CARD15 sequence (SEQ ID NO:55) and the location of JW15.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed to the exciting discovery of disease-predisposing alleles that are closely associated with the fibrostenosing disease subtype of Crohn's disease. These fibrostenosis-predisposing alleles are linked to a NOD2/CARD15 locus as described further below and can be used to diagnose or predict susceptibility to the fibrostenosing disease subtype of Crohn's disease.

As disclosed herein, genotyping and other clinical characterization approaches were used to identify a strong association between disease-predisposing alleles and the fibrostenosing disease subtype of Crohn's disease. In particular, two cohorts of Crohn's disease patients were assembled and clinically characterized (see Example I and Table 1). These patients were also genotyped for three single nucleotide polymorphisms (SNPs) in the NOD2/CARD15 gene, SNP 8, SNP 12, and SNP 13, which are polymorphic markers

associated with Crohn's disease. As disclosed herein, univariate analysis indicated that a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus was significantly associated with fibrostenosing disease in Cohort 1 (p=0.049, see Table 5). In addition, a positive association at a less stringent significance level was also observed with small bowel involvement and younger age of onset, and a negative association was observed with ulcerative colitis-like disease in this cohort. With respect to serologic markers, patients with the "2" allele at SNP 13 were more likely to express anti-*Saccharomyces cerevisiae* antibodies (ASCA) (p=0.053).

The results obtained with Cohort 1 were further tested using Cohort 2 as disclosed herein in Example IV. As with Cohort 1, Cohort 2 demonstrated a significant association between a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus and fibrostenosing disease (p=0.002, see Table 6). Furthermore, the significance between a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus and fibrostenosing disease increased when the two cohorts were analyzed together (p=0.001, see Figure 2).

As further disclosed herein in Example V, a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus was associated with fibrostenosing disease in both Jewish and non-Jewish individuals. Approximately 46% of Crohn's disease patients with fibrostenosing disease (Jewish individuals 52% vs. non-Jewish individuals 42%) had at least one of these rare variant alleles compared with only 23% (Jewish individuals 21.6% vs. non-Jewish individuals 25%) of Crohn's disease patients without fibrostenosing disease (Odds ratio, 2.8; 95% Confidence

interval, 1.56-5.18). Of the three rare variant alleles, the "2" allele at SNP 13, which is a frameshift mutation denoted "3020insC," demonstrated the greatest association with fibrostenosing disease (47% vs. 17%, p=0.006 for cohorts combined). These results indicate that fibrostenosis-predisposing alleles can be linked to the NOD2/CARD15 locus.

As further disclosed herein in Example VI, patients who were carriers of two fibrostenosis-predisposing alleles in NOD2/CARD15 were significantly more likely to have fibrostenosing disease as compared with patients who were not carriers of NOD2/CARD15 mutations at SNP 8, SNP 12 or SNP 13 (85% vs. 43%; odds ratio 7.4; 95% confidence interval 1.9-28.9, p=0.004). See Figure 3. Patients who were carriers of a single NOD2/CARD15 fibrostenosis- predisposing allele were also significantly more likely to have fibrostenosing disease when compared with patients who were not carriers of any of the three NOD2/CARD15 fibrostenosis-predisposing alleles assayed (64% vs. 43%; odds ratio 2.37; 95% confidence interval 1.26-4.47; p=0.008). These results confirm that patients who have a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus can have the fibrostenosing subtype of Crohn's disease and further indicate that Crohn's disease patients with multiple fibrostenosis-predisposing alleles (homozygous mutations or compound heterozygous mutations) linked to NOD2/CARD15 have an increased risk of fibrostenosing disease as compared to individuals carrying a single fibrostenosis-predisposing allele.

Fibrostenosing and perforating disease can occur together in the same patient. Patients with fibrostenosing disease can be characterized, for example,

as i) having only fibrostenosing disease or ii) having both fibrostenosing and perforating disease. As disclosed herein in Example VII, the percentage of patients having only fibrostenosing disease that carried a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus was 48.3%, which was similar to that seen in patients with both fibrostenosing and perforating complications (46.0%; p=0.8). As seen in Figure 4, when patients with fibrostenosing disease were compared with those patients described as having perforating disease only (perianal or internal), the frequency of the "2" allele at SNP 8, SNP 12 or SNP 13 of the NOD2/CARD15 locus in patients with fibrostenosing disease (with or without perforating complications) was significantly greater than that seen in patients with only perforating complications (46.6% versus 18.6%; p=0.002).

As further disclosed herein in Example VIII, multivariant analysis was performed to investigate the association of a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus with clinical phenotypes. For multivariant analysis, all variables with at least borderline significance ($p < 0.1$) in either cohort were tested simultaneously for their association with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus using logistic regression. As shown in Table 7, the clinical phenotype of fibrostenosing disease was significantly associated ($p < 0.05$) with these rare alleles at the NOD2/CARD15 locus (odds ratio 2.8; 95% confidence interval, 1.3-6.0). These results confirm that fibrostenosing disease is independently associated with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus.

Because fibrostenosing disease is more likely to occur in patients with small-bowel involvement, patients were stratified on the basis of small-bowel involvement to analyze whether the association between fibrostenosing disease and NOD2/CARD15 variant alleles was a primary association (see Example IX). Among patients with small-bowel involvement, 26.4% of patients who did not have fibrostenosing disease (n=53) had a "2" allele at SNP 8, SNP 12, or SNP 13, whereas 46.1% of patients who had fibrostenosing disease (n=102) had a "2" allele at SNP 8, SNP 12, or SNP 13 (p=0.017). A similar trend was observed among patients without small-bowel involvement (p=0.05), and the combined analysis conditioning on small-bowel involvement yielded a significance level of 0.009. After controlling for fibrostenosing disease, small-bowel involvement was not associated with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus (p= 0.63). This result agrees with the results from logistic regression analysis (see Example VIII) and indicates that the association between fibrostenosing disease and a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is independent of small-bowel involvement. These results further indicate that the observed small-bowel association with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is secondary to the presence of fibrostenosing disease.

Based on these discoveries, the present invention provides a method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease by determining the presence or absence in an individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, where the presence of the

fibrostenosis-predisposing allele is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease. The methods of the invention can be advantageous in that they are noninvasive and can be conveniently practiced, for example, with a blood sample from an individual. The methods of the invention can be used to quickly, easily and reliably diagnose or predict susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease as described further herein below.

In one embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele located within the NOD2/CARD15 locus. In another embodiment, NF-kappa B activation by a NOD2/CARD15 polypeptide encoded by the fibrostenosis-predisposing allele is reduced as compared to NF-kappa B activation by a wild-type NOD2/CARD15 polypeptide. In a further embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele located in a coding region of the NOD2/CARD15 locus, for example, within a region encoding residues 744 to 1020 of NOD2/CARD15. In still a further embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele which is a "2" allele at SNP 8, SNP 12, or SNP 13. In yet a further embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele which is a "2" allele at SNP 13. In another embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele which is located in a non-coding region of the NOD2/CARD15 locus. Such an allele can be, without limitation, a JW1, JW15, or JW16 variant allele. In another embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele which is located in a promoter region of the

NOD2/CARD15 locus. Useful fibrostenosis-predisposing alleles in the promoter region of NOD2/CARD15 include, but are not limited to, JW17 and JW18 variant alleles.

The present invention relates to genetic markers which localize to the IBD1 locus on chromosome 16. Utilizing genome wide scan linkage strategies, the IBD1 locus was mapped to the proximal region of the long arm of chromosome 16 (16q12) in the Caucasian population (Hugot et al., Nature 379:821-823 (1996)). This finding has been replicated in many studies, including an international collaborative study reporting a high multipoint linkage score (MLS) for a complex disease (MLS = 5.7 at marker D16S411 in 16q12). See Cho et al., Inflamm. Bowel Dis. 3:186-190 (1997), Akolkar et al., Am. J. Gastroenterol. 96:1127-1132 (2001), Ohmen et al., Hum. Mol. Genet. 5:1679-1683 (1996), Parkes et al., Lancet 348:1588 (1996), Cavanaugh et al., Ann. Hum. Gent. (1998), Brant et al., Gastroenterology 115:1056-1061 (1998), Curran et al., Gastroenterlology 115:1066-1071 (1998), Hampe et al., Am. J. Hum. Genet. 64:808-816 (1999), and Annese et al., Eur. J. Hum. Genet. 7:567-573 (1999). NOD2/CARD15 within the IBD1 locus was simultaneously identified by a positional-cloning strategy (Hugot et al., Nature 411:599-603 (2001)) and a positional candidate gene strategy (Ogura et al., Nature 411:603-606 (2001), Hampe et al., Lancet 357:1925-1928 (2001)). The encoded NOD2/CARD15 protein contains amino-terminal caspase recruitment domains (CARDs), which can activate NF-kappa B (NF-κB), and several carboxy-terminal leucine-rich repeat domains (Ogura et al, J. Biol. Chem. 276:4812-4818 (2001)). Figure 1 shows an illustration of the NOD2/CARD15 locus.

The sequence of the human NOD2/CARD15 gene can be found in GenBank as accession number NM_022162, which is incorporated by reference herein. In addition, the complete sequence of human chromosome 16 clone RP11-327F22, which includes NOD2/CARD15, can be found in GenBank as accession number AC007728, which is incorporated by reference herein. Furthermore, the sequence of NOD2/CARD15 from other species can be found in the GenBank database.

Variations at three single nucleotide polymorphisms in the coding region of NOD2/CARD15 have been previously described. These three SNPs, designated SNP 8, SNP 12 and SNP 13, are located in the carboxy-terminal region of the NOD2/CARD15 gene (Hugot et al., *supra*, 2001).

The invention relies, in part, on determining the presence or absence in an individual of a fibrostenosing-predisposing allele linked to a NOD2/CARD15 locus. The term "fibrostenosis-predisposing allele," as used herein, means a stably heritable molecular variation that is linked to the NOD2/CARD15 locus and that tends to be inherited together with the clinical subtype of Crohn's disease characterized by fibrostenosing disease more often than would be expected according to traditional Mendelian genetics. A fibrostenosis-predisposing allele useful in the invention can be, without limitation, a single nucleotide polymorphism (SNP), microsatellite (ms), variable number tandem repeat (VNTR) polymorphism, or a substitution, insertion or deletion of one or more nucleotides. One skilled in the art understands that a fibrostenosis-predisposing allele also can be a molecular variation such as abnormal methylation or other

modification that does not produce a difference in the primary nucleotide sequence of the fibrostenosis-predisposing allele as compared to the wild type allele.

The term "linked to," as used herein in reference to a fibrostenosis-predisposing allele and a NOD2/CARD15 locus, means that the fibrostenosis-predisposing allele and the NOD2/CARD15 locus are inherited together more often than would be expected according to traditional Mendelian genetics. It is understood that an allele and locus are linked when there is less than 50% recombination between the two sites. A fibrostenosis-predisposing allele is generally separated from a NOD2/CARD15 locus by at most 50 centiMorgan (cM). As non-limiting examples, a fibrostenosis- predisposing allele can be within 50 centiMorgan (cM), 40 cM, 30 cM, 20 cM, 10 cM, 5 cM, or 1 cM of the NOD2/CARD15 locus. The distance between a linked fibrostenosis-predisposing allele and a NOD2/CARD15 locus can also be, for example, 50,000,000 base pairs (bps), 40,000,000 bps, 30,000,000 bps, 20,000,000 bps, 10,000,000 bps, 5,000,000 bps, 1,000,000 bps, 500,000 bps, 100,000 bps, 50,000 bps, 10,000 bps, 1,000 bps or 100 bps.

The methods of the invention are useful for diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease (regional enteritis), which is a disease of chronic inflammation that can involve any part of the gastrointestinal tract. Commonly the distal portion of the small intestine (ileum) and cecum are affected in Crohn's disease. In other cases, the disease is confined to the small intestine, colon or anorectal region. Crohn's disease occasionally involves the

duodenum and stomach, and more rarely the esophagus and oral cavity.

The variable clinical manifestations of Crohn's disease are, in part, a result of the varying anatomic localization of the disease. The most frequent symptoms of Crohn's disease are abdominal pain, diarrhea and recurrent fever. Crohn's disease is commonly associated with intestinal obstruction or fistula, which is an abnormal passage, for example, between diseased loops of bowel. Crohn's disease also can include extra-intestinal complications such as inflammation of the eye, joints and skin; liver disease; kidney stones or amyloidosis; and is associated with an increased risk of intestinal cancer.

Several features are characteristic of the pathology of Crohn's disease. The inflammation associated with Crohn's disease, known as transmural inflammation, involves all layers of the bowel wall. Thickening and edema, for example, typically appear throughout the bowel wall, with fibrosis also present in long-standing disease. The inflammation characteristic of Crohn's disease also is discontinuous, with segments of inflamed tissue, known as "skip lesions," separated by apparently normal intestine. Furthermore, linear ulcerations, edema, and inflammation of the intervening tissue lead to a "cobblestone" appearance of the intestinal mucosa, which is distinctive of Crohn's disease.

A hallmark of Crohn's disease is the presence of discrete aggregations of inflammatory cells, known as granulomas, which are generally found in the submucosa. About half of Crohn's disease cases display the typical discrete granulomas, while others show a diffuse

granulomatous reaction or nonspecific transmural inflammation. As a result, the presence of discrete granulomas is indicative of Crohn's disease, although the absence granulomas also is consistent with the disease. Thus, transmural or discontinuous inflammation, rather than the presence of granulomas, is a preferred diagnostic indicator of Crohn's disease (Rubin and Farber, Pathology (Second Edition) Philadelphia: J.B. Lippincott Company (1994)).

Crohn's disease is a classification representing a number of heterogeneous disease subtypes that affect the gastrointestinal tract and may produce similar symptoms. As non-limiting examples, patients with Crohn's disease can be characterized as having subtypes characterized by fibrostenosing disease, internal-perforating disease, perianal fistulizing disease or ulcerative colitis (UC)-like disease based on previously described criteria (Gasche et al., Inflammatory Bowel Diseases 6:8-15 (2000); Vasiliauskas et al., Gut 47:487-496 (2000); Vasiliauskas et al., Gastroenterology 110:1810-1819 (1996); and Greenstein et al., Gut 29:588-592 (1988)).

According to well-established criteria fibrostenosing disease is defined by documented persistent intestinal obstruction or an intestinal resection for an intestinal obstruction. Radiographic, endoscopic, surgical or histopathological documentation can be used to confirm a diagnosis of the fibrostenosing subtype of Crohn's disease. The fibrostenosing subtype of Crohn's disease can be accompanied by other symptoms such as perforations, abscesses or fistulae. In addition, the fibrostenosing subtype of Crohn's disease can be characterized by persistent symptoms of intestinal

blockage such as nausea, vomiting, abdominal distention and inability to eat solid food. Intestinal X-rays of patients with the fibrostenosing subtype of Crohn's disease can show, for example, distention of the bowel before the point of blockage.

