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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
17 September 2009 (17.09.2009)

PCT

(10) International Publication Number
WO 2009/114756 A2

(51) International Patent Classification:
C12Q 1/68 (2006.01)

(21) International Application Number:
PCT/US2009/037065

(22) International Filing Date:
13 March 2009 (13.03.2009)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/036,632 14 March 2008 (14.03.2008) US
61/097,109 15 September 2008 (15.09.2008) US

(71) Applicant *(for all designated States except US)*: **EXAGEN DIAGNOSTICS, INC.** [US/US]; 801 University Boulevard S.E., Suite 209, Albuquerque, NM 87106 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **HARRIS, Cole** [US/US]; 16375 Havenpark Drive, Houston, TX 77059 (US). **ALSOBROOK, John** [US/US]; 643 Coronado Road, Corrales, NM 87048 (US).

(74) Agent: **HARPER, David, S.**; McDonnell Boehnen Hulbert & Berghoff LLP, 300 S. Wacker Drive, Suite 3100, Chicago, IL 60606 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR), OAPI (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 (Rule 48.2(g))*

— *with sequence listing part of description (Rule 5.2(a))*

WO 2009/114756 A2

(54) Title: BIOMARKERS FOR INFLAMMATORY BOWEL DISEASE AND IRRITABLE BOWEL SYNDROME

(57) Abstract: The present invention provides compositions and their use in diagnosing and/or distinguishing inflammatory bowel disease and irritable bowel syndrome.

Biomarkers for Inflammatory Bowel Disease and Irritable Bowel Syndrome

Cross Reference

This application claims priority to U.S. Provisional Patent Application Serial Nos. 61/036,632 filed March 14, 2008 and 61/097,109 filed September 15, 2008, both references incorporated by reference herein in their entirety.

Field of the Invention

The invention relates generally to the fields of nucleic acids, nucleic acid detection, and intestinal disorders

Background

Irritable Bowel Syndrome (IBS) is a chronic condition characterized by abdominal pain, constipation and/or diarrhea. It is fairly common and responsible for 20–50% of visits to gastroenterologists. IBS does not result in damage to the gastrointestinal tract and is not associated with nor develops into more serious gastrointestinal conditions such as colon cancer or colitis, and it can often be controlled with drugs aimed at symptom relief, diet changes, and stress management techniques. However, more serious conditions must be ruled out before making a definitive diagnosis of IBS, and thus setting an appropriate course of treatment.

Inflammatory Bowel Disease (IBD) refers to at least two distinct diseases that cause inflammation of the intestinal tract: Ulcerative Colitis affects the colon, while Crohn's Disease most often affects the last part of the small intestine, but can attack any part of the digestive tract. IBD is rare by comparison to IBS, and IBD patients may experience many of the same symptoms as IBS patients, complicating the diagnosis of IBD. Furthermore, patients with IBD are at greater risk of developing colon cancer. Currently, IBD can only be definitively diagnosed by colonoscopy, a rather invasive procedure; even this invasive procedure is incapable of diagnosing approximately 10% of patients undergoing colonoscopy (Burczynski, J. Mol. Diag. 8(1): 51 (2006)). IBD may be treated with anti-inflammatory drugs, immunosuppressive agents, and/or surgery to remove damaged tissues.

Thus, there is a need in the art for better and more specific diagnostic tests capable of distinguishing between IBD and IBS.

Summary of the Invention

In a first aspect, the present invention provides biomarkers consisting of between 2 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3); and

(b) a second probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3),

wherein the first probe set and the second probe set do not selectively hybridize to the same nucleic acid.

In a second aspect, the present invention provides biomarker, comprising:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3); and

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID

NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3),

wherein the first primer pair and the second primer pair do not selectively amplify the same nucleic acid.

In a third aspect, the present invention provides methods for diagnosing IBD and/or IBS comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD or IBS under hybridizing conditions with 2 or more probes sets, wherein at least a first probe set and a second probe set selectively hybridize under high stringency conditions to a nucleic acid target selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3); wherein the first probe set and the second probe set do not selectively hybridize to the same nucleic acid;

(b) detecting formation of hybridization complexes between the 2 or more probe sets and nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD, IBS, or neither based on the gene expression of the nucleic acid targets.

In one embodiment of the third aspect of the invention, diagnosing whether the subject is likely to have IBD, IBS, or neither comprises analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

In a fourth aspect, the present invention provides methods for diagnosing IBD and/or IBS comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD or IBS under amplifying conditions with 2 or more primer pairs, wherein at least a first primer pair and a second primer pair are capable of selectively

amplifying a detectable portion of a nucleic acid target selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3); wherein the first primer pair and the second primer pair do not selectively amplify the same nucleic acid;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the two or more primer pairs, wherein the amplification products provide a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD, IBS, or neither based on the amplification of the nucleic acid targets.

In one embodiment of the fourth aspect of the invention, diagnosing whether the subject is likely to have IBD, IBS, or neither based on the amplification of the nucleic acid targets comprises analyzing the amplification products by applying a weight to the number of amplification products formed for each nucleic acid target.

Brief Description of the Figures

Figure 1 is a graph of the weighted-sum regression score for each training set patient in an IBD vs. Normal analysis.

Figure 2 shows the boxplots of the logistic regression scores based on expression levels of 5 of the 8 genes for the five patient cohorts. Note the separation of the normal and IBD patients (UC and Crohn's).

Figure 3 shows the boxplots of the logistic regression scores based on expression levels of 7 of the 8 genes for the five patient cohorts. Note the separation of the normal and IBS from the IBD patients (UC and Crohn's).

Figure 4 shows the boxplots of the logistic regression scores based on expression levels of 4 of the 8 genes for the five patient cohorts. Note the separation of the Normal and IBS patients.