Additional subtypes of Crohn's disease can be identified using defined clinical criteria. For example, internal perforating disease can be defined as current or previous evidence of entero-enteric or entero-vesicular fistulae, intraabdominal abscesses, or small bowel perforation. Perianal perforating disease can be defined by current or previous evidence of either perianal fistulae or abscesses or rectovaginal fistula. UC-like disease can be defined by current or previous evidence of left-sided colonic involvement, symptoms of bleeding or urgency, and crypt abscesses on colonic biopsies as previously described. Disease location can be classified as small bowel, colon, or both based on one or more endoscopic, radiologic or pathologic studies.

The fibrostenosing subtype of Crohn's disease can occur in patients having disease with small-bowel involvement. As disclosed herein, after controlling for fibrostenosing disease, small-bowel involvement was not associated with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus ($p=0.63$; see Example IX). This result agrees with the results from logistic regression analysis disclosed in Example VIII and indicates that the association between fibrostenosing disease and a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is independent of small-bowel involvement. Based on these findings, the present invention provides a method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by

fibrostenosing disease independent of small bowel involvement by determining the presence or absence in an individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, where the presence of the fibrostenosis-predisposing allele is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease independent of small bowel involvement.

The diagnostic methods of the invention are practiced in an individual. As used herein, the term "individual" means an animal, such as a human or other mammal, capable of having the fibrostenosing subtype of Crohn's disease. An individual can have one or more symptoms of Crohn's disease or the fibrostenosing subtype of Crohn's disease or can be asymptomatic. The methods of the invention can be useful, for example, for diagnosing the fibrostenosing subtype of Crohn's disease in an individual with one or more symptoms, or for predicting susceptibility to the fibrostenosing subtype of Crohn's disease in an asymptomatic individual such as an individual at increased risk for having the fibrostenosing subtype of Crohn's disease. In one embodiment, the methods of the invention are used to determine the presence or absence of the fibrostenosing subtype of Crohn's disease in an individual known to have Crohn's disease.

The methods of the invention can be useful, for example, to diagnose or predict susceptibility to the fibrostenosing subtype of Crohn's disease in an Ashkenazi Jewish individual. Crohn's disease is significantly more common (2 to 8 fold higher) in Ashkenazi Jews than in non-Jewish Caucasians (Brant et al., Gastroenterol. 115:1056-1061 (1998)). Furthermore, among persons of

Jewish ethnicity, American or European Ashkenazi Jews have a 2 to 4 fold increased risk of having this inflammatory bowel disease compared with Sephardic or Oriental Jews (Yang and Rotter in Kirschner and Shorter (Eds.), Inflammatory Bowel Disease Baltimore: Williams and Wilkins, p. 301-331 (1995); Rozen et al., Gastroenterol. 76:25-30 (1979)). The empiric risk of Crohn's disease for a first degree relative of a proband with Crohn's disease is 7.8% for Jews compared with 5.2% for non-Jews (p=0.005; Yang et al., Gut 34:517-524 (1993)). Thus, the Jewish population and especially the Ashkenazi Jewish population represents a group at increased risk for Crohn's and autoimmune diseases of related etiology.

The methods of the invention rely on fibrostenosis-predisposing alleles linked to the NOD2/CARD15 locus. NOD2/CARD15 has structural homology with both apoptosis regulators Apaf-1/CED-4 and a class of plant disease resistant gene products (Ogura et al., J. Biol. Chem, 276:4812-4818 (2001)). Similar to plant disease resitant gene products, NOD2/CARD15 has an amino-terminal effector domain, a nucleotide-binding domain and leucine rich repeats (LRRs). Wild-type NOD2/CARD15 activates nuclear factor NF-kappa B, making it responsive to bacterial lipopolysaccharides (LPS; Ogura et al., J. Biol. Chem, 276:4812-4818 (2001); Inohara et al., J. Biol. Chem. 276:2551-2554 (2001). NOD2/CARD15 can function as an intercellular receptor for LPS, with the leucine rich repeats required for responsiveness. Like NOD2/CARD15, cytosolic plant disease resistant polypeptides have carboxy-terminal leucine rich repeats that are important for the recognition of pathogen components and induction of pathogen-specific responses (Parniske et al., Cell

91:821-832 (1997); Ellis et al., Plant Cell 11:495-506 (1999); Dixon et al., Proc. Natl. Acad. Sci. USA 97: 8807-8814 (2000)).

In one embodiment, the fibrostenosis-predisposing allele is located within the NOD2/CARD15 locus, a schematic of which is shown in Figure 1. The NOD2/CARD15 locus includes coding regions of the NOD2/CARD15 gene as well as non-coding regions such as introns and 5' and 3' untranslated regions. One skilled in the art understands that the NOD2/CARD15 locus can include, for example, promoter regions 5' of the gene, enhancer regions 5' or 3' of the gene or in intronic sequences, and mRNA stability regions 3' of the gene.

In another embodiment, the fibrostenosis-predisposing allele is located in a coding region of the NOD2/CARD15 locus, for example within a region encoding residues 744 to 1020 of NOD2/CARD15. Residues 744 to 1020 of the NOD2/CARD15 polypeptide contain several leucine-rich repeats in the carboxy-terminal portion of the NOD2/CARD15 polypeptide. Fibrostenosis-predisposing alleles located in a region encoding residues 744 to 1020 of NOD2/CARD15 include, without limitation, SNP 12 and SNP 13. A fibrostenosis-predisposing allele useful in the invention also can be an allele which encodes a NOD2/CARD15 polypeptide with reduced NF-kappa B activation as compared to NF-kappa B activation by a wild-type NOD2/CARD15 polypeptide. As an example, a rare variant allele at SNP 13 results in a truncated NOD2/CARD15 polypeptide which has reduced ability to induce NF-kappa B in response to LPS stimulation (Ogura et al., Nature 411:603-606 (2001)).

A fibrostenosis-predisposing allele useful in the invention can be, for example, a "2" allele at SNP 8, SNP 12 or SNP 13. SNP 8, SNP 12, and SNP 13 are located within the coding region of NOD2/CARD15 as shown in Figure 1. In one embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele which is the SNP 8 "2" allele. As used herein, the term "SNP 8" means a single nucleotide polymorphism within exon 4 in the NOD2/CARD15 gene, which occurs within a triplet encoding amino acid 702 of the NOD2/CARD15 protein. The "1" allele, in which cytosine (c) resides at position 138,991 of the AC007728 sequence, is the common or "wild-type" SNP 8 allele and occurs within a triplet encoding an arginine at amino acid 702. The "2" allele of SNP 8, in which thymine (t) resides at position 138,991 of the AC007728 sequence, is a rare variant that results in an arginine (R) to tryptophan (W) substitution at amino acid 702 of the NOD2/CARD15 protein. Accordingly, the rare "2" allele at SNP 8 is denoted "R702W" or "702W" and can also be denoted "R675W" based on the earlier numbering system of Hugot et al., *supra*, 2001. The NCBI SNP ID number for SNP 8 is rs2066844, which is incorporated herein by reference. As disclosed herein and described further below, the presence of allele "1" or "2" at SNP 8, or another SNP described below, can be conveniently detected, for example, by allelic discrimination assays or sequence analysis.

A method of the invention also can be practiced with a fibrostenosis-predisposing allele which is the SNP 12 "2" allele. As used herein, the term "SNP 12" means a single nucleotide polymorphism within exon 8 in the NOD2/CARD15 gene, which occurs within a triplet encoding amino acid 908 of the NOD2/CARD15 protein. The

"1" allele, in which guanine (g) resides at position 128,377 of the AC007728 sequence, is the common or "wild-type" SNP 12 allele and occurs within a triplet encoding glycine at amino acid 908. The "2" allele of SNP 12, in which cytosine (c) resides at position 128,377 of the AC007728 sequence, is a rare variant that results in a glycine (G) to arginine (R) substitution at amino acid 908 of the NOD2/CARD15 protein. This rare "2" allele at SNP 12 is denoted "G908R" or "908R" and can also be denoted "G881R" based on the earlier numbering system of Hugot et al., *supra*, 2001. SNP 12 is located within the leucine rich repeat region of the NOD2/CARD15 gene. The NCBI SNP ID number for SNP 12 is rs2066845, which is incorporated herein by reference.

A method of the invention also can be practiced with a fibrostenosis-predisposing allele which is the SNP 13 "2" allele. This allele is an insertion of a single nucleotide that results in a frame shift in the tenth leucine-rich repeat of the NOD2/CARD15 protein and is followed by a premature stop codon. The resulting truncation of the NOD2/CARD15 protein appears to prevent activation of NF-kB in response to bacterial lipopolysaccharides (Ogura et al., *supra*, 2001). As used herein, the term "SNP 13" means a single nucleotide polymorphism within exon 11 in the NOD2/CARD15 gene, which occurs in a triplet encoding amino acid 1007 of the NOD2/CARD15 protein. The "2" allele of SNP 13, in which a cytosine has been added at position 121,139 of the AC007728 sequence, is a rare variant resulting in a frame shift mutation at amino acid 1007. Accordingly, the rare "2" allele at SNP 13 is denoted "1007fs" and can also be denoted "3020insC," or "980fs" based on the earlier numbering system of Hugot et al., *supra*, 2001. The NCBI

SNP ID number for SNP 13 is rs2066847, which is incorporated herein by reference.

One skilled in the art recognizes that a particular polymorphic allele can be conveniently defined, for example, in comparison to a Centre d'Etude du Polymorphisme Humain (CEPH) reference individual such as the individual designated 1347-02 (Dib et al., Nature 380:152-154 (1996)), using commercially available reference DNA obtained, for example, from PE Biosystems (Foster City, CA). In addition, specific information on SNPs can be obtained from the dbSNP of the National Center for Biotechnology Information (NCBI).

A fibrostenosis-predisposing allele also can be located in a non-coding region of the NOD2/CARD15 locus. Non-coding regions include, for example, intron sequences as well as 5' and 3' untranslated sequences. Examples of a fibrostenosis-predisposing allele in an intron sequence of the NOD2/CARD15 gene include, but are not limited to, the JW1 variant allele, which is described below. Examples of fibrostenosis-predisposing alleles located in the 3' untranslated region of the NOD2/CARD15 gene include, without limitation, JW15 and JW16 variant alleles, which are described below. Examples of fibrostenosis-predisposing alleles located in the 5' untranslated region of the NOD2/CARD15 gene include, without limitation, the JW17 and JW18 variant alleles, which are described below. In one embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele located in a non-coding region of the NOD2/CARD15 locus which is a JW1, JW15 or JW16 variant allele. In another embodiment, a method of the invention is practiced with a fibrostenosis-predisposing allele located in a promoter

region of the NOD2/CARD15 locus which is a JW17 or JW18 variant allele.

As used herein, the term "JW1 variant allele" means a genetic variation at nucleotide 158 of intervening sequence 8 (intron 8) of a NOD2/CARD15 gene. In relation to the AC007728 sequence, the JW1 variant is located at position 128,143. The genetic variation at nucleotide 158 of intron 8 can be, but is not limited to, a single nucleotide substitution, multiple nucleotide substitutions, or a deletion or insertion of one or more nucleotides. The wild type sequence of intron 8 has a cytosine at position 158; as non-limiting examples, a JW1 variant allele can have a cytosine (C) to adenine (A), cytosine to guanine (G), or cytosine to thymine (T) substitution at nucleotide 158 of intron 8. In one embodiment, the JW1 variant allele is a change from a cytosine to a thymine at nucleotide 158 of NOD2/CARD15 intron 8.

As used herein, the term "JW15 variant allele" means a genetic variation in the 3' untranslated region of NOD2/CARD15 at nucleotide position 118,790 of the AC007728 sequence. The genetic variation at nucleotide 118,790 can be, but is not limited to, a single nucleotide substitution, multiple nucleotide substitutions, or a deletion or insertion of one or more nucleotides. The wild type sequence has an adenine (A) at position 118,790; as non-limiting examples, a JW15 variant allele can have an adenine (A) to cytosine (C), adenine to guanine (G), or adenine to thymine (T) substitution at nucleotide 118,790. In one embodiment, the JW15 variant allele is a change from an adenine to a cytosine at nucleotide 118,790.

As used herein, the term "JW16 variant allele" means a genetic variation in the 3' untranslated region of NOD2/CARD15 at nucleotide position 118,031 of the AC007728 sequence. The genetic variation at nucleotide 118,031 can be, but is not limited to, a single nucleotide substitution, multiple nucleotide substitutions, or a deletion or insertion of one or more nucleotides. The wild type sequence has a guanine (G) at position 118,031; as non-limiting examples, a JW16 variant allele can have a guanine (G) to cytosine (C), guanine to adenine (A), or guanine to thymine (T) substitution at nucleotide 118,031. In one embodiment, the JW16 variant allele is a change from a guanine to an adenine at nucleotide 118,031.

As used herein, the term "JW17 variant allele" means a genetic variation in the 5' untranslated region of NOD2/CARD15 at nucleotide position 154,688 of the AC007728 sequence. The genetic variation at nucleotide 154,688 can be, but is not limited to, a single nucleotide substitution, multiple nucleotide substitutions, or a deletion or insertion of one or more nucleotides. The wild type sequence has a cytosine (C) at position 154,688; as non-limiting examples, a JW17 variant allele can have a cytosine (C) to guanine (G), cytosine to adenine (A), or cytosine to thymine (T) substitution at nucleotide 154,688. In one embodiment, the JW17 variant allele is a change from a cytosine to a thymine at nucleotide 154,688.

As used herein, the term "JW18 variant allele" means a genetic variation in the 5' untranslated region of NOD2/CARD15 at nucleotide position 154,471 of the AC007728 sequence. The genetic variation at nucleotide 154,471 can be, but is not limited to, a

single nucleotide substitution, multiple nucleotide substitutions, or a deletion or insertion of one or more nucleotides. The wild type sequence has a cytosine (C) at position 154,471; as non-limiting examples, a JW18 variant allele can have a cytosine (C) to guanine (G), cytosine to adenine (A), or cytosine to thymine (T) substitution at nucleotide 154,471. In one embodiment, the JW18 variant allele is a change from a cytosine to a thymine at nucleotide 154,471.

Further provided herein is a method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease by determining the presence or absence in an individual of at least two fibrostenosis-predisposing alleles linked to a NOD2/CARD15 locus, where the presence of one or more of the fibrostenosis-predisposing alleles is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease. In a method of the invention, the at least two fibrostenosis-predisposing alleles are "2" alleles at SNP 8, SNP 12 or SNP 13.

Further provided herein is a method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease by determining the presence or absence in an individual of at least two fibrostenosis-predisposing alleles linked to a NOD2/CARD15 locus, where the presence of one or more of the fibrostenosis-predisposing alleles is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease. In one embodiment, the at least two

fibrostenosis-predisposing alleles are "2" alleles at SNP 8, SNP 12, or SNP 13. In another embodiment, a method of the invention for diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease is practiced by determining the presence or absence in the individual of (i) a "2" allele at SNP 8, (ii) a "2" allele at SNP 12, and (iii) a "2" allele at SNP 13, where the presence of one or more of the "2" alleles at SNP 8, SNP 12, and SNP 13 is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease.