Figure 5 is a boxplot of the logistic regression scores based on expression levels of 5 genes whose combination differentiates IBD vs. Normal.

Detailed Description of the Invention

All references cited are herein incorporated by reference in their entirety.

Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in *Methods in Enzymology* (M.P. Deutshcer, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA), *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R.I. Freshney. 1987. Liss, Inc. New York, NY), *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, TX).

In a first aspect, the invention provides biomarkers consisting of between 2 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3); and

(b) a second probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3), wherein the first probe set and the second probe set do not selectively hybridize to the same nucleic acid.

The recited nucleic acids are human nucleic acids recited by SEQ ID NO and gene name; as will be understood by those of skill in the art, such human nucleic acid sequences also include the mRNA counterpart to the sequences disclosed herein. For ease

of reference, the nucleic acids will be referred to by gene name throughout the rest of the specification; it will be understood that as used herein the gene name means the recited SEQ. ID. NO(S). for each gene listed in Table 1, complements thereof, and RNA counterparts thereof.

In one non-limiting example, the first probe set selectively hybridizes under high stringency conditions to TH1L, and thus selectively hybridizes under high stringency conditions to the nucleic acid of SEQ ID NO:4 (NM_198978) a mRNA version thereof, or complements thereof, and the second probe set selectively hybridizes under high stringency conditions to RAP1A, thus selectively hybridizing under high stringency conditions to one or both of the nucleic acid of SEQ ID NOS: 1-2, a mRNA version thereof, or complements thereof. Further embodiments will be readily apparent to those of skill in the art based on the teachings herein and Table 1 below.

Table 1. Nucleic acid sequences

Gene name	NCBI accession #	SEQ ID #	Hs.ID	gene description
TH1L	NM_198976	4	Hs.517148	TH1-like (Drosophila)
HIST1H2AC	NM_003512	11	Hs.484950	histone 1, H2ac
TFE3	NM_006521	12	Hs.274184	Transcription factor binding to IGHM enhancer 3
HIST1H2BK	NM_080593	9	Hs.437275	Histone 1, H2bk
UBE2G1	NM_003342.4	5	Hs.462035	Ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)
NONO	NM_007363	13	Hs.533282	Non-POU domain containing, octamer-binding
PCBP1	NM_006196	14	Hs.2853	Poly(rC) binding protein 1
RAP1A (1) RAP1A (2)	NM_001010935.1 NM_002884.2	1 2	Hs.190334	RAP1A, member of RAS oncogene family
PPP2R5A	NM_006243	10	Hs.497684	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform
PGRMC1	NM_006667	15	Hs.90061	Progesterone receptor membrane component 1
BLCAP	NM_006698	3	Hs.472651	Bladder cancer associated protein
GPX1 (1) GPX1 (2)	NM_000581.2 NM_201397.1	7 8	Hs.76686	Glutathione peroxidase 1
HMGB1	NM_002128	16	Hs.434102	High-mobility group box 1
CALM3	NM_005184	6	Hs.515487	Calmodulin 3 (phosphorylase kinase, delta)

As is described in more detail below, the inventors have discovered that the biomarkers of the invention can be used, for example, as probes for diagnosing IBD and IBS. The biomarkers can be used, for example, to determine the expression levels in

tissue mRNA for the recited genes. The biomarkers of this first aspect of the invention are especially preferred for use in RNA expression analysis from the genes in a tissue of interest, such as blood samples (for example, peripheral blood mononuclear cells (PBMCs) or RBC-depleted whole blood).

As used herein with respect to all aspects and embodiments of the invention, a "probe set" is one or more isolated polynucleotides that each selectively hybridize under high stringency conditions to the same target nucleic acid (for example, a single specific mRNA). Thus, a single "probe set" may comprise any number of different isolated polynucleotides that selectively hybridize under high stringency conditions to the same target nucleic acid, such as a mRNA expression product. For example, a probe set that selectively hybridizes to a BLCAP mRNA may consist of a single polynucleotide of 100 nucleotides that selectively hybridizes under high stringency conditions to BLCAP mRNA, may consist of two separate polynucleotides 100 nucleotides in length that each selectively hybridize under high stringency conditions to BLCAP mRNA, or may consist of twenty separate polynucleotides 25 nucleotides in length that each selectively hybridize under high stringency conditions to BLCAP mRNA (such as, for example, fragmenting a larger probe into many individual shorter polynucleotides). Those of skill in the art will understand that many such permutations are possible.

The biomarkers of the invention consist of between 2 and 35 probe sets. In various embodiments, the biomarker can include 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 probe sets that selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3, wherein each of the 3-14 different probe sets selectively hybridize under high stringency conditions to a different nucleic acid target. Thus, as will be clear to those of skill in the art, the biomarkers may include further probe sets that, for example, (a) are additional probe sets that also selectively hybridize under high stringency conditions to the recited human nucleic acid (e.g.RAP1A expresses alternative products that share much overlap; thus, one probe set could selectively hybridize to one transcript (or a cDNA derived therefrom) and another probe set could selectively hybridize to the other alternative transcript (or a cDNA derived therefrom; GPX is a similar example with alternative transcripts); or (b) do not selectively hybridize under high stringency conditions to any of the recited human nucleic acids. Such further probe sets of type (b)

may include those consisting of polynucleotides that selectively hybridize to other nucleic acids of interest, and may further include, for example, probe sets consisting of control sequences, such as competitor nucleic acids, sequences to provide a standard of hybridization for comparison, etc.

In various embodiments of this first aspect, the biomarker consists of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 probe sets. In various further embodiments, at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more of the different probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3. As will be apparent to those of skill in the art, as the percentage of probe sets that selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3 increases, the maximum number of probe sets in the biomarker will decrease accordingly. Thus, for example, where at least 50% of the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3, or their complements, the biomarker will consist of between 2 and 28 probe sets. Those of skill in the art will recognize the various other permutations encompassed by the compositions according to the various embodiments of this aspect of the invention.