The strength of the association between a fibrostenosing-predisposing allele and Crohn's disease can be characterized by a particular odds ratio such as an odds ratio of at least 2 with a lower 95% confidence interval limit of greater than 1. Such an odds ratio can be, for example, at least 3.0, 4.0, 5.0, 6.0, 7.0, or 8.0 or greater with a lower 95% confidence interval limit of greater than 1, such as an odds ratio of at least 7.4 with a 95% confidence interval of 1.9-28.9 (see Figure 3). In addition, an odds ratio can be, for example, at least 2.37 with a lower confidence interval limit of 1.26-4.47 (see Figure 3). In one embodiment, the fibrostenosis- predisposing allele is associated with the clinical subtype of Crohn's disease characterized by fibrostenosing disease with an odds ratio of at least 2 and a lower 95% confidence limit greater than 1. Methods for determining an odds ratio are well known in the art (see, for example, Schlesselman et al., Case Control Studies: Design, Conduct and Analysis Oxford University Press, New York (1982)).

In one embodiment, a fibrostenosis-predisposing allele is associated with the fibrostenosing subtype of Crohn's disease with a p value of equal to or less than 0.05. In other embodiments, a fibrostenosis-predisposing allele is associated with the fibrostenosing subtype of Crohn's disease with a p value of equal to or less than 0.1. As used herein, the term "p value" is synonymous with "probability value." As is well known in the art, the expected p value for the association between a random allele and disease is 1.00. A p value of less than about 0.05 indicates that the allele and disease do not appear together by chance but are influenced by positive factors. Generally, the statistical threshold for significance of linkage has been set at a level of allele sharing for which false positives would occur once in twenty genome scans (p=0.05). In particular embodiments, a fibrostenosis-predisposing allele is associated with a clinical subtype of Crohn's disease characterized by fibrostenosis with a p value of equal to or less than 0.1, 0.05, 0.04, 0.03, 0.02, 0.01, 0.009, 0.008, 0.007, 0.006, 0.005, 0.004, 0.003, 0.002 or 0.001, or with a p value of less than 0.00095, 0.0009, 0.00085, 0.0008 or 0.0005. It is recognized that, in some cases, p values may need to be corrected, for example, to account for factors such as sample size (number of families), genetic heterogeneity, clinical heterogeneity, or analytical approach (parametric or nonparametric method).

A variety of means can be used to determine the presence or absence of a fibrostenosing-predisposing allele in a method of the invention. As an example, enzymatic amplification of nucleic acid from an individual can be conveniently used to obtain nucleic acid for subsequent analysis. The presence or absence of

a fibrostenosis-predisposing allele also can be determined directly from the individual's nucleic acid without enzymatic amplification.

Analysis of nucleic acid from an individual, whether amplified or not, can be performed using any of various techniques. Useful techniques include, without limitation, polymerase chain reaction based analysis, sequence analysis and electrophoretic analysis, which can be used alone or in combination. As used herein, the term "nucleic acid" means a polynucleotide such as a single- or double-stranded DNA or RNA molecule including, for example, genomic DNA, cDNA and mRNA. The term nucleic acid encompasses nucleic acid molecules of both natural and synthetic origin as well as molecules of linear, circular or branched configuration representing either the sense or antisense strand, or both, of a native nucleic acid molecule. It is understood that such nucleic acid can be attached to a synthetic material such as a bead or column matrix.

The presence or absence of a fibrostenosing-predisposing allele can involve amplification of an individual's nucleic acid by the polymerase chain reaction. Use of the polymerase chain reaction for the amplification of nucleic acids is well known in the art (see, for example, Mullis et al. (Eds.), The Polymerase Chain Reaction, Birkhäuser, Boston, (1994)). In one embodiment, polymerase chain reaction amplification is performed using one or more fluorescently labeled primers. In another embodiment, polymerase chain reaction amplification is performed using one or more labeled or unlabeled primers that contain a DNA minor grove binder.

Several different primers can be used to amplify an individual's nucleic acid by the polymerase chain reaction. For example, the PCR primers listed in Table 2 (SEQ ID NOS: 37-44) and shown in Figures 5 to 8 can be used to amplify specific regions in the NOD2/CARD15 locus of an individual's nucleic acid. For example, the region surrounding SNP 8 can be amplified using SEQ ID NO: 39 and 40; SNP 12 can be amplified using SEQ ID NOS: 41 and 42, and the region surrounding SNP 13 can be amplified using SEQ ID NOS: 43 and 44. In addition, for example, the region surrounding. As understood by one skilled in the art, additional primers for PCR analysis can be designed based on the sequence flanking the region of interest. As a non-limiting example, a sequence primer can contain about 15 to 30 nucleotides of a sequence upstream or downstream of the region of interest. Such primers are generally designed to have sufficient guanine and cytosine content to attain a high melting temperature which allows for a stable annealing step in the amplification reaction. Several computer programs, such as Primer Select, are available to aid in the design of PCR primers.

A Taqman® allelic discrimination assay available from Applied Biosystems can be useful for determining the presence or absence of a fibrostenosing-predisposing allele. In a Taqman® allelic discrimination assay, a specific, fluorescent, dye-labeled probe for each allele is constructed. The probes contain different fluorescent reporter dyes such as FAM and VICTM to differentiate the amplification of each allele. In addition, each probe has a quencher dye at one end which quenches fluorescence by fluorescence resonance energy transfer (FRET). During PCR, each probe anneals specifically to complementary sequences in the

nucleic acid from the individual. The 5' nuclease activity of Taq polymerase is used to cleave only probe that hybridize to the allele. Cleavage separates the reporter dye from the quencher dye, resulting in increased fluorescence by the reporter dye. Thus, the fluorescence signal generated by PCR amplification indicates which alleles are present in the sample. Mismatches between a probe and allele reduce the efficiency of both probe hybridization and cleavage by Taq polymerase, resulting in little to no fluorescent signal. Improved specificity in allelic discrimination assays can be achieved by conjugating a DNA minor grove binder (MGB) group to a DNA probe as described, for example, in Kutyavin et al., Nuc. Acids Research 28:655-661 (2000). Minor grove binders include, but are not limited to, compounds such as dihydrocyclopyrroloindole tripeptide (DPI3).

Sequence analysis also can be useful for determining the presence or absence of a fibrostenosing-predisposing allele in a method of the invention. A fibrostenosing-predisposing allele can be detected by sequence analysis using primers disclosed herein, for example, as the PCR primers listed in Table 2 (SEQ ID NOS: 37-44) and shown in Figures 5 to 8. As understood by one skilled in the art, additional primers for sequence analysis can be designed based on the sequence flanking the region of interest. As a non-limiting example, a sequence primer can contain about 15 to 30 nucleotides of a sequence about 40 to 400 base pairs upstream or downstream of the region of interest. Such primers are generally designed to have sufficient guanine and cytosine content to attain a high melting temperature which allows for a stable annealing step in the sequencing reaction.

The term "sequence analysis," as used herein in reference to one or more nucleic acids, means any manual or automated process by which the order of nucleotides in the nucleic acid is determined. As an example, sequence analysis can be used to determine the nucleotide sequence of a sample of DNA. The term sequence analysis encompasses, without limitation, chemical and enzymatic methods such as dideoxy enzymatic methods including, for example, Maxam-Gilbert and Sanger sequencing as well as variations thereof. The term sequence analysis further encompasses, but is not limited to, capillary array DNA sequencing, which relies on capillary electrophoresis and laser-induced fluorescence detection and can be performed using instruments such as the MegaBACE 1000 or ABI 3700. As additional non-limiting examples, the term sequence analysis encompasses thermal cycle sequencing (Sears et al., Biotechniques 13:626-633 (1992)); solid-phase sequencing (Zimmerman et al., Methods Mol. Cell Biol. 3:39-42 (1992); and sequencing with mass spectrometry such as matrix-assisted laser desorption/ionization time-of-flight mass spectrometry MALDI-TOF MS (Fu et al., Nature Biotech. 16: 381-384 (1998)). The term sequence analysis also includes, yet is not limited to, sequencing by hybridization (SBH), which relies on an array of all possible short oligonucleotides to identify a segment of sequences present in an unknown DNA (Chee et al., Science 274:610-614 (1996); Drmanac et al., Science 260:1649-1652 (1993); and Drmanac et al., Nature Biotech. 16:54-58 (1998)). One skilled in the art understands that these and additional variations are encompassed by the term sequence analysis as defined herein. See, in general, Ausubel et al., *supra*, Chapter 7 and supplement 47.

The invention also provides a method of diagnosing or predicting susceptibility to a clinical

subtype of Crohn's disease characterized by fibrostenosing disease by determining the presence or absence in an individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, where the presence of the fibrostenosis-predisposing allele is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease, and where the method includes the steps of obtaining material containing nucleic acid including the NOD2/CARD15 locus from the individual. As used herein, the term "material" means any biological matter from which nucleic acid can be prepared. As non-limiting examples, the term material encompasses whole blood, plasma, saliva, cheek swab, or other bodily fluid or tissue that contains nucleic acid. In one embodiment, a method of the invention is practiced with whole blood, which can be obtained readily by non-invasive means and used to prepare genomic DNA, for example, for enzymatic amplification or automated sequencing. In another embodiment, a method of the invention is practiced with tissue obtained from an individual such as tissue obtained during surgery or biopsy procedures.

Electrophoretic analysis also can be useful in the methods of the invention. Elecrophoretic analysis, as used herein in reference to one or more nucleic acids such as amplified fragments, means a process whereby charged molecules are moved through a stationary medium under the influence of an electric field. Electrophoretic migration separates nucleic acids primarily on the basis of their charge, which is in proportion to their size, with smaller molecules migrating more quickly. The term electrophoretic analysis includes, without limitation, analysis using slab gel electrophoresis, such as agarose or

polyacrylamide gel electrophoresis, or capillary electrophoresis. Capillary electrophoretic analysis generally occurs inside a small-diameter (50-100- m) quartz capillary in the presence of high (kilovolt-level) separating voltages with separation times of a few minutes. Using capillary electrophoretic analysis, nucleic acids are conveniently detected by UV absorption or fluorescent labeling, and single-base resolution can be obtained on fragments up to several hundred base pairs. Such methods of electrophoretic analysis, and variations thereof, are well known in the art, as described, for example, in Ausubel et al., Current Protocols in Molecular Biology Chapter 2 (Supplement 45) John Wiley & Sons, Inc. New York (1999).

Restriction fragment length polymorphism (RFLP) analysis also can be useful for determining the presence or absence of a fibrostenosis-predisposing allele in a method of the invention (Jarcho et al. in Dracopoli et al., Current Protocols in Human Genetics pages 2.7.1-2.7.5, John Wiley & Sons, New York; Innis et al.,(Ed.), PCR Protocols, San Diego: Academic Press, Inc. (1990)). As used herein, restriction fragment length polymorphism analysis is any method for distinguishing genetic polymorphisms using a restriction enzyme, which is an endonuclease that catalyzes the degradation of nucleic acid and recognizes a specific base sequence, generally a palindrome or inverted repeat. One skilled in the art understands that the use of RFLP analysis depends upon an enzyme that can differentiate two alleles at a polymorphic site.

Allele-specific oligonucleotide hybridization also can be used to detect the presence or absence of a fibrostenosis-predisposing allele. Allele-specific

oligonucleotide hybridization is based on the use of a labeled oligonucleotide probe having a sequence perfectly complementary, for example, to the sequence encompassing a fibrostenosis-predisposing allele. Under appropriate conditions, the allele-specific probe hybridizes to a nucleic acid containing the fibrostenosis-predisposing allele but does not hybridize to the one or more other alleles, which have one or more nucleotide mismatches as compared to the probe. If desired, a second allele-specific oligonucleotide probe that matches an alternate allele also can be used. Similarly, the technique of allele-specific oligonucleotide amplification can be used to selectively amplify, for example, a fibrostenosis-predisposing allele by using an allele-specific oligonucleotide primer that is perfectly complementary to the nucleotide sequence of the fibrostenosis-predisposing allele but which has one or more mismatches as compared to other alleles (Mullis et al., *supra*, 1994). One skilled in the art understands that the one or more nucleotide mismatches that distinguish between the fibrostenosis-predisposing allele and one or more other alleles are often located in the center of an allele-specific oligonucleotide primer to be used in allele-specific oligonucleotide hybridization. In contrast, an allele-specific oligonucleotide primer to be used in PCR amplification generally contains the one or more nucleotide mismatches that distinguish between the disease-associated and other alleles at the 3' end of the primer.

A heteroduplex mobility assay (HMA) is another well known assay that can be used to detect the presence or absence of a fibrostenosis-predisposing allele in a method of the invention. HMA is useful for detecting the presence of a polymorphic sequence since a DNA duplex

carrying a mismatch has reduced mobility in a polyacrylamide gel compared to the mobility of a perfectly base-paired duplex (Delwart et al., Science 262:1257-1261 (1993); White et al., Genomics 12:301-306 (1992)).

The technique of single strand conformational polymorphism (SSCP) also can be used to detect the presence or absence of a fibrostenosis-predisposing allele in a method of the invention (see Hayashi, Methods Applic. 1:34-38 (1991)). This technique is used to detect mutations based on differences in the secondary structure of single-strand DNA that produce an altered electrophoretic mobility upon non-denaturing gel electrophoresis. Polymorphic fragments are detected by comparison of the electrophoretic pattern of the test fragment to corresponding standard fragments containing known alleles.

Denaturing gradient gel electrophoresis (DGGE) also can be used to detect a fibrostenosis-predisposing allele in a method of the invention. In DGGE, double-stranded DNA is electrophoresed in a gel containing an increasing concentration of denaturant; double-stranded fragments made up of mismatched alleles have segments that melt more rapidly, causing such fragments to migrate differently as compared to perfectly complementary sequences (Sheffield et al., "Identifying DNA Polymorphisms by Denaturing Gradient Gel Electrophoresis" in Innis et al., *supra*, 1990).

Other molecular methods useful for determining the presence or absence of a fibrostenosis-predisposing allele are known in the art and useful in the methods of the invention. Other well-known approaches for

determining the presence or absence of a fibrostenosis-predisposing allele include, without limitation, automated sequencing and RNAase mismatch techniques (Winter et al., Proc. Natl. Acad. Sci. 82:7575-7579 (1985)). Furthermore, one skilled in the art understands that, where the presence or absence of multiple alleles or a fibrostenosis-predisposing haplotype is to be determined, individual alleles can be detected by any combination of molecular methods. See, in general, Birren et al. (Eds.) Genome Analysis: A Laboratory Manual Volume 1 (Analyzing DNA) New York, Cold Spring Harbor Laboratory Press (1997). In addition, one skilled in the art understands that multiple alleles can be detected in individual reactions or in a single reaction (a "multiplex" assay). In view of the above, one skilled in the art realizes that the methods of the invention for diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease can be practiced using one or any combination of the well known assays described above or known in the art.

The present invention further provides a method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease by determining the presence or absence in an individual of a fibrostenosis-predisposing haplotype, where the presence of the fibrostenosis-predisposing haplotype is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease. In one embodiment, the fibrostenosis-predisposing haplotype is associated with a clinical subtype of Crohn's disease characterized by fibrostenosing disease with an odds ratio of at least 2 and a lower 95%

confidence limit greater than 1. In another embodiment, the fibrostenosis-predisposing haplotype is associated with a clinical subtype of Crohn's disease characterized by fibrostenosing disease with an odds ratio of at least 3, at least 4, at least 5, at least 6, and a lower 95% confidence limit greater than 1.