As used herein with respect to each aspect and embodiment of the invention, the term "selectively hybridizes" means that the isolated polynucleotides are fully complementary to at least a portion of their nucleic acid target so as to form a detectable hybridization complex under the recited hybridization conditions, where the resulting hybridization complex is distinguishable from any hybridization that might occur with other nucleic acids. The specific hybridization conditions used will depend on the length of the polynucleotide probes employed, their GC content, as well as various other factors as is well known to those of skill in the art. (See, for example, Tijssen (1993) Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes part I, chapter 2, "Overview of principles of hybridization and the strategy of

nucleic acid probe assays," Elsevier, N.Y. ("Tijssen")). As used herein, "stringent hybridization conditions" are selected to be nor more than 5°C lower than the thermal melting point (Tm) for the specific polynucleotide at a defined ionic strength and pH. The Tm is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. High stringency conditions are selected to be equal to the Tm for a particular polynucleotide probe. An example of stringent conditions are those that permit selective hybridization of the isolated polynucleotides to the genomic or other target nucleic acid to form hybridization complexes in 0.2X SSC at 65°C for a desired period of time, and wash conditions of 0.2X SSC at 65°C for 15 minutes. It is understood that these conditions may be duplicated using a variety of buffers and temperatures. SSC (see, e.g., Sambrook, Fritsch, and Maniatis, in: Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1989) is well known to those of skill in the art, as are other suitable hybridization buffers. .

The polynucleotides in the probe sets can be of any length that permits selective hybridization under high stringency conditions to the nucleic acid of interest. In various preferred embodiments of this aspect of the invention and related aspects and embodiments disclosed below, the isolated polynucleotides are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, or more contiguous nucleotides in length of one of the recited SEQ ID NOS., full complements thereof, or corresponding RNA sequences.

The term "polynucleotide" as used herein refers to DNA or RNA, preferably DNA, in either single- or double-stranded form. In a preferred embodiment, the polynucleotides are single stranded nucleic acids that are "anti-sense" to the recited nucleic acid (or its corresponding RNA sequence). The term "polynucleotide" encompasses nucleic-acid-like structures with synthetic backbones. DNA backbone analogues provided by the invention include phosphodiester, phosphorothioate, phosphorodithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-carbamate, morpholino carbamate, and peptide nucleic acids (PNAs), methylphosphonate linkages or alternating methylphosphonate and phosphodiester linkages (Strauss-Soukup (1997) Biochemistry 36:8692-8698), and benzylphosphonate linkages, as discussed in US 6,664,057; see also Oligonucleotides and Analogues, a Practical Approach, edited by F. Eckstein, IRL Press

at Oxford University Press (1991); Antisense Strategies, Annals of the New York Academy of Sciences, Volume 600, Eds. Baserga and Denhardt (NYAS 1992); Milligan (1993) J. Med. Chem. 36:1923-1937; Antisense Research and Applications (1993, CRC Press).

An "isolated" polynucleotide as used herein for all of the aspects and embodiments of the invention is one which is free of sequences which naturally flank the polynucleotide in the genomic DNA of the organism from which the nucleic acid is derived, and preferably free from linker sequences found in nucleic acid libraries, such as cDNA libraries. Moreover, an "isolated" polynucleotide is substantially free of other cellular material, gel materials, and culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. The polynucleotides of the invention may be isolated from a variety of sources, such as by PCR amplification from genomic DNA, mRNA, or cDNA libraries derived from mRNA, using standard techniques; or they may be synthesized in vitro, by methods well known to those of skill in the art, as discussed in US 6,664,057 and references disclosed therein. Synthetic polynucleotides can be prepared by a variety of solution or solid phase methods. Detailed descriptions of the procedures for solid phase synthesis of polynucleotide by phosphite-triester, phosphotriester, and H-phosphonate chemistries are widely available. (See, for example, US 6,664,057 and references disclosed therein). Methods to purify polynucleotides include native acrylamide gel electrophoresis, and anion-exchange HPLC, as described in Pearson (1983) J. Chrom. 255:137-149. The sequence of the synthetic polynucleotides can be verified using standard methods.

In one embodiment, the polynucleotides are double or single stranded nucleic acids that include a strand that is “anti-sense” to all or a portion of the SEQ ID NOS shown above for each gene of interest or its corresponding RNA sequence (ie: it is fully complementary to the recited SEQ ID NOs). In one non-limiting example, the first probe set selectively hybridizes under high stringency conditions to TH1L, and is fully complementary to all or a portion of the nucleic acid of SEQ ID NO:4 (NM_198978) or a mRNA version thereof, and the second probe set selectively hybridizes under high stringency conditions to RAP1A and is fully complementary to one or both of the nucleic acid of SEQ ID NOS: 1-2 or a mRNA version thereof.

In one preferred embodiment of the first aspect of the invention, the biomarker comprises or consists of at least 3, 4, or 5 probe sets that selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3. As disclosed in more detail below, such probe sets can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from those subjects suffering from IBS. Examples of such preferred probe sets are provided in **Table 17.** Thus, in a preferred embodiment, the invention provides a biomarker consisting of between 3 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

(b) a second probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof; and

(c) a third probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

wherein each of the between 3 and 35 different probe sets consists of one or more probes of 15 or more contiguous nucleotides, or full complements thereof, of a single mRNA different from that of the other probe sets, and wherein each of the different probe sets is optionally detectably labeled. In a further preferred version of this embodiment, the first probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; the second probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of TH1L, or a full complement thereof; the third probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; and a fourth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof.