The term "fibrostenosis-predisposing haplotype," as used herein, means a combination of alleles that tend to be inherited together with the clinical subtype of Crohn's disease characterized by fibrostenosing disease more often than would be expected according to traditional Mendelian genetics. In a method of the invention, the clinical subtype of Crohn's disease can be, for example, characterized by fibrostenosing disease independent of small bowel involvement. In one embodiment, the fibrostenosis-predisposing haplotype includes at least one allele linked to the NOD2/CARD15 locus. In another embodiment, the fibrostenosis-predisposing haplotype includes a fibrostenosis-predisposing allele. In a further embodiment, a fibrostenosis-predisposing haplotype contains, for example, a variant allele at the NOD2/CARD15 locus. In another embodiment, the fibrostenosis-predisposing haplotype includes the "2" allele at SNP 8, SNP 12, or SNP 13. In a futher embodiment, the fibrostenosis-predisposing haplotype includes the "2" allele at SNP 13. In still further embodiments, the fibrostenosis-predisposing haplotype includes the "2" allele at SNP 8, SNP 12, and SNP 13. In another embodiment, the fibrostenosis-predisposing haplotype includes a JW1, JW15, JW16, JW17, or JW18 variant allele. One skilled in the art understands that a fibrostenosis-predisposing haplotype can contain alleles that individually are not significantly

associated the fibrostenosing subtype of Crohn's disease, so long as the combination of alleles making up the haplotype tend to be inherited together with the fibrostenosing subtype of Crohn's disease more often than would be expected according to traditional Mendelian genetics.

The presence or absence of a fibrostenosis-predisposing haplotype can be accomplished using any of the methods described herein above for determining the presence or absence of a fibrostenosis-predisposing allele. As an example, enzymatic amplification such as polymerase chain reaction amplification, for example, using one or more fluorescently labeled probes or one or more probes containing a DNA minor grove binder can be useful for determining the presence or absence of a fibrostenosis-predisposing haplotype in a method of the invention.

Antibody based methods also can be useful for determining the presence or absence of a fibrostenosis-predisposing allele or fibrostenosis-predisposing haplotype in a method of the invention. As an example, an antibody that is specifically reactive with a polypeptide or fragment thereof encoded by fibrostenosis-predisposing allele can be used to detect the presence or absence of that allele in an individual. Such an antibody can be, for example, specifically reactive with the truncated version of NOD2/CARD15 generated by a "2" allele at SNP 13 but not reactive with full-length or wild type NOD2/CARD15.

Antibodies useful in the methods of the invention include, without limitation, monoclonal and

polyclonal antibodies, single chain antibodies, chimeric antibodies, bifunctional or bispecific antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, including compounds which include CDR or antigen-binding sequences, which differentially bind to a polypeptide or fragment encoded by a fibrostenosis-predisposing allele but not to other, non-predisposing alleles. Antibody fragments, including Fab, Fab', $F(ab')_2$, and Fv, also can be useful in the methods of the invention as can plastic antibodies or molecularly imprinted polymers (MIPs; Haupt and Mosbauch, TIBTech 16:468-475 (1998)). Screening assays to determine differential binding specificity of an antibody are well known in the art (see Harlow et al. (Eds), Antibodies: A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, N.Y. (1988)).

Antibodies useful in a method of the invention can be produced using any method well known in the art, using a polypeptide, or immunogenic fragment thereof, encoded by a fibrostenosis-predisposing allele. Immunogenic polypeptides or fragments can be isolated from natural sources, from recombinant host cells, or can be chemically synthesized. Methods for synthesizing such peptides are known in the art as described, for example, in Merrifield, J. Amer. Chem. Soc. 85: 2149-2154 (1963); Krstenansky et al., FEBS Lett. 211:10 (1987).

Antibodies that differentially bind to polypeptides encoded by fibrostenosis-predisposing alleles of the invention can be labeled with a detection moiety and used to detect the presence, absence or amount of the encoded polypeptide *in vivo*, *in vitro*, or *in situ*. A moiety, such as a fluorescent molecule, can be linked to an antibody for use in a method of the invention. A

moiety such as detection moiety can be linked to an antibody using, for example, carbodiimide conjugation (Bauminger and Wilchek, Meth. Enzymol. 70:151-159 (1980)).

Antibodies that differentially bind to polypeptides encoded by a fibrostenosis-predisposing allele can be used in immunoassays. Immunoassays include, without limitation, radioimmunoassays, enzyme-linked immunosorbent assays (ELISAs) and immunoassays with fluorescently labeled antibodies, which are well known in the art. Antibodies can also be used to detect the presence or absence of a polypeptide of interest in a cell or tissue using immunohistochemistry or other *in situ* assays. Furthermore, cells containing a polypeptide of interest either on the surface of the cell or internally can be detected by an antibody using assays such as fluorescence activated cell sorting (FACS). One skilled in the art understands that these and other routine assays can be useful for determining the presence or absence of the gene product of a fibrostenosis-predisposing allele according to a method of the invention.

The methods of the invention optionally include generating a report indicating the presence or absence in a individual of a fibrostenosis-predisposing allele or fibrostenosis-predisposing haplotype. The methods of the invention also optionally include generating a report indicating the presence or absence in the individual of a clinical subtype of Crohn's disease characterized by fibrostenosing disease or the risk that an individual has of having or developing the fibrostenosing subtype of Crohn's disease.

A report can be in a variety of forms, for example, a report can be printed on paper or a report can be an electronic report that is not printed but is transmitted over an electronic medium such as electronic mail or a computer diskette. A report also can be an oral report that indicates the presence or absence in the individual of a fibrostenosis-predisposing allele or a clinical subtype of Crohn's disease characterized by fibrostenosing disease.

The invention also provides a method of optimizing therapy in an individual by determining the presence or absence in the individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus, diagnosing individuals in which the fibrostenosis-predisposing allele is present as having a fibrostenosing subtype of Crohn's disease, and treating the individual having a fibrostenosing subtype of Crohn's disease based on the diagnosis. Treatment for the fibrostenosing subtype of Crohn's disease currently includes, for example, surgical removal of the affected, strictured part of the bowel. In one embodiment, the presence or absence of a fibrostenosis-predisposing allele is determined in an individual having a known diagnosis of Crohn's disease. In another embodiment, the diagnosis is recorded in the form of a report as described above.

The following examples are intended to illustrate but not limit the present invention.

EXAMPLE I

SELECTION AND CHARACTERIZATION OF STUDY SUBJECTS

This example describes the clinical characterization of how two cohorts of Crohn's disease patients.

A. Selection of Study Subjects

Two cohorts of Crohn's disease patients were consecutively identified from an inflammatory bowel disease referral center (Cedars-Sinai Medical Center Inflammatory Bowel Disease Center). The first cohort of 142 patients, ascertained between 1993-1996 and designated "CD1", was previously described in Vasiliauskas et al., Gut 47:487-496 (2000)). The second cohort of 59 patients (Cohort 2) was collected between 1999-2001 and designated "CD2". A cohort of 175 patients with ulcerative colitis was used as an inflammatory bowel disease control group. This study, which was reviewed and approved for human subject participation by the Cedars-Sinai Institutional Review Board, involved the collection of clinical, serologic and genetic data from patients consenting to the study.

A diagnosis of Crohn's disease in the cohort patients was defined by the presence of a combination of established features from at least two of the following categories: 1) clinical - perforating or fistulizing disease, obstructive symptoms secondary to small bowel stenosis or stricture; 2) endoscopic - deep linear or serpiginous ulcerations, discrete ulcers in normal-appearing mucosa, cobblestoning, or discontinuous or asymmetric inflammation; 3) radiographic - segmental disease (skip lesions), small bowel or colon strictures,

stenosis, or fistula, and; 4) histopathologic-submucosal or transmural inflammation, multiple granulomas, marked focal cryptitis or focal chronic inflammatory infiltration within and between biopsies, or skip lesions including rectal sparing in the absence of local therapy.

To identify clinical features and immunological traits associated with allelic variants of the NOD2/CARD15 gene, the study was designed to analyze two consecutively ascertained cohorts of patients with Crohn's disease. The first cohort was used to explore the relationship of NOD2/CARD15 alleles with an array of clinical and serologic variables, thereby generating hypotheses. The second cohort was then used to confirm the specific hypotheses generated from analysis of the first cohort. To minimize type I error and maximize statistical power, the significance of the associations in the first cohort were permitted to be less stringent ($p < 0.1$) than in the second cohort ($p < 0.05$). By avoiding a highly stringent correction for the number of variables examined in the first cohort, there was an increased ability to identify specific associations between NOD2/CARD15 allele variants and clinical variables.

B. Clinical Characterization of Study Subjects

Patients with Crohn's disease were characterized as having fibrostenosing disease, internal-perforating disease, perianal fistulizing disease or ulcerative colitis (UC)-like disease based on previously described criteria (Gasche et al., Inflammatory Bowel Diseases 6:8-15 (2000); Vasiliauskas et al., Gut 47:487-496 (2000);

Vasiliauskas et al., Gastroenterology 110:1810-1819 (1996); and Greenstein et al., Gut 29:588-592 (1988)). According to well established criteria, fibrostenosing disease was defined by documented persistent intestinal obstruction or an intestinal resection for an intestinal obstruction. Internal perforating disease was defined as current or previous evidence of entero-enteric or entero-vesicular fistulae, intraabdominal abscesses, or small bowel perforation. Perianal perforating disease was defined by current or previous evidence of either perianal fistulae or abscesses or rectovaginal fistula. UC-like disease was defined by current or previous evidence of left-sided colonic involvement, symptoms of bleeding or urgency, and crypt abscesses on colonic biopsies as previously described. Disease location was classified as small bowel, colon, or both based on one or more endoscopic, radiologic or pathologic studies. A panel of inflammatory bowel disease physicians unaware of the results of serologic and genetic testing reached a consensus on phenotype based on the clinical data.

Serum ANCA expression and ANCA subtype characterization were performed by fixed neutrophil enzyme-linked immunosorbent assay (ELISA) as previously described (Saxon et al., J. Allergy Clin. Immunol. 86:202-210 (1990)). Briefly, human peripheral blood neutrophils fixed with methanol were reacted with control and coded sera at a 1:100 dilution. Anti-human immunoglobulin G (IgG) (chain-specific) antibody (Jackson Immunoresearch Labs, Inc.; West Grove, PA) conjugated to alkaline phosphatase was added to label neutrophil-bound antibody, and a colorimetric reaction was performed. Levels were determined relative to a standard consisting of pooled sera obtained from well-characterized pANCA+ UC patients. Results were

expressed as ELISA units (EU) per milliliter. ANCA+ sera were further subtyped via indirect immunofluorescent staining to determine the ANCA neutrophil binding pattern, as previously described (Saxon et al., *supra*, 1990). Sera showing the characteristic perinuclear highlighting and losing the characteristic staining pattern when treated with deoxyribonuclease were termed pANCA+ (Vidrich et al., J. Clin. Immunol. 15:293-299 (1995)). For the purposes of this study, patients were considered pANCA+ if they were both positive for ANCA by ELISA and lost perinuclear immunofluorescence staining with deoxyribonuclease treatment.

Sera were analyzed for ASCA expression in a blinded fashion by using a fixed ELISA assay (Vasiliauskas et al., Gut 47:487-496 (2000); and Vermeire et al., Gastroenterology 120:827-833 (2001)). Two patients in the second cohort did not undergo ASCA testing. High-binding polystyrene microtiter plates were coated with purified phosphopeptidomannans extracted from yeast S. uvarum, a subspecies of S. cerevisiae. Coded patient sera were diluted and added to the wells, followed by an enzyme-linked colorimetric reaction. Color development was proportional to concentrations of ASCA antibody present in the sera. Levels were determined and results expressed as EU per milliliter, relative to a standard, which was derived from a pool of patient sera with well-characterized Crohn's disease found to have reactivity to this antigen. Sera showing ASCA IgG reactivity of >40 EU/mL or IgA reactivity of >20 EU/mL were termed ASCA+. Serological assays were performed at Cedars-Sinai Medical Center and Prometheus Laboratories (San Diego, CA) using substantially identical methodology. The clinical characteristics of the two Crohn's disease cohorts are shown in Table 1.

TABLE 1

Clinical Characteristics of Two Crohn's Disease Cohorts

Clinical characteristics	CD1	CD2	
	n=142	n=59	p
Gender (M/F)	79/63	33/26	0.969
Age at onset	22 (4-67)	22(2-58)	0.6621
Ethnicity (Jew/Non-Jew)	60/82	23/36	0.668
Disease location (%)			
SB only	19.0	26.4	0.496
Colon only	20.4	20.8	
SB and Colon	60.6	52.8	
Perianal perforating (%)	35.9	28.8	0.332
Internal perforating (%)	47.2	23.7	0.002
Fibrostenosing disease (%)	59.9	30.5	0.001
UC-like (%)	39.4	22.0	0.018
pANCA-positive (%)	19.7	12.5	0.295
ASCA-positive* (%)	57.0	38.6	0.019

EXAMPLE II

PATIENTS WITH CROHN'S DISEASE HAVE AN INCREASED FREQUENCY OF RARE ALLELIC VARIANTS OF NOD2/CARD15

This example describes the association of a "2" allele at SNP 8, SNP 12, or SNP 13 within the NOD2/CARD15 locus (rare allelic variants of NOD2/CARD15) with Crohn's disease in a North American population.

In order to determine whether the North American Crohn's disease patient populations in Cohorts 1 and 2 expressed allelic variants of NOD2/CARD15, Cohort 1 (hypothesis-generating) and Cohort 2 (hypothesis-confirming) were genotyped for the rare allelic variant of SNP 8 (R675W), SNP 12 (G881R) and

SNP 13 (3020insC). A cohort of ulcerative colitis patients was used for comparison.

Genotyping was performed using a genotyping assay employing 5'-exonuclease technology, the TaqMan MGB™ assay (PE Biosystems; Foster City, CA). Primers were designed using the software PrimerExpress 1.5™ (PE Biosystems) and sequence information found in dbSNP for NOD2/CARD15 SNP 5, 8, 12, and 13. The MGB™ design adds a "minor groove binder" to the 3' end of the TaqMan™ probes, thereby increasing the binding temperature of the probe and enabling the use of shorter probes than in conventional TaqMan™ assays (Kutyavin et al., Nucleic Acids Res. 25:3718-3723 (1997)). This has the effect of increasing the discrimination between the alleles in the assay (Kutyavin et al., Nucleic Acids Res. 28:655-661 (2000)). Assays were performed following the manufacturer's recommendations (PE Biosystems bulletin 4317594) in an ABI 7900 instrument. Genotyping was performed blinded to clinical status of the subjects. Primers and probes used in the genotyping assay are shown in Tables 2 and 3.