In another preferred embodiment of the first aspect of the invention, the biomarker comprises or consists of at least 5 or 6 probe sets that probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO. As disclosed in more detail below, such probe sets can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from those subjects suffering from IBD. Examples of such preferred probe sets are provided in **Table 18.** In one preferred version of this embodiment, the biomarker consists of between 5 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(b) a second probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(c) a third probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(d) a fourth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof; and

(e) a fifth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1),

SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

wherein each of the between 5 and 35 different probe sets consists of one or more probes of 15 or more contiguous nucleotides, or full complements thereof, of a single mRNA different from that of the other probe sets, and wherein each of the different probe sets is optionally detectably labeled. In another version, the first probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; the second probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; the third probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; the fourth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; the fifth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of GPX1, or a full complement thereof; and a sixth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of NONO or a full complement thereof.

In a further preferred embodiment of the first aspect of the invention, the biomarker comprises or consists of at least 6 or 7 probe sets that selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A. As disclosed in more detail below, such probe sets can be used in preferred embodiments of the methods of the invention for distinguishing those subjects suffering from IBS from those subjects suffering from IBD. Examples of such preferred probe sets are provided in **Table 19.** In one preferred embodiment, the biomarker consists of

(a) a first probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(b) a second probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3),

SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(c) a third probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(d) a fourth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(e) a fifth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof; and

(f) a sixth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

wherein each of the between 6 and 35 different probe sets consists of one or more probes of 15 or more contiguous nucleotides, or full complements thereof, of a single mRNA different from that of the other probe sets, and wherein each of the different probe sets is optionally detectably labeled. In a further preferred embodiment, the first probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; the second probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; the third probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; the fourth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of GPX1, or a full complement thereof; the fifth probe set consists of one or more

nucleotide probes of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof; the sixth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of PPP2R5A, or a full complement thereof; and a seventh probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof.

In one specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to BLCAP, a second probe set that selectively hybridizes under high stringency conditions to TH1L, a third probe set that selectively hybridizes under high stringency conditions to CALM3, and a fourth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBS patients.

In a second specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to BLCAP, a second probe set that selectively hybridizes under high stringency conditions to TH1L, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, and a fourth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBS patients.

In a third specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to GPX1. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBD patients.

In a fourth specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions

to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to CALM3, and a fifth probe set that selectively hybridizes under high stringency conditions to GPX1. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBD patients.

In a fifth specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to CALM3, a fifth probe set that selectively hybridizes under high stringency conditions to GPX1, and a sixth probe set that selectively hybridizes under high stringency conditions to NONO. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBD patients.

In a sixth specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to CALM3, a fifth probe set that selectively hybridizes under high stringency conditions to GPX1, a sixth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK, and a seventh probe set that selectively hybridizes under high stringency conditions to PPP2RR5A. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish normal and IBS patients from IBD patients.

In a seventh specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to UBE2G1, a third probe set that selectively hybridizes under high stringency conditions to CALM3, a fourth probe set that selectively hybridizes under high stringency conditions to GPX1, a fifth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK1, and a sixth probe set that selectively hybridizes

under high stringency conditions to PPP2R5A. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish IBS patients from IBD patients.

In an eighth specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to UBE2G1, a third probe set that selectively hybridizes under high stringency conditions to CALM3, a fourth probe set that selectively hybridizes under high stringency conditions to GPX1, a fifth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK, a sixth probe set that selectively hybridizes under high stringency conditions to PPP2R5A, and a seventh probe set that selectively hybridizes under high stringency conditions to BLCAP. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish IBS patients from IBD patients.

In a ninth specific embodiment of this first aspect of the invention, the biomarker includes a first probe set that selectively hybridizes under high stringency conditions to BLCAP, a second probe set that selectively hybridizes under high stringency conditions to CALM3, a third probe set that selectively hybridizes under high stringency conditions to GPX1, a fourth probe set that selectively hybridizes under high stringency conditions to TH1L, a fifth probe set that selectively hybridizes under high stringency conditions to RAP1A, and a sixth probe set that selectively hybridizes under high stringency conditions to NONO. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish IBS and IBD patients from normal patients.

Thus, in various other embodiments of this first aspect of the invention, the biomarker comprises or consists of one or more of:

(a) a first probe set that selectively hybridizes under high stringency conditions to RAP1A and a second probe set that selectively hybridizes under high stringency conditions to GPX1 (used as a probe set pair common to biomarkers for diagnosing IBD from normal patients; IBD from normal and IBS patients; IBD from IBS patients; and IBD and IBS patients from normal patients);

(b) a first probe set that selectively hybridizes under high stringency conditions to UBE2G1 and a second probe set that selectively hybridizes under high

stringency conditions to BLCAP (used as a probe set pair that can be added to probe set pair (a) to generate a 4-gene biomarker specific for diagnosing IBD from normal);

(c) a first probe set that selectively hybridizes under high stringency conditions to UBE2G1, a second probe set that selectively hybridizes under high stringency conditions to BLCAP and a third probe set that selectively hybridizes under high stringency conditions to CALM3 (used as a probe trio that can be added to probe set pair (a) to generate a 5-gene biomarker for diagnosing IBD from normal);

(d) a first probe set that selectively hybridizes under high stringency conditions to NONO and a second probe set that selectively hybridizes under high stringency conditions to CALM3 (used as a probe set pair that, can be added to probe sets (a) and (b) to generate a 6-gene biomarker for diagnosing IBD from normal);

(e) a first probe set that selectively hybridizes under high stringency conditions to PPP2R5A and a second probe set that selectively hybridizes under high stringency conditions to HIST1H2BK (used as a probe set pair common to biomarkers for diagnosing IBD from IBS patients). The probe set (e), when combined with probe sets (a), and (c) disclosed above for distinguishing IBD from normal, generates a biomarker for diagnosing normal and IBS patients from IBD patients). The probe set combination of (e), (a), and (c) can also be used as a biomarker to distinguish between IBS and IBD patients when the expression values of the individual genes are given different weights as discussed herein;

(f) a first probe set that selectively hybridizes under high stringency conditions to UBE2G1 and a second probe set that selectively hybridizes under high stringency conditions to CALM3 (used as a probe set pair that can be added to probe sets (a), and (e) described above, to generate a 6-gene biomarker that can be used to distinguish IBD from IBS patients);

(g) a first probe set that selectively hybridizes under high stringency conditions to BLCAP and a second probe set that selectively hybridizes under high stringency conditions to TH1L (used as probe set pair that when added to (a) and (d) above can be used to generate a 6-gene biomarker that can distinguish patients with IBS or IBD from normal patients);

h) a first probe set that selectively hybridizes under high stringency conditions to HIST1H2KB and a second probe set that selectively hybridizes under high stringency conditions to CALM3; (used as probe set pair that when added to (g) above

can be used to generate a 4- gene biomarker that can distinguish patients with IBS from normal patients); and

i) a first probe set that selectively hybridizes under high stringency conditions to HIST1H2KB and a second probe set that selectively hybridizes under high stringency conditions to UBE2G1 (used as probe set pair that when added to (g) above can be used to generate a different 4-gene biomarker that can distinguish patients with IBS from normal patients).

In a second aspect, the present invention provides biomarkers, comprising or consisting of

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3; and

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3;

wherein the first primer pair and the second primer pair do not selectively amplify the same nucleic acid.

As is described in more detail below, the inventors have discovered that the biomarkers of the invention can be used, for example, as primers for amplification assays for diagnosing IBD and IBS. The biomarkers can be used, for example, to determine the expression levels in tissue mRNA for the recited genes. The biomarkers of this second aspect of the invention are especially preferred for use in RNA expression analysis from the genes in a tissue of interest, such as blood samples (PBMCs or RBC-depleted whole blood).

The nucleic acid targets have been described in detail above, as have polynucleotides in general. As used herein, "selectively amplifying" means that the primer pairs are complementary to their targets and can be used to amplify a detectable portion of the nucleic acid target that is distinguishable from amplification products due to non-specific amplification. In a preferred embodiment, the primers are fully complementary to their target.

As is well known in the art, polynucleotide primers can be used in various assays (PCR, RT-PCR, RTQ-PCR, spPCR, qPCR, and allele-specific PCR, etc.) to amplify portions of a target to which the primers are complementary. Thus, a primer pair would include both a "forward" and a "reverse" primer, one complementary to the sense strand (ie: the strand shown in the sequences provided herein) and one complementary to an "antisense" strand (ie: a strand complementary to the strand shown in the sequences provided herein), and designed to hybridize to the target so as to be capable of generating a detectable amplification product from the target of interest when subjected to amplification conditions. The sequences of each of the target nucleic acids are provided herein, and thus, based on the teachings of the present specification, those of skill in the art can design appropriate primer pairs complementary to the target of interest (or complements thereof). In various embodiments, each member of the primer pair is a single stranded DNA polynucleotide at least 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more nucleotides in length that are fully complementary to the nucleic acid target. In various further embodiments, the detectable portion of the target nucleic acid that is amplified is at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, or more nucleotides in length.

In various embodiments, the biomarker can comprise or consist of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 primer pairs that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3, wherein none of the 3-14 primer pairs selectively amplify the same nucleic acid. In a preferred embodiment, the primers are fully complementary to their target. Thus, as will be clear to those of skill in the art, the biomarkers may include further primer pairs that do not selectively amplify any of the recited human nucleic acids. Such further primer pairs may include those consisting of polynucleotides that selectively amplify other nucleic acids of interest, and may further include, for example, primer pairs to provide a standard of amplification for comparison, etc.

In various embodiments of this second aspect, the biomarker consists of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 primer pairs. In various further embodiments, at least 10%, 15%,

20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more of the different primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3.

In one preferred embodiment of the second aspect of the invention, the biomarker comprises or consists of at least 3, 4, or 5 primer pairs that selectively amplify a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3. As disclosed in more detail below, such primer pairs can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from those subjects suffering from IBS. Examples of such preferred primer pairs are those that amplify a detectable portion of the nucleic acids provided in **Table 17.** Thus, in one preferred version of this embodiment, the biomarker consists of between 3 and 35 different nucleic acid primer pairs, wherein:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), wherein each primer in the second primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof; and

(c) a third primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), wherein each primer in the third primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L),

SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

wherein each of the between 3 and 35 different primer pairs consists of one or more primer pairs of 15 or more contiguous nucleotides, or full complements thereof, for a single mRNA different from that of the other primer pairs, and wherein each of the different primer pairs is optionally detectably labeled. In a further preferred version of this embodiment, each primer in the first primer pair consists of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; each primer in the second primer pair consists of 15 or more contiguous nucleotides of TH1L, or a full complement thereof; each primer in the third primer pair consists of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; and each primer in a fourth primer pair consists of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof.

In another preferred embodiment of the second aspect of the invention, the biomarker comprises or consists of at least 5 or 6 primer pairs that selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO. As disclosed in more detail below, such primer pairs can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from those subjects suffering from IBD. Examples of such preferred primer pairs are those that amplify a detectable portion of the nucleic acids provided in **Table 18.** In one preferred version of this embodiment, the biomarker consists of between 5 and 35 different nucleic acid primer pairs, wherein:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A),

SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO)), wherein each primer in the second primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(c) a third primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the third primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(d) a fourth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof; and

(e) a fifth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the fifth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

wherein each of the between 5 and 35 different primer pairs consists of one or more primer pairs of 15 or more contiguous nucleotides, or full complements thereof, for a single mRNA different from that of the other primer pairs, and wherein each of the

different primer pairs is optionally detectably labeled. In a further embodiment, each primer in the first primer pair consists of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; each primer in the second primer pair consists of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; each primer in the third primer pair consists of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; each primer in the fifth primer pair consists of 15 or more contiguous nucleotides of GPX1, or a full complement thereof; and each primer in a sixth primer pair consists of 15 or more contiguous nucleotides of NONO, or a full complement thereof.