Table 2
Primers Used in Taqman MGB™ Assay for SNPs 5, 8, 12 and 13

SNP Primer	Forward Primer	Reverse Primer	SEQ ID NO
5	5'GGTGGCTGGGC TCTTCT 3'	5'CTCGCTTCCTCAGTACCTAT GATG 3'	for 37 rev 38
8	5'CTGGCTGAGTG CCAGACATCT 3'	5'GGCGGGATGGAGTGGAA 3'	for 39 rev 40
12	5'CCACCTCAAGC TCTGGTGATC 3'	5'GTTGACTCTTTTGGCCTTTT CAG 3'	for 41 rev 42
13	5'CCTTACCAGAC TTCCAGGATGGT 3'	5'TGTCCAATAACTGCATCACC TACCT 3'	for 43 rev 44

Table 3
TAQMAN PROBES

Allele detected	Probe sequence	Seq ID NO
SNP5 wild type allele ("1")	6FAM-CATGGCTGGACCC-MGBNFQ	45
SNP5 variant allele ("2")	TET-CATGGCTGGATCC-MGBNFQ	46
SNP8 wild type allele ("1")	6FAM-TGCTCCGGCGCCA-MGBNFQ	47
SNP8 variant allele ("2")	TET-CTGCTCTGGCGCCA-MGBNFQ	48
SNP12 wild type allele ("1")	6FAM-CTCTGTTGCCCCAGAA-MGBNFQ	49
SNP12 wild type allele ("1")	TET-CTCTGTTGCGCCAGA-MGBNFQ	50
SNP13 wild type allele ("1")	TET-CTTTCAAGGGCCTGC-MGBNFQ	51
SNP13 variant allele ("2")	6FAM-CCTTTCAAGGGGCCT-MGBNFQ	52
JW1 wild type allele	6FAM-AAGACTCGAGTGTCCT-MGBNFQ	53
JW1 variant	VIC-AGACTCAAGTGTCCTC-MGBNFQ	54

As shown in Table 4, each of three rare allelic variants of NOD2/CARD15 (a "2" allele at SNP 8, SNP 12, or SNP 13) was significantly more frequent in patients

with Crohn's disease compared with ulcerative colitis. In addition, as can be seen in Table 4, the frequency of each of the NOD2/CARD15 rare allelic variants was similar in each cohort of Crohn's disease patients, supporting the combined use of the two cohorts. The overall frequency of any of the three NOD2/CARD15 rare allelic variants was 35% in Crohn's disease patients compared with 11% in ulcerative colitis patients (p=0.001).

Within the combined Crohn's disease cohort, the frequency of homozygotes with a "2" allele at SNP 13 (3020insC) and compound rare allelic heterozygotes was 1% and 4%, respectively, while none of the ulcerative colitis patients had such a genotype. These results demonstrate that rare allelic variants of NOD2/CARD15 are associated with Crohn's disease across diverse geographic and ethnically-defined patient populations.

Table 4

Frequency of NOD2/CARD15 Rare Allelic Variants in CD and UC Patient Populations

Allelic variants	UC (n=175)	CD1 (n=142)	CD2 (n=59)	Combined CD1 and CD2 (n=201)	p (UC vs. Combined CD)
R675W (SNP 8 "2" allele)	5.7%	16.9%	15.3%	16.4%	0.001
G881R (SNP 12 "2" allele)	1.7%	12.0%	10.2%	11.4%	0.0001
3020insC (SNP 13 "2" allele)	3.4%	11.3%	11.9%	11.4%	0.004
Carriage of any allelic variant	10.9%	36.6%	32.2%	35.3%	0.001

EXAMPLE III

RARE VARIANT ALLELES IN THE NOD2/CARD15 LOCUS ARE ASSOCIATED WITH THE FIBROSTENOSING SUBTYPE OF CROHN'S DISEASE IN COHORT 1

This example demonstrates that a "2" allele at SNP 8, SNP 12, or SNP 13 is significantly associated with fibrostenosing disease in Cohort 1.

Patients with Crohn's disease express diverse clinical phenotypes that can be due to differences in underlying genetic factors. In order to determine whether rare variant alleles at the NOD2/CARD15 locus were associated with specific Crohn's disease-related clinical phenotypes or disease-related serum immune markers, univariate analysis was performed. The univariate analysis evaluated the association between NOD2/CARD15 allelic variants at SNP 8, SNP 12, or SNP 13 and predefined clinical characteristics, including age of onset, disease location, and disease phenotype (fibrostenosing disease, internal-perforating disease, perianal fistulizing disease or ulcerative colitis-like disease). The association between NOD2/CARD15 allelic variants and expression of the serum immune markers ASCA and pANCA was also tested.

As shown in Table 5, univariate analysis indicated that a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus was significantly associated with fibrostenosing disease in Cohort 1 ($p=0.049$) for the three allelic variants combined. A positive association at a less stringent significance level ($p< 0.1$) was also observed with small bowel involvement and younger age of onset, and a negative association was observed with

UC-like disease in this cohort. With respect to serologic markers, patients with the "2" allele at SNP 13 were more likely to express ASCA (p=0.053). These results demonstrate that a "2" allele at SNP 8, SNP 12, or SNP 13 is significantly associated with fibrostenosing disease in Cohort 1.

Statistical analysis was performed using SAS computer software (Version 6.10; SAS Institute, Inc.; Cary, NC). Quantitative variables were described as medians with a range. Nonparametric statistical tests were used to test differences in quantitative variables between two groups. A Chi-square test or Fisher's exact test (when the expected number was less than 5) was used to evaluate associations between carriers and non-carriers of the rare alleles or between genotypes and categorical variables, such as type of IBD, disease location, disease behavior, and antibody positivity. In addition, a Mantel Haenszel stratified association test was performed for all genotype and phenotype associations by controlling for potential confounding effect due to ethnic variation. This stratified association test was also used to evaluate whether the small bowel involvement and fibrostenosing disease were independently associated with NOD2/CARD15 variants (see Example IX below).

Table 5

Relationship of NOD2/CARD15 Rare Variant Alleles and Clinical Phenotypes of Crohn's Disease in Cohort 1

			Qualitative Trait %NOD2 variant carriers			
Clinical phenotypes			R675W (SNP 8)	G881R (SNP 12)	3020insC (SNP 13)	Carriage of any allelic variant
		n				
Small bowel involvement	yes	113	19.47%	11.50%	14.16%	40.71%
	no	29	6.90%	13.79%	0.00%	20.69%
p value			0.081	0.494	0.04	0.063
Perianal perforating	yes	51	11.76%	11.76%	13.73%	35.29%
	no	91	19.78%	12.09%	9.89%	37.36%
p value			0.248	0.839	0.547	0.747
Internal perforating	yes	67	13.43%	16.42%	11.94%	37.31%
	no	75	20.00%	8.00%	10.67%	36.00%
p value			0.346	0.178	0.91	0.96
Fibrostenosing	yes	85	18.82%	14.12%	15.29%	43.53%
	no	57	14.04%	8.77%	5.26%	26.32%
p value			0.389	0.458	0.084	0.049
UC-like	yes	56	17.86%	10.71%	5.36%	30.36%
	no	86	16.28%	12.79%	15.12%	40.70%
p value			0.822	0.736	0.076	0.22
pANCA positive	yes	28	17.86%	14.29%	7.14%	32.14%
	no	114	16.67%	11.40%	12.28%	37.72%
p value			0.82	0.793	0.394	0.529
ASCA positive	yes	81	18.52%	9.88%	16.05%	38.27%
	no	61	14.75%	14.75%	4.92%	34.43%
p value			0.467	0.234	0.053	0.744

			Quantitative Trait median (range)			
			R675W (SNP 8)	G881R (SNP 12)	3020insC (SNP 13)	Carriage of any allelic variant
Age of onset						
carrier of NOD2 variant	yes		22 (6-67)	22 (4-62)	19 (10-50)	20 (4-67)
	no		22 (4-63)	22 (4-67)	22 (4-67)	22 (4-63)
p			0.715	0.937	0.074	0.238

EXAMPLE IV

RARE VARIANT ALLELES IN THE NOD2/CARD15 LOCUS ARE ASSOCIATED WITH THE FIBROSTENOSING SUBTYPE OF CROHN'S DISEASE IN COHORT 2

This example demonstrates that a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is significantly associated with fibrostenosing disease in Cohort 2.

The results obtained with Cohort 1 in Example III indicated that NOD2/CARD15 rare variant alleles were positively associated with fibrostenosing Crohn's disease, small bowel involvement, ASCA positivity, and younger age of onset, and negatively associated with UC-like disease (see Table 5). These hypotheses were further tested using Cohort 2; the results are shown in Table 6. As with Cohort 1, Cohort 2 demonstrated a significant association between a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus and fibrostenosing disease ($p=0.002$, with Bonferroni correction $p=0.01$; see Table 6). These results indicate that a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is significantly associated with fibrostenosing disease in Cohort 2.

Table 6
Relationship of NOD2/CARD15 Rare Variant Alleles and Clinical Phenotypes of Crohn's Disease in Cohort 2

Clinical phenotypes		n	Qualitative Trait %NOD2 variant carriers: R675W (SNP 8)	G881R (SNP 12)	3020insC (SNP 13)	Carriage of any allelic variant
Fibrostenosing	yes	18	22.22%	22.22%	27.78%	61.11%
	no	41	12.20%	4.88%	4.88%	19.51%
p			0.315	**0.048**	**0.018**	**0.002**
Small bowel involvement	yes	42	19.05%	9.52%	14.29%	35.71%
	no	17	5.88%	11.76%	5.88%	23.53%
p			0.22	0.828	0.288	0.354
ASCA positive	yes	22	9.09%	13.64%	13.64%	31.82%
	no	35	17.14%	8.57%	11.43%	31.43%
p			0.4	0.542	0.735	0.956

		Quantitative Trait median (range): R675W (SNP 8)	G881R (SNP 12)	3020ins C (SNP 13)	Carriage of any allelic variant
Age of onset carrier of NOD2 variant	yes	27 (10-58)	26 (7-33)	17 (13-35)	22 (7-58)
	no	19 (2-55)	20 (2-58)	24 (2-58)	22 (2-55)
p		0.332	0.9	0.566	0.981

EXAMPLE V

RARE VARIANT ALLELES IN THE NOD2/CARD15 LOCUS ARE ASSOCIATED WITH THE FIBROSTENOSING SUBTYPE OF CROHN'S DISEASE IN A COMBINED COHORT REPRESENTING COHORTS 1 AND 2

This example demonstrates that a "2" allele at SNP 8, SNP 12, or SNP 13 is significantly associated with fibrostenosing disease in a combined cohort representing cohorts 1 and 2.

As seen in Figure 2, the association between a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus (NOD2 variant carrier) and fibrostenosing disease was even more significant ($p=0.001$) when the two cohorts were analyzed together than when analyzed separately.

The association between a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus (NOD2 variant carrier) and fibrostenosing disease was observed in both Jewish and non-Jewish individuals. Approximately 46% of Crohn's disease patients with fibrostenosing disease (Jews 52% vs. non-Jews 42%) had at least one of these rare alleles compared with only 23% (Jews 21.6% vs. non-Jews 25%) of Crohn's disease patients without fibrostenosing disease (Odds ratio, 2.8; 95% Confidence interval, 1.56-5.18). Of the three rare variant alleles, the frameshift mutation 3020insC (a "2" allele at SNP 13) demonstrated the greatest association with fibrostenosing disease (47% vs. 17%, $p=0.006$ for cohorts combined). These results indicate that rare variant alleles in the NOD2/CARD15 locus are associated with the fibrostenosing subtype of Crohn's disease in a combined cohort representing Cohorts 1 and 2.

EXAMPLE VI

CROHN'S DISEASE PATIENTS WITH HOMOZYGOUS MUTATIONS OR COMPOUND HETEROZYGOUS MUTATIONS IN NOD2/CARD15

This example describes the increased risk of fibrostenosing disease in Crohn's disease patients carrying homozygous mutations or compound heterozygous mutations in NOD2/CARD15 locus.

As shown in Figure 3, compared with patients who were not carriers of NOD2/CARD15 mutations at SNP 8, SNP 12 or SNP 13, patients who were carriers of two mutations in NOD2/CARD15 were significantly more likely to have fibrostenosing disease (85% vs. 43%; odds ratio 7.4; 95% confidence interval 1.9-28.9, p=0.004). Patients who were carriers of a single NOD2/CARD15 mutation were also significantly more likely to have fibrostenosing disease when compared with patients who were not carriers of these NOD2/CARD15 mutations (64% vs. 43%; Odds ratio 2.37; 95% Confidence interval 1.26-4.47; p=0.008). These results indicate that Crohn's disease patients with homozygous mutations or compound heterozygous mutations in NOD2/CARD15 have an increased risk of fibrostenosing disease.

EXAMPLE VII

FIBROSTENOSING DISEASE ONLY COMPARED TO FIBROSTENOSING AND PERFORATING DISEASE

This example describes the association of the "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus in patients with fibrostenosing disease compared to patients with fibrostenosing and perforating disease.

Fibrostenosing and perforating disease often occur in the same patient. Patients with fibrostenosing disease can be characterized as i) having only fibrostenosing disease or ii) having both fibrostenosing and perforating disease. In order to address these phenotypes individually, patients in each of the two cohorts were separated by the presence of fibrostenosing disease with perforating complications (Fib + perf) or without perforating complications (Fib only) and compared with patients with perforating complications without evidence of fibrostenosis (Perf only). The percentage of patients having only fibrostenosing disease that carried a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus was 48.3%, which was similar to that seen in patients with both fibrostenosing and perforating complications (46.0%; p=0.8). As seen in Figure 3, when patients with fibrostenosing disease were compared with those patients described as having perforating disease only (perianal or internal), the frequency of the "2" allele at SNP 8, SNP 12 or SNP 13 of the NOD2/CARD15 locus in patients with fibrostenosing disease (with or without perforating complications) was significantly greater than that seen in patients with only perforating complications (46.6% versus 18.6%; p=0.002).

EXAMPLE VIII

MULTIVARIANT ANALYSIS OF THE COMBINED PATIENT COHORT

This example demonstrates that fibrostenosing disease is independently associated with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus.

For multivariant analysis, all variables with at least borderline significance ($p < 0.1$) in either cohort were tested simultaneously for their association with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus by using logistic regression. As shown in Table 7, the clinical phenotype of fibrostenosing disease was significantly associated ($p < 0.05$) with these rare alleles at NOD2/CARD15 locus (OR 2.8; 95% CI, 1.3-6.0). These results confirm that fibrostenosing disease is independently associated with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus.

Table 7

Multivariate Analysis in the Combined Cohort for 5 Phenotypic Variables

Clinical phenotypes	OR	95% CI	P
Fibrostenosing disease	2.8	1.3-6.0	0.011
Small bowel involvement	1.3	0.5-3.4	0.561
UC-like	0.9	0.4-1.7	0.658
ASCA positive	0.7	0.3-1.3	0.250
Age of onset	1.0	0.9-1.0	0.874

EXAMPLE IX

FIBROSTENOSING DISEASE AND SMALL-BOWEL INVOLVEMENT

This example demonstrates that the association between fibrostenosing disease and a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is independent of small-bowel involvement.

Because fibrostenosing disease is more likely to occur in patients with small-bowel involvement, patients were stratified on the basis of small-bowel involvement to analyze whether the association between fibrostenosing disease and NOD2/CARD15 variant alleles was a primary association. Among patients with small-bowel involvement, 26.4% of patients who did not have fibrostenosing disease (n=53) had a "2" allele at SNP 8, SNP 12, or SNP 13, whereas 46.1% of patients who had fibrostenosing disease (n=102) had a "2" allele at SNP 8, SNP 12, or SNP 13(p=0.017). A similar trend was observed among patients without small-bowel involvement (p=0.05), and the combined analysis conditioning on small-bowel involvement yielded a significance level of 0.009.

After controlling for fibrostenosing disease, small-bowel involvement was not associated with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus (p= 0.63). This result agrees with the results from logistic regression analysis (see Example VIII) and indicates that the association between fibrostenosing disease and a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is independent of small-bowel involvement. These results further indicate that the observed small-bowel association with a "2" allele at SNP 8, SNP 12, or SNP 13 of the NOD2/CARD15 locus is secondary to the presence of fibrostenosing disease.

All journal article, reference, and patent citations provided above, in parentheses or otherwise, whether previously stated or not, are incorporated herein by reference.

Although the invention has been described with reference to the examples above, it should be understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims.

We claim:

1. A method of diagnosing or predicting susceptibility to a clinical subtype of Crohn's disease characterized by fibrostenosing disease, comprising

determining the presence or absence in an individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus,

wherein the presence of said fibrostenosis-predisposing allele is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease.

2. The method of claim 1, wherein said clinical subtype of Crohn's disease is characterized by fibrostenosing disease independent of small bowel involvement.

3. The method of claim 1, wherein said fibrostenosis-predisposing allele is located within said NOD2/CARD15 locus.

4. The method of claim 3, wherein NF-kappa B activation by a NOD2/CARD15 polypeptide encoded by said fibrostenosis-predisposing allele is reduced as compared to NF-kappa B activation by a wild-type NOD2/CARD15 polypeptide.

5. The method of claim 3, wherein said fibrostenosis-predisposing allele is located in a coding region of said NOD2/CARD15 locus.

6. The method of claim 5, wherein said fibrostenosis-predisposing allele is located in a region encoding residues 744 to 1020 of NOD2/CARD15.

7. The method of claim 5, wherein said fibrostenosis-predisposing allele is a "2" allele at a SNP selected from SNP 8, SNP 12, and SNP 13.

8. The method of claim 7, wherein said fibrostenosis-predisposing allele is a "2" allele at SNP 13.

9. The method of claim 3, wherein said fibrostenosis-predisposing allele is located in a non-coding region of said NOD2/CARD15 locus.

10. The method of claim 9, wherein said fibrostenosis-predisposing allele is selected from a JW1, JW15, and JW16 variant allele.

11. The method of claim 9, wherein said fibrostenosis-predisposing allele is located in a promoter region of said NOD2/CARD15 locus.

12. The method of claim 11, wherein said fibrostenosis-predisposing allele is an allele selected from a JW17 and JW18 variant allele.

13. The method of claim 1, comprising determining the presence or absence in said individual of at least two fibrostenosis-predisposing alleles linked to a NOD2/CARD15 locus,

wherein the presence of one or more of said fibrostenosis-predisposing alleles is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease.

14. The method of claim 13, wherein said at least two fibrostenosis-predisposing alleles are "2" alleles at a SNP selected from SNP 8, SNP 12, and SNP 13.

15. The method of claim 14, comprising determining the presence or absence in said individual of

(i) a "2" allele at SNP 8,

(ii) a "2" allele at SNP 12, and

(iii) a "2" allele at SNP 13,

wherein the presence of one or more of said "2" alleles at SNP 8, SNP 12, and SNP 13 is diagnostic of or predictive of susceptibility to the clinical subtype of Crohn's disease characterized by fibrostenosing disease.

16. The method of claim 1, wherein said fibrostenosis-predisposing allele is associated with said clinical subtype of Crohn's disease characterized by fibrostenosing disease with an odds ratio of at least 2 and a lower 95% confidence limit greater than 1.

17. The method of claim 1, further comprising generating a report indicating the presence or absence in said individual of said fibrostenosis-predisposing allele.

18. The method of claim 1, further comprising generating a report indicating the presence or absence in said individual of said clinical subtype of Crohn's disease characterized by fibrostenosing disease.

19. The method of claim 1, wherein determining the presence or absence of said fibrostenosis-predisposing allele comprises enzymatic amplification of nucleic acid from said individual.

20. The method of claim 19, wherein said amplification is polymerase chain reaction amplification.

21. The method of claim 20, wherein said polymerase chain reaction amplification is performed using one or more fluorescently labeled probes.

22. The method of claim 20, wherein said polymerase chain reaction amplification is performed using one or more probes comprising a DNA minor grove binder.

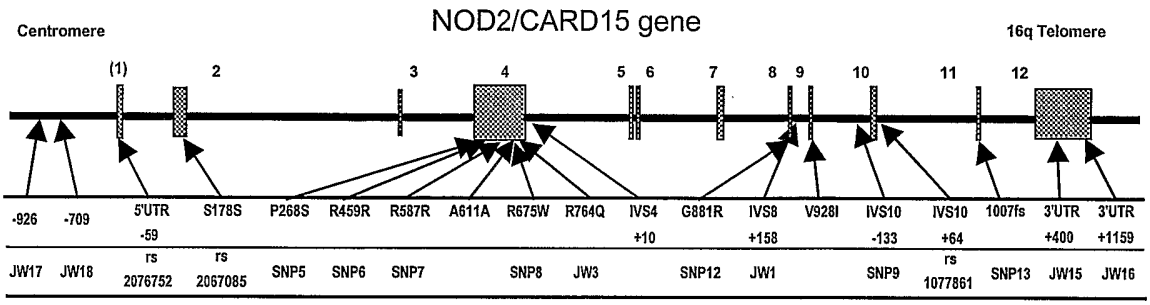
23. A method of optimizing therapy in an individual, comprising

(a) determining the presence or absence in said individual of a fibrostenosis-predisposing allele linked to a NOD2/CARD15 locus,

(b) diagnosing individuals in which said fibrostenosis-predisposing allele is present as having a fibrostenosing subtype of Crohn's disease, and

(c) treating said individual having a fibrostenosing subtype of Crohn's disease based on said diagnosis.

Figure 1


NOD2/CARD15 gene
Centromere
16q Telomere
(1)
2
3
4
5
6
7
8
9
10
11
12
-926
-709
5'UTR -59
S178S
P268S
R459R
R587R
A611A
R675W
R764Q
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G881R
IVS8 +158
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JW18
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rs 2067085
SNP5
SNP6
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SNP8
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SNP12
JW1
SNP9
rs 1077861
SNP13
JW15
JW16

Figure 2

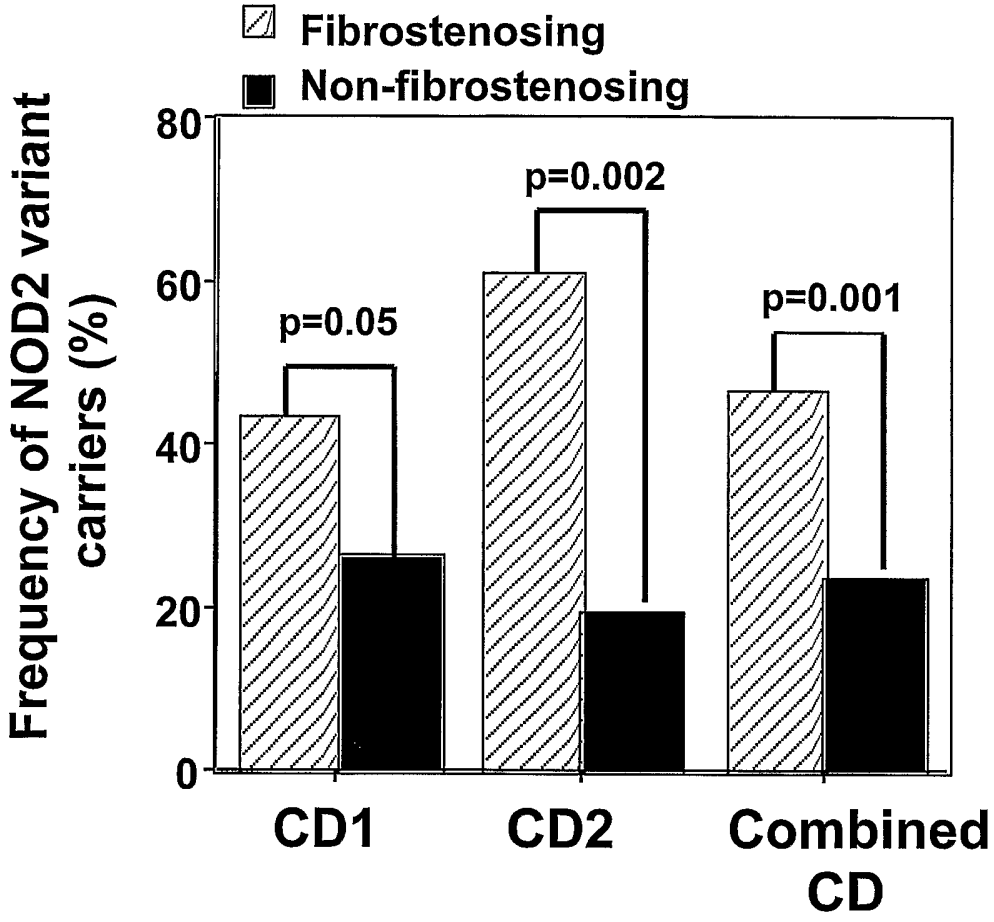
Fibrostenosing
Non-fibrostenosing
Frequency of NOD2 variant carriers (%)
80
60
40
20
0
p=0.05
p=0.002
p=0.001
CD1
CD2
Combined CD

Figure 3

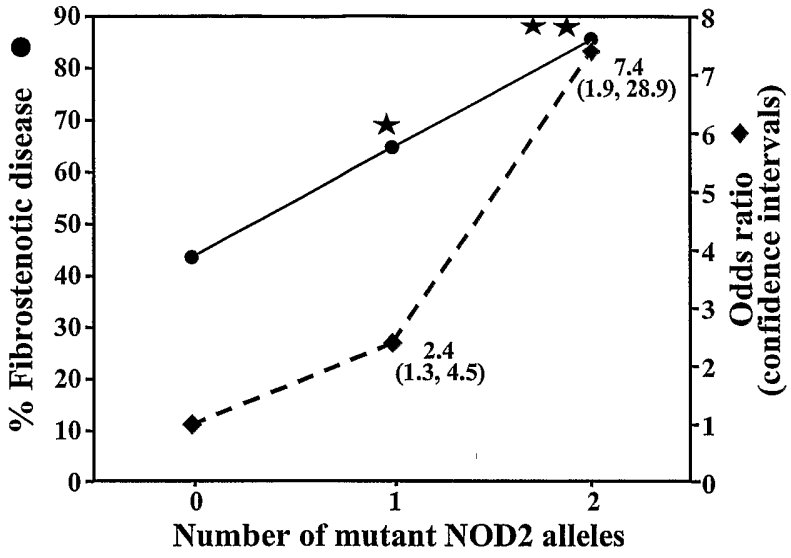
% Fibrostenotic disease
Odds ratio (confidence intervals)
Number of mutant NOD2 alleles
7.4
(1.9, 28.9)
2.4
(1.3, 4.5)
0
10
20
30
40
50
60
70
80
90
1
2
3
4
5
6
7
8

Figure 4

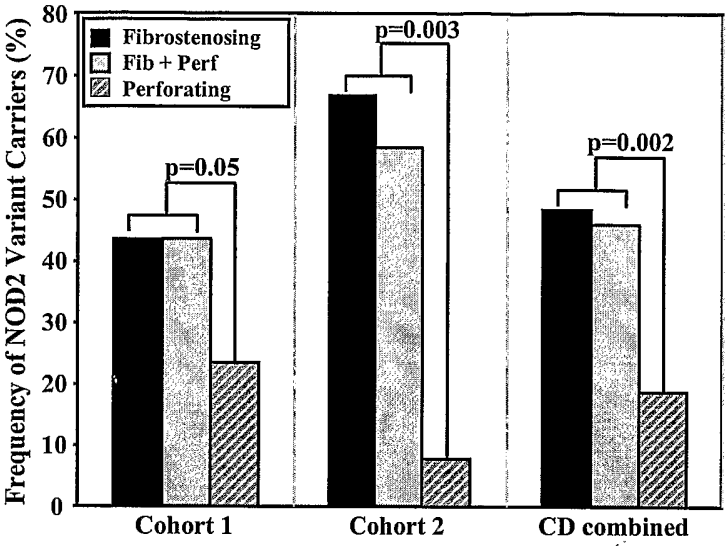
Fibrostenosing
Fib + Perf
Perforating
Frequency of NOD2 Variant Carriers (%)
0
10
20
30
40
50
60
70
80
p=0.05
p=0.003
p=0.002
Cohort 1
Cohort 2
CD combined