In a further preferred embodiment of the second aspect of the invention, the biomarker comprises or consists of at least 6 or 7 primer pairs that selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A. As disclosed in more detail below, such primer pairs can be used in preferred embodiments of the methods of the invention for distinguishing those subjects suffering from IBS from those subjects suffering from IBD. Examples of such preferred primer pairs are those that amplify a detectable portion of the nucleic acids provided in **Table 19.** In one preferred embodiment, the biomarker consists of between 6 and 35 different nucleic acid primer pairs, wherein:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1),

SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the second primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(c) a third primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the third primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(d) a fourth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(e) a fifth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the fifth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof; and

(f) a sixth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the sixth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

wherein each of the between 6 and 35 different primer pairs consists of one or more primer pairs of 15 or more contiguous nucleotides, or full complements thereof, for a single mRNA different from that of the other primer pairs, and wherein each of the different primer pairs is optionally detectably labeled. In another preferred embodiment, each primer in the first primer pair consists of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; each primer in the second primer pair consists of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; each primer in the third primer pair consists of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of GPX1, or a full complement thereof; each primer in the fifth primer pair consists of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof; each primer in the sixth primer pair consists of 15 or more contiguous nucleotides of PPP2R5A, or a full complement thereof; and wherein each primer in a seventh primer pair consists of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof.

In one specific embodiment, a biomarker according to this second aspect of the invention comprises or consists of a first primer pair that selectively amplifies a detectable portion of BLCAP a second primer pair that selectively amplifies a detectable portion of TH1L, a third primer pair that selectively amplifies a detectable portion of CALM3, and a fourth primer pair that selectively amplifies a detectable portion of HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBS patients.

In a second specific embodiment of this second aspect of the invention, a biomarker according to this second aspect of the invention comprises or consists of a first

primer pair that selectively amplifies a detectable portion of BLCAP, a second primer pair that selectively amplifies a detectable portion of TH1L, a third primer pair that selectively amplifies a detectable portion of UBE2G1, and a fourth primer pair that selectively amplifies a detectable portion of HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBS patients.

In a third specific embodiment of this second aspect of the invention, the biomarker includes a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of BLCAP, a third primer pair that selectively amplifies a detectable portion of UBE2G1, and a fourth primer pair that selectively amplifies a detectable portion of GPX1. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBD patients.

In a fourth specific embodiment of this second aspect of the invention, the biomarker of this second aspect comprises or consists of a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of BLCAP, a third primer pair that selectively amplifies a detectable portion of UBE2G1, a fourth primer pair that selectively amplifies a detectable portion of CALM3, and a fifth primer pair that selectively amplifies a detectable portion of GPX1. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBD patients

In a fifth specific embodiment of this second aspect of the invention, the biomarker of this second aspect comprises or consists of a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of BLCAP, a third primer pair that selectively amplifies a detectable portion of UBE2G1, a fourth primer pair that selectively amplifies a detectable portion of CALM3, a fifth primer pair that selectively amplifies a detectable portion of GPX1, and a sixth primer pair that selectively amplifies a detectable portion of NONO. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between normal and IBD patients.

In a sixth specific embodiment of this second aspect of the invention, the biomarker of this second aspect comprises or consists of a primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a

detectable portion of BLCAP, a third primer pair that selectively amplifies a detectable portion of UBE2G1, a fourth primer pair that selectively amplifies a detectable portion of CALM3, a fifth primer pair that selectively amplifies a detectable portion of GPX1, a sixth primer pair that selectively amplifies a detectable portion of HIST1H2BK, and a seventh primer pair that selectively amplifies a detectable portion of PPP2RR5A. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish normal and IBS patients from IBD patients.

In a seventh specific embodiment of this second aspect of the invention, the biomarker of this second aspect comprises or consists of a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of UBE2G1, a third primer pair that selectively amplifies a detectable portion of CALM3, a fourth primer pair that selectively amplifies a detectable portion of GPX1, a fifth primer pair that selectively amplifies a detectable portion of HIST1H2BK, and a sixth primer pair that selectively amplifies a detectable portion of PPP2R5A. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish between IBS patients and IBD patients.

In an eighth specific embodiment of this second aspect of the invention, the biomarker of this second aspect comprises or consists of a primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of UBE2G1, a third primer pair that selectively amplifies a detectable portion of CALM3, a fourth primer pair that selectively amplifies a detectable portion of GPX1, a fifth primer pair that selectively amplifies a detectable portion of HIST1H2BK, a sixth primer pair that selectively amplifies a detectable portion of PPP2R5A, and a seventh primer pair that selectively amplifies a detectable portion of BLCAP. As disclosed in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish IBS patients from IBD patients.

In a ninth specific embodiment of this second aspect of the invention, the biomarker of this second aspect comprises or consists of a first primer pair that selectively amplifies a detectable portion of BLCAP, a second primer pair that selectively amplifies a detectable portion of CALM3, a third primer pair that selectively amplifies a detectable portion of GPX1, a fourth primer pair that selectively amplifies a detectable portion of TH1L, a fifth primer pair that selectively amplifies a detectable portion of RAP1A, and a sixth primer pair that selectively amplifies a detectable portion of NONO. As disclosed

in more detail below, the inventors have discovered that such biomarkers can be used as probes to distinguish IBS and IBD patients from normal patients.