FIGURE 5

SNP 8

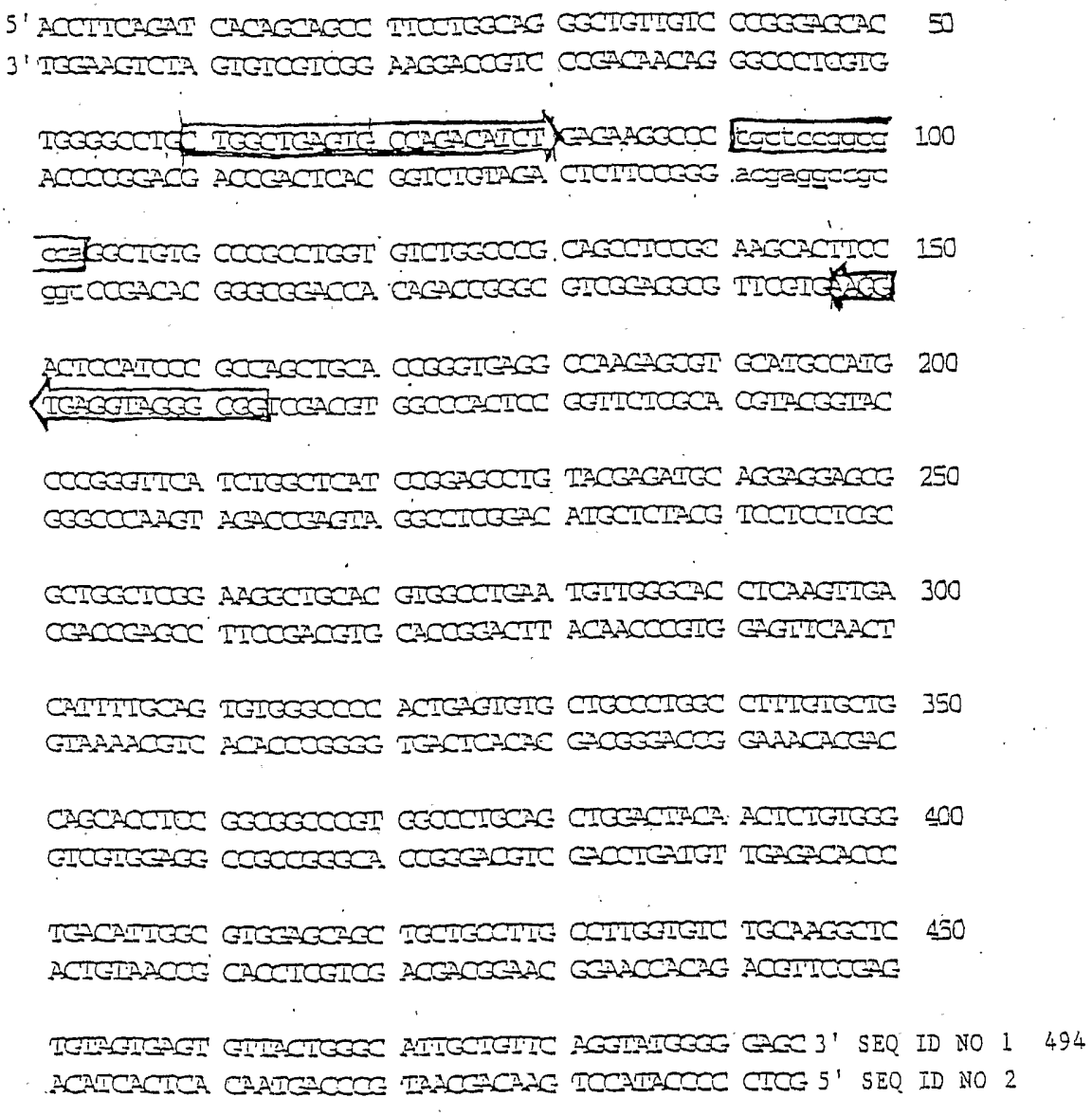

Figure 6

SNP 12

FIGURE 7

SNP 13

FIGURE 8

SNP 5

FIGURE 9

JW1


5'GCACTGGGCA CCCACTACCA ATGGATTGGA ATTGGTCCTT AAGATAAAAT 50
3'CGTGACCCGT GGGTGATGGT TACCTAACCT TAACCAGGAA TTCTATTTTA
GTACCTGATC CAGCCCAATA TCTTCAATTT ACAGATACTG TATCAAAACC 100
CATGGACTAG GTCGGGTTAT AGAAGTTAAA TGTCTATGAC ATAGTTTTGG
CTGAGAGGAC AAGGGACATT TCCAAGTCAC CCAGAaagac tcgagtgtcc 150
GACTCTCCTG TTCCCTGTAA AGGTTCAGTG GGTCTttctg agctcacagg
tCTCTTGAAA TCCAATGGTC TTTTTTCCTT ACTCCATTGC CTAACATTGT 200
aGAGAACTTT AGGTTACCAG AAAAAAGGAA TGAGGTAACG GATTGTAACA
GGGGTAGAAA TAAAGTTCAA AGACCTTCAG AACTGGCCCC AGCTCCTCCC 250
CCCCATCTTT ATTTCAAGTT TCTGGAAGTC TTGACCGGGG TCGAGGAGGG
TCTTCACCTG ATCTCCCCAA GAAAACTGCA GGATAGACTC TGAAGCTTAC 300
AGAAGTGGAC TAGAGGGGTT CTTTTGACGT CCTATCTGAG ACTTCGAATG
CTGAGCCACC TCAAGCTCTG GTGATCACCC AAGGCTTCAG CCAGGGCCTG 350
GACTCGGTGG AGTTCGAGAC CACTAGTGGG TTCCGAAGTC GGTCCCCGAC
GGCCCCCTCG TCACCCACTC TGTTGCCCCA GAATCTGAAA AGGCCAAAAG 400
CCGGGGGAGC AGTGGGTGAG ACAACGGGGT CTTAGACTTT TCCGGTTTTC
AGTCAACAGA CAGTGTCAGT GAGTACCTGA TATGTGTTCT AGACATGAAC 450
TCAGTTGTCT GTCACAGTCA CTCATGGACT ATACACAAGA TCTGTACTTG
TAACAGTCCT CCTCCCTCTG CAGTCCCAGC CAGAGGGGCA GGACCACTCA 500
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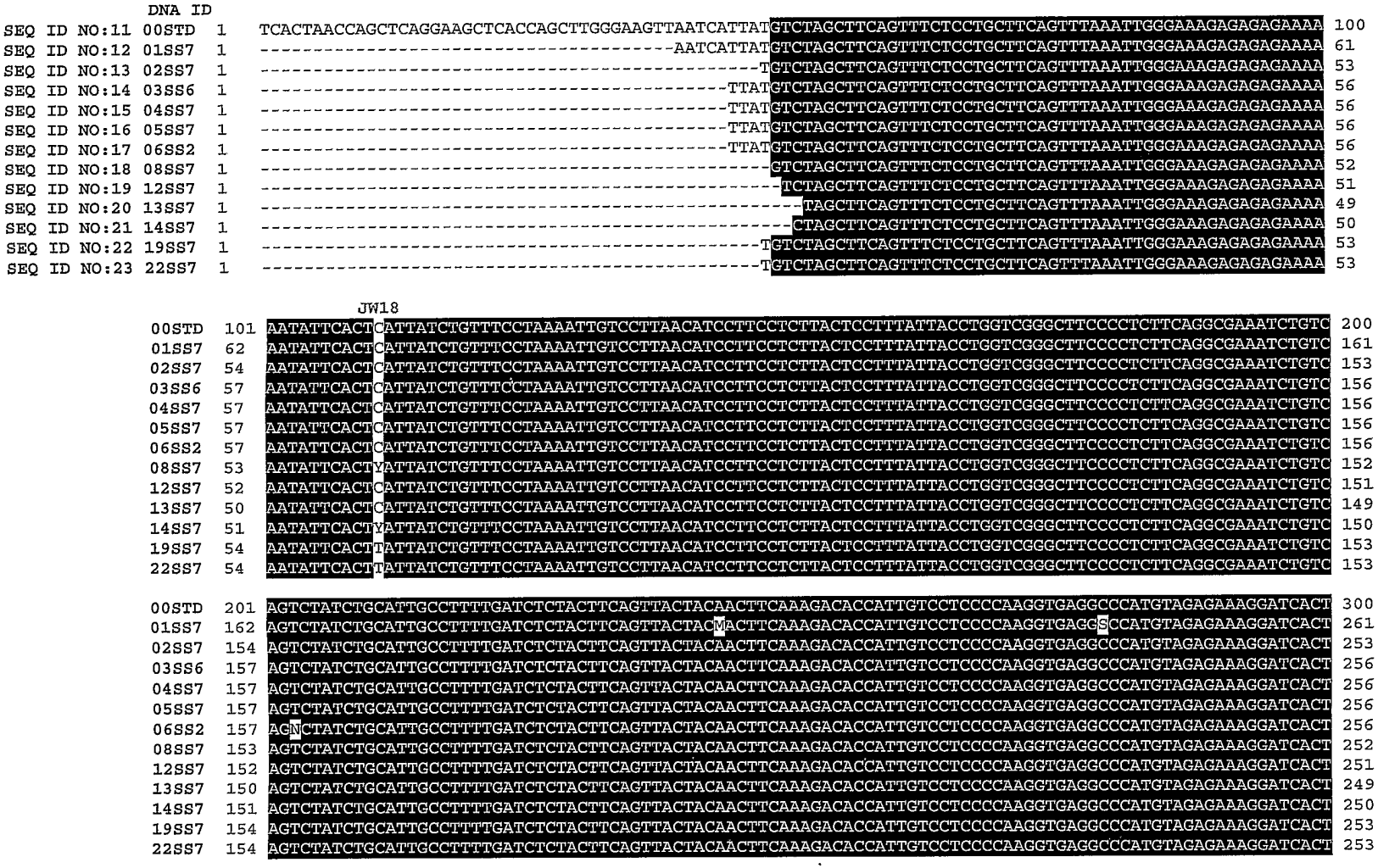
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SEQ ID NO:15 04SS7 1 --TTATGTCTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 56
SEQ ID NO:16 05SS7 1 --TTATGTCTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 56
SEQ ID NO:17 06SS2 1 --TTATGTCTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 56
SEQ ID NO:18 08SS7 1 --GTCTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 52
SEQ ID NO:19 12SS7 1 --TCTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 51
SEQ ID NO:20 13SS7 1 --TAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 49
SEQ ID NO:21 14SS7 1 --CTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 50
SEQ ID NO:22 19SS7 1 --TGTCTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 53
SEQ ID NO:23 22SS7 1 --TGTCTAGCTTCAGTTTCTCCTGCTTCAGTTTAAATTGGGAAAGAGAGAGAAAA 53
JW18
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02SS7 54 AATATTCACTCATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 153
03SS6 57 AATATTCACTCATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 156
04SS7 57 AATATTCACTCATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 156
05SS7 57 AATATTCACTCATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 156
06SS2 57 AATATTCACTCATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 156
08SS7 53 AATATTCACTYATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 152
12SS7 52 AATATTCACTCATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 151
13SS7 50 AATATTCACTCATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 149
14SS7 51 AATATTCACTYATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 150
19SS7 54 AATATTCACTTATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 153
22SS7 54 AATATTCACTTATTATCTGTTTCCTAAAATTGTCCTTAACATCCTTCCTCTTACTCCTTTATTACCTGGTCGGGCTTCCCCTCTTCAGGCGAAATCTGTC 153
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01SS7 162 AGTCTATCTGCATTGCCTTTTGATCTCTACTTCAGTTACTACMACTTCAAAGACACCATTGTCCTCCCCAAGGTGAGGSCCATGTAGAGAAAGGATCACT 261
02SS7 154 AGTCTATCTGCATTGCCTTTTGATCTCTACTTCAGTTACTACAACTTCAAAGACACCATTGTCCTCCCCAAGGTGAGGCCCATGTAGAGAAAGGATCACT 253
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04SS7 157 AGTCTATCTGCATTGCCTTTTGATCTCTACTTCAGTTACTACAACTTCAAAGACACCATTGTCCTCCCCAAGGTGAGGCCCATGTAGAGAAAGGATCACT 256
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13SS7 150 AGTCTATCTGCATTGCCTTTTGATCTCTACTTCAGTTACTACAACTTCAAAGACACCATTGTCCTCCCCAAGGTGAGGCCCATGTAGAGAAAGGATCACT 249
14SS7 151 AGTCTATCTGCATTGCCTTTTGATCTCTACTTCAGTTACTACAACTTCAAAGACACCATTGTCCTCCCCAAGGTGAGGCCCATGTAGAGAAAGGATCACT 250
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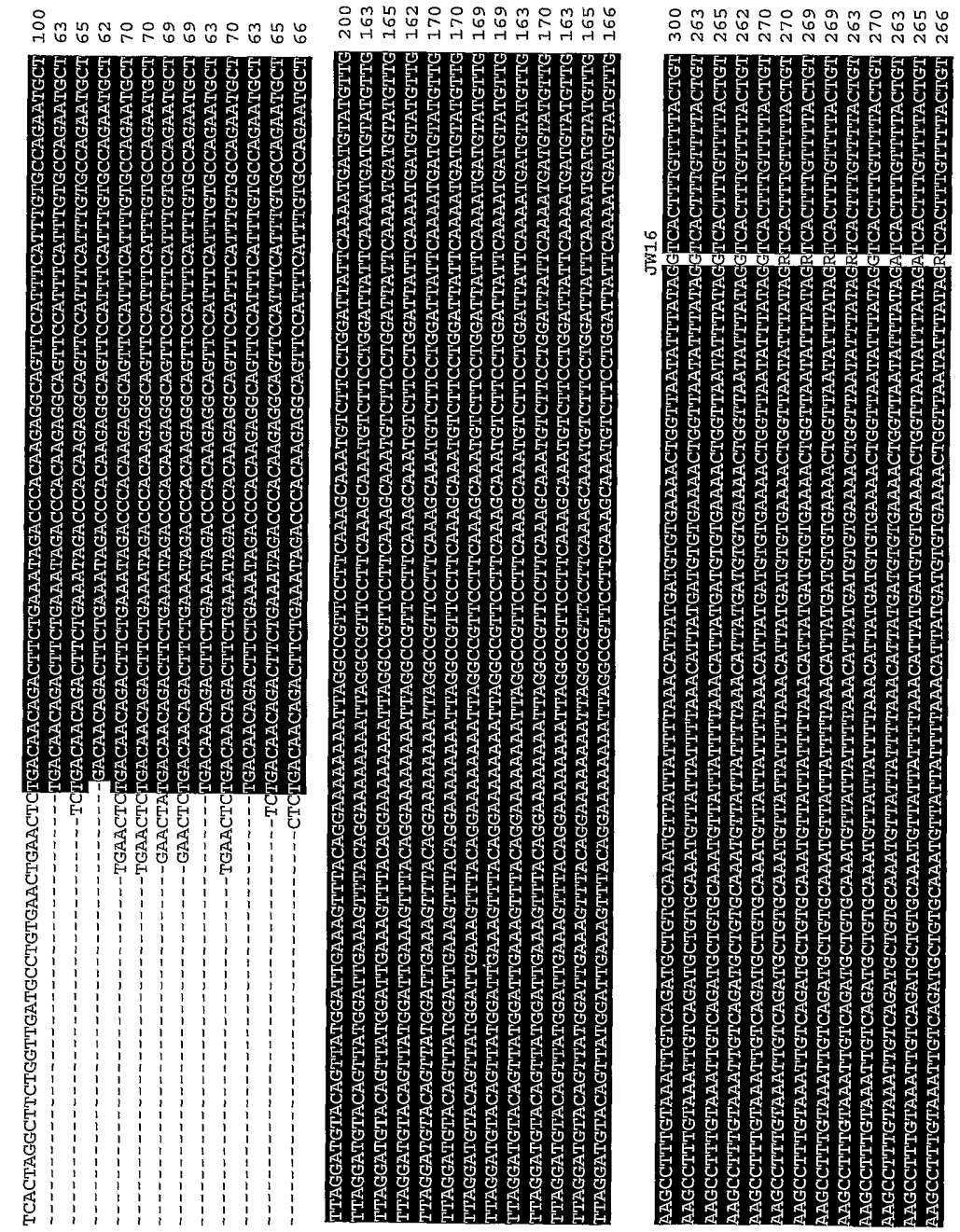
22SS7 154 AGTCTATCTGCATTGCCTTTTGATCTCTACTTCAGTTACTACAACTTCAAAGACACCATTGTCCTCCCCAAGGTGAGGCCCATGTAGAGAAAGGATCACT 253

FIGURE 10

FIGURE 10 (continued)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JW16

FIGURE 11A

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04SS6  271 CTTAAGTTTATACTCTTATAGACAACATGGCCGTGAACTTTATGCTGTAAATAATCAGAGGGCAATAAACTGTTGAGTCAAAACAGCCATCTTCCTTGTG 370
05SS2  271 CTTAAGTTTATACTCTTATAGACAACATGGCCGTGAACTTTATGCTGTAAATAATCAGAGGGCAATAAACTGTTGAGTCAAAACAGCCATCTTCCTTGTG 370
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14SS6  264 CTTAAGTTTATACTCTTATAGACAACATGGCCGTGAACTTTATGCTGTAAATAATCAGAGGGCAATAAACTGTTGAGTCAAAACAGCCATCTTCCTTGTG 363
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22SS6  267 CTTAAGTTTATACTCTTATAGACAACATGGCCGTGAACTTTATGCTGTAAATAATCAGAGGGCAATAAACTGTTGAGTCAAAACAGCCATCTTCCTTGTG 366