Thus, in various other embodiments of this second aspect of the invention, the biomarker comprises or consists of:

(a) a first primer pair that selectively amplifies a detectable portion of RAP1A and a second primer pair that selectively amplifies a detectable portion of GPX1 (used as a primer pair set common to biomarkers for diagnosing IBD from normal patients; IBD from normal and IBS; IBD from IBS; and IBD and IBS from normal);

(b) a first primer pair that selectively amplifies a detectable portion of UBE2G1 and a second primer pair that selectively amplifies a detectable portion of BLCAP (used as a primer pair set that can be added to primer pair set (a) to generate a 4-gene biomarker specific for diagnosing IBD from normal);

(c) a first primer pair that selectively amplifies a detectable portion of UBE2G1, a second primer pair that selectively amplifies a detectable portion of BLCAP, and a third primer pair that selectively amplifies a detectable portion of CALM3 (used as a primer pair trio that can be added to primer pair (a) to generate a 5-gene biomarker for diagnosing IBD from normal);

(d) a first primer pair that selectively amplifies a detectable portion of NONO and a second primer pair that selectively amplifies a detectable portion of CALM3 (used as a primer pair set that, can be added to primer pair sets (a) and (b) to generate a 6-gene biomarker for diagnosing IBD from normal);

(e) a first primer pair that selectively amplifies a detectable portion of PPP2R5A and a second primer pair that selectively amplifies a detectable portion of HIST1H2BK (used as a primer pair set pair common to biomarkers for diagnosing IBD from IBS patients). The primer pair set (e), when combined with primer pair sets (a), and (c) disclosed above for distinguishing IBD from normal, generates a biomarker for diagnosing normal and IBS patients from IBD patients). The primer pair set combination of (e), (a), and (c) can also be used as a biomarker to distinguish between IBS and IBD patients when the expression values of the individual genes are given different weights as discussed herein;

(f) a first primer pair that selectively amplifies a detectable portion of UBE2G1 and a second primer pair that selectively amplifies a detectable portion of CALM3 (used as a primer pair that can be added to primer pair sets (a), and (e) described

above, to generate a 6-gene biomarker that can be used to distinguish IBD from IBS patients);

(g) a first primer pair that selectively amplifies a detectable portion of BLCAP and a second primer pair that selectively amplifies a detectable portion of TH1L (used as primer pair set that when added to (a) and (d) above can be used to generate a 6-gene biomarker that can distinguish patients with IBS or IBD from normal patients;

h) a first primer pair that selectively amplifies a detectable portion of HIST1H2KB and a second primer pair that selectively amplifies a detectable portion of CALM3 (used as primer pair set that when added to (g) above can be used to generate a 4- gene biomarker that can distinguish patients with IBS from normal patients; and

i) a first primer pair that selectively amplifies a detectable portion of HIST1H2KB and a second primer pair that selectively amplifies a detectable portion of UBE2G1 (used as primer pair set that when added to (h) above can be used to generate a different 4-gene biomarker that can distinguish patients with IBS from normal patients.

The biomarkers of the first and second aspects of the invention can be stored frozen, in lyophilized form, or as a solution containing the different probe sets or primer pairs. Such a solution can be made as such, or the composition can be prepared at the time of hybridizing the polynucleotides to target, as discussed below. Alternatively, the compositions can be placed on a solid support, such as in a microarray or microplate format.

In all of the above aspects and embodiments, the polynucleotides can be labeled with a detectable label. In a preferred embodiment, the detectable labels for polynucleotides in different probe sets are distinguishable from each other to, for example, facilitate differential determination of their signals when conducting hybridization reactions using multiple probe sets. Methods for detecting the label include, but are not limited to spectroscopic, photochemical, biochemical, immunochemical, physical or chemical techniques. For example, useful detectable labels include but are not limited to radioactive labels such as ^{32}P, ^{3}H, and ^{14}C; fluorescent dyes such as fluorescein isothiocyanate (FITC), rhodamine, lanthanide phosphors, and Texas red, ALEXIS™ (Abbott Labs), CY™ dyes (Amersham); electron-dense reagents such as gold; enzymes such as horseradish peroxidase, beta-galactosidase, luciferase, and alkaline phosphatase; colorimetric labels such as colloidal gold; magnetic labels such as those sold under the mark DYNABEADS™; biotin; dioxigenin; or haptens and proteins for which

antisera or monoclonal antibodies are available. The label can be directly incorporated into the polynucleotide, or it can be attached to a probe or antibody which hybridizes or binds to the polynucleotide. The labels may be coupled to the probes by any suitable means known to those of skill in the art. In various embodiments, the polynucleotides are labeled using nick translation, PCR, or random primer extension (see, e.g., Sambrook et al. *supra*).

In a third aspect, the present invention provides methods for diagnosing IBD and/or IBS comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD or IBS under hybridizing conditions with 2 or more probes sets, wherein at least a first probe set and a second probe set selectively hybridize under high stringency conditions to a nucleic acid target selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3; wherein the first probe set and the second probe set do not selectively hybridize to the same nucleic acid;

(b) detecting formation of hybridization complexes between the 2 or more probe sets and nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD, IBS, or neither based on the gene expression of the nucleic acid targets.

The inventors have discovered that the methods of the invention can be used, for example, in diagnosing IBD and IBS. The specific genes, probe sets, hybridizing conditions, probe types, polynucleotides, etc. are as defined above for the first and/or second aspects of the invention.

The subject is any human subject that may be suffering from IBS or IBD. As discussed above, IBS is a chronic condition characterized by abdominal pain, constipation and/or diarrhea, and/or a change in bowel habits while IBD patients may suffer from the same symptoms, as well as vomiting, hematochezia, weight loss, and/or weight gain; thus, for example, subjects with one or more of these symptoms would be candidate subjects for the methods of the invention.