00STD  401 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 497
01SS6  364 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 460
02SS6  366 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 462
03SS6  363 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 459
04SS6  371 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 467
05SS2  371 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 467
06SS6  370 ACCAAACATTTAAAAATATTCTGGCTGGGCACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 466
08SS6  370 ACCAAACATTTAAAAATATTCTGGCTGGGCACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 466
12SS6  364 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 460
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14SS6  364 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 460
19SS6  366 ACCAAACATTTAAAAATATTCTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTTGGG 462
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FIGURE 11A (continued)

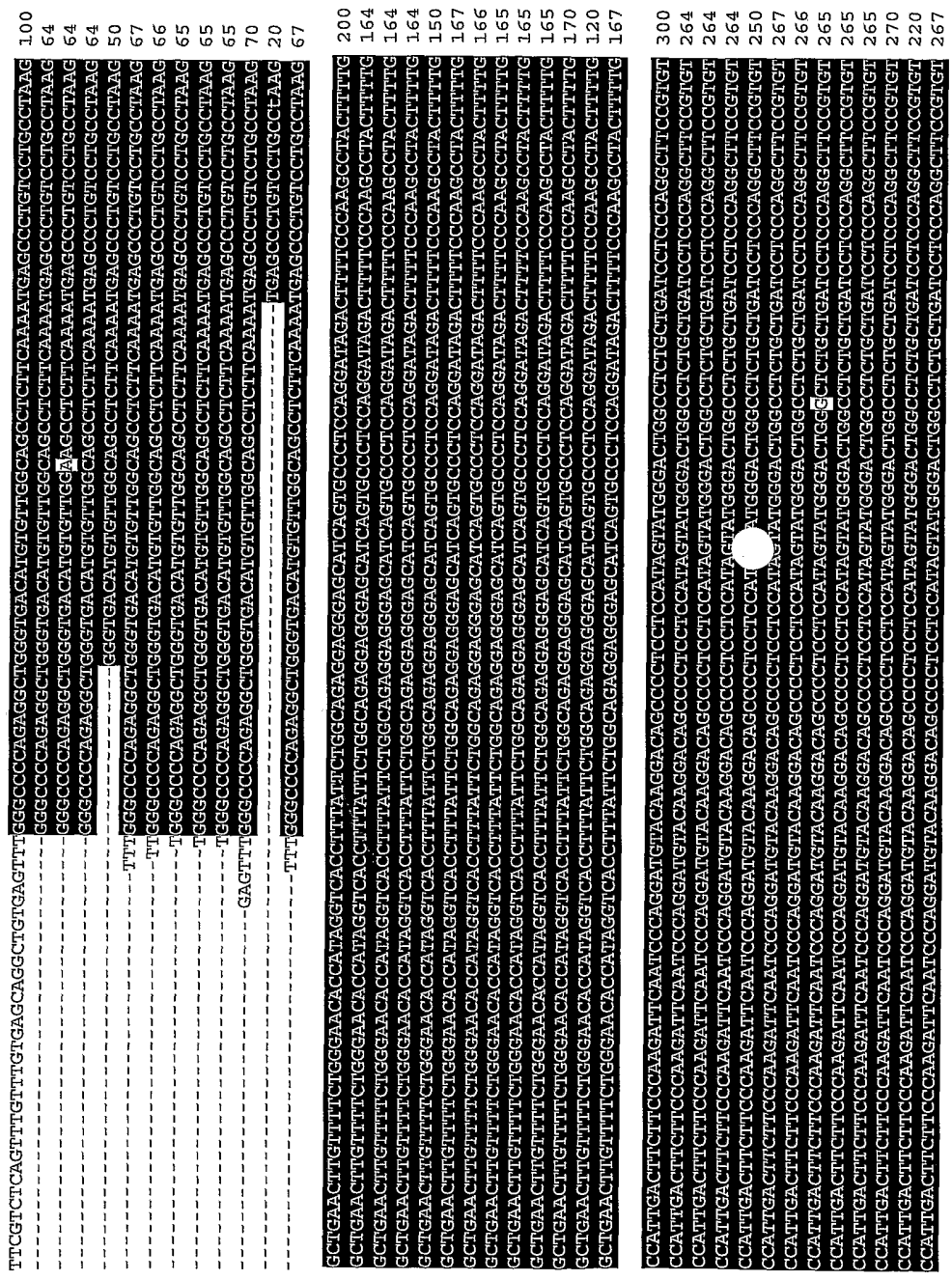
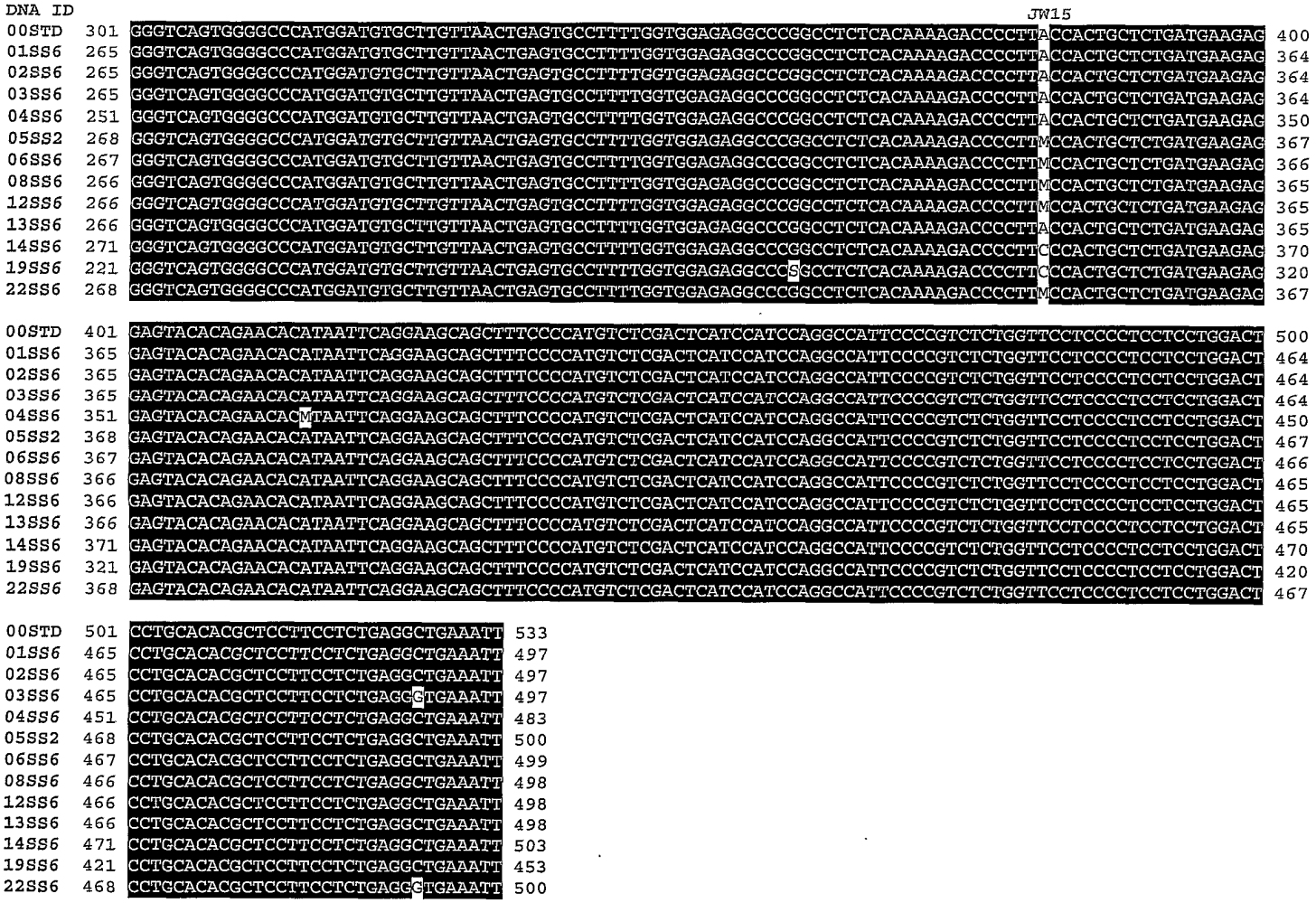


FIGURE 11B



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Abreu, Maria T.
Taylor, Kent D.
Rotter, Jerome I.
Yang, Huiying
Sugimura, Kazuhito
Targan, Stephan R.

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Fibrostenosing Disease in Patients with Crohn's Disease

<130> 66783-138

<150> US 60/407,391
<151> 2002-08-30

<150> US 10/356,736
<151> 2003-01-30

<160> 67

<170> FastSEQ for Windows Version 4.0

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tgtgatctga aggt 494

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<212> DNA
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<210> 7
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<212> DNA
<213> Homo sapiens

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<210> 8
<211> 540
<212> DNA
<213> Homo sapiens

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<210> 9
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<212> DNA

<213> Homo sapeins

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gagtacctga tatgtgttct agacatgaac taacagtcct cctccctctg cagtcccagc 480
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<210> 10
<211> 520
<212> DNA
<213> Homo sapiens

<400> 10
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cttttggcct tttcagattc tggggcaaca gagtgggtga cgagggggcc caggccctgg 180
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<211> 535
<212> DNA
<213> Homo sapiens

<400> 11
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<210> 12
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<212> DNA
<213> Homo sapiens

<400> 12
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tattacctgg tcgggcttcc cctcttcagg cgaaatctgt cagtctatct gcattgcctt 180
ttgatctcta cttcagttac tacmacttca aagacaccat tgtcctcccc aaggtgaggs 240

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gccctccctg aaacccaggc ccaggcctga gcctggacac ctccttcctt cctgagacca 360
cagccagccc ggtttctctg gggccaagag caaatgcttt gcttaagtgc tgaaatctca 420
gcccactgac cccttgcmga caggagagga ggggaagccc agggaagctc aacttcccaa 480
gtgtcctgag tctctg 496

<210> 13
<211> 488
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 434
<223> n = A,T,C or G

<400> 13
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amccccttgca gacnggagag gaggggaagc ccagggaagc tcaacttccc aagtgtcctg 480
agtctctg 488

<210> 14
<211> 491
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 437
<223> n = A,T,C or G

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<210> 15
<211> 491
<212> DNA
<213> Homo sapiens

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ctgagtctct g 491

<210> 16
<211> 491
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 437
<223> n = A,T,C or G

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<210> 17
<211> 491
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 159
<223> n = A,T,C or G

<400> 17
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ctgacccctt gcagacagga gaggagggga agcccaggga agctcaactt cccaagtgtc 480
ctgagtctct g 491

<210> 18
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 433
<223> n = A,T,C or G

<400> 18
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cggtttctct ggggccaaga gcaaatgctt tgcttaagtg ctgaaatctc agcccactga 420
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gtctctg 487

<210> 19
<211> 486
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 432
<223> n = A,T,C or G

<400> 19
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tctctg 486

<210> 20
<211> 484
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 430
<223> n = A,T,C or G

<400> 20
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tttctctggg gccaagagca aatgctttgc ttaagtgctg aaatctcagc ccactgaccc 420
cttgcagacn ggagaggagg ggaagcccag ggaagctcaa cttcccaagt gtcctgagtc 480
tctg 484

<210> 21
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 431
<223> n = A,T,C or G

<400> 21
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cgggcttccc ctcttcaggc gaaatctgtc agtctatctg cattgccttt tgatctctac 180
ttcagttact acaacttcaa agacaccatt gtcctcccca aggtgaggcc catgtagaga 240
aaggatcact tccttgctga aagagagggt caaggggcga cccacgtggg ccctccctga 300
aacccaggcc caggcctgag cctggacacc tccttccttc ctgagaccac agccagcccg 360
gtttctctgg ggccaagagc aaatgctttg cttaagtgct gaaatctcag cccactgacc 420
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ctctg 485

<210> 22
<211> 488
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 434
<223> n = A,T,C or G

<400> 22
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ggtcgggctt cccctcttca ggcgaaatct gtcagtctat ctgcattgcc ttttgatctc 180
tacttcagtt actacaactt caaagacacc attgtcctcc ccaaggtgag gcccatgtag 240
agaaaggatc acttccttgc tgaaagagag ggtcaagggg cgacccacgt gggccctccc 300
tgaaacccag gcccaggcct gagcctggac acctccttcc ttcctgagac cacagccagc 360
ccggtttctc tggggccaag agcaaatgct ttgcttaagt gctgaaatct cagcccactg 420
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<210> 23
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<212> DNA
<213> Homo sapiens

<220>
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<223> n = A,T,C or G

<400> 23
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ggtcgggctt cccctcttca ggcgaaatct gtcagtctat ctgcattgcc ttttgatctc 180
tacttcagtt actacaactt caaagacacc attgtcctcc ccaaggtgag gcccatgtag 240
agaaaggatc acttccttgc tgaaagagag ggtcaagggg cgacccacgt gggccctccc 300
tgaaacccag gcccaggcct gagcctggac acctccttcc ttcctgagac cacagccagc 360
ccggtttctc tggggccaag agcaaatgct ttgcttaagt gctgaaatct cagcccactg 420
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agtctctg 488

<210> 24
<211> 497
<212> DNA
<213> Homo sapiens

<400> 24
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<210> 25
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<212> DNA
<213> Homo sapiens

<400> 25
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<210> 26
<211> 462
<212> DNA
<213> Homo sapiens

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<210> 27
<211> 459
<212> DNA
<213> Homo sapiens

<400> 27
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<210> 28
<211> 467
<212> DNA
<213> Homo sapiens

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cttccttgtg accaaacatt taaaaatatt ctggctgggc acagtggctc acgcctgtaa 420
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<210> 29
<211> 467
<212> DNA
<213> Homo sapiens

<400> 29
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<210> 30
<211> 466
<212> DNA
<213> Homo sapiens

<400> 30
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<210> 31
<211> 466
<212> DNA
<213> Homo sapiens

<400> 31
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<210> 32
<211> 460
<212> DNA
<213> Homo sapiens

<400> 32
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<210> 33
<211> 467
<212> DNA
<213> Homo sapiens

<400> 33
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<210> 34
<211> 460

<212> DNA
<213> Homo sapiens

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<210> 35
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<212> DNA
<213> Homo sapiens

<400> 35
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<210> 36
<211> 463
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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<400> 37
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<210> 38
<211> 24
<212> DNA
<213> Homo sapiens

<400> 38
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<210> 39
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<212> DNA
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<400> 39
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<210> 40
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<400> 40
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<210> 41
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<210> 43
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<210> 44
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<400> 44
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<210> 45
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<213> Homo sapiens

<400> 45
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<210> 46
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<210> 55
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<213> Homo sapiens

<400> 56
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<210> 57

<211> 497
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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 59
<211> 483
<212> DNA
<213> Homo sapiens

<400> 59
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<211> 500
<212> DNA
<213> Homo sapiens

<400> 60
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<210> 61
<211> 499
<212> DNA
<213> Homo sapiens

<400> 61
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<211> 498
<212> DNA
<213> Homo sapiens

<400> 62
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<210> 63
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<212> DNA
<213> Homo sapiens

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<210> 64
<211> 498
<212> DNA
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<400> 64
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<210> 65
<211> 503
<212> DNA
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