As used herein, a "mRNA-derived nucleic acid sample" is a sample containing mRNA from the subject, or a cDNA (single or double stranded) generated from the mRNA obtained from the subject. The sample can be from any suitable tissue source, including but not limited to blood samples, such as PBMCs or RBC-depleted whole blood.

In one embodiment, the mRNA sample is a human mRNA sample. It will be understood by those of skill in the art that the RNA sample does not require isolation of an individual or several individual species of RNA molecules, as a complex sample mixture containing RNA to be tested can be used, such as a cell or tissue sample analyzed by in situ hybridization.

In a further embodiment, the probe sets comprise single stranded anti-sense polynucleotides of the nucleic acid compositions of the invention. For example, in mRNA fluorescence in situ hybridization (FISH) (ie. FISH to detect messenger RNA), only an anti-sense probe strand hybridizes to the single stranded mRNA in the RNA sample, and in that embodiment, the "sense" strand oligonucleotide can be used as a negative control.

Alternatively, the probe sets may comprise DNA probes. In either of these embodiments (anti-sense probes or cDNA probes), it is preferable to use controls or processes that direct hybridization to either cytoplasmic mRNA or nuclear DNA. In the absence of directed hybridization, it is preferable to distinguish between hybridization to cytoplasmic RNA and hybridization to nuclear DNA.

Any method for evaluating the presence or absence of hybridization products in the sample can be used, such as by Northern blotting methods, in situ hybridization (for example, on blood smears), polymerase chain reaction (PCR) analysis, qPCR (quantitative PCR), RT-PCR (Real Time PCR), or array based methods.

In one embodiment, detection is performed by in situ hybridization ("ISH"). In situ hybridization assays are well known to those of skill in the art. Generally, in situ hybridization comprises the following major steps (see, for example, US 6,664,057): (1) fixation of sample or nucleic acid sample to be analyzed; (2) pre-hybridization treatment of the sample or nucleic acid sample to increase accessibility of the nucleic acid sample (within the sample in those embodiments) and to reduce nonspecific binding; (3) hybridization of the probe sets to the nucleic acid sample; (4) post-hybridization washes to remove polynucleotides not bound in the hybridization; and (5) detection of the

hybridized nucleic acid fragments. The reagent used in each of these steps and their conditions for use varies depending on the particular application. In a particularly preferred embodiment, ISH is conducted according to methods disclosed in US Patent Nos. 5,750,340 and/or 6,022,689, incorporated by reference herein in their entirety.

In a typical in situ hybridization assay, cells are fixed to a solid support, typically a glass slide. The cells are typically denatured with heat or alkali and then contacted with a hybridization solution to permit annealing of labeled probes specific to the nucleic acid sequence encoding the protein. The polynucleotides of the invention are typically labeled, as discussed above. In some applications it is necessary to block the hybridization capacity of repetitive sequences. In this case, human genomic DNA or Cot-1 DNA is used to block non-specific hybridization.

When performing an in situ hybridization to cells fixed on a solid support, typically a glass slide, it is preferable to distinguish between hybridization to cytoplasmic RNA and hybridization to nuclear DNA. There are two major criteria for making this distinction: (1) copy number differences between the types of targets (hundreds to thousands of copies of RNA vs. two copies of DNA) which will normally create significant differences in signal intensities and (2) clear morphological distinction between the cytoplasm (where hybridization to RNA targets would occur) and the nucleus will make signal location unambiguous. Thus, when using double stranded DNA probes, it is preferred that the method further comprises distinguishing the cytoplasm and nucleus in cells being analyzed within the bodily fluid sample. Such distinguishing can be accomplished by any means known in the art, such as by using a nuclear stain such as Hoeschst 33342 or DAPI, which delineate the nuclear DNA in the cells being analyzed. In this embodiment, it is preferred that the nuclear stain is distinguishable from the detectable probe. It is further preferred that the nuclear membrane be maintained, i.e. that all the Hoeschst or DAPI stain be maintained in the visible structure of the nucleus.

In a further embodiment, an array-based format can be used in which the probe sets can be arrayed on a surface and the RNA sample is hybridized to the polynucleotides on the surface. In this type of format, large numbers of different hybridization reactions can be run essentially "in parallel." This embodiment is particularly useful when there are many genes whose expressions in one specimen are to be measured, or when isolated nucleic acid from the specimen, but not the intact specimen, is available. This provides rapid, essentially simultaneous, evaluation of a large number of gene expression assays.

Methods of performing hybridization reactions in array based formats are also described in, for example, Pastinen (1997) Genome Res. 7:606-614; (1997) Jackson (1996) Nature Biotechnology 14:1685; Chee (1995) Science 274:610; WO 96/17958. Methods for immobilizing the polynucleotides on the surface and derivatizing the surface are known in the art; see, for example, US 6,664,057.

In each of the above aspects and embodiments, detection of hybridization is typically accomplished through the use of a detectable label on the polynucleotides in the probe sets, such as those described above; in some alternatives, the label can be on the target nucleic acids. The label can be directly incorporated into the polynucleotide, or it can be attached to a probe or antibody which hybridizes or binds to the polynucleotide. The labels may be coupled to the probes in a variety of means known to those of skill in the art, as described above. The label can be detected by any suitable technique, including but not limited to spectroscopic, photochemical, biochemical, immunochemical, physical or chemical techniques, as discussed above.

The methods may comprise comparing gene expression of the nucleic acid targets to a control. Any suitable control known in the art can be used in the methods of the invention. For example, the expression level of a gene known to be expressed at a relatively constant level in IBS, IBD, and normal patients can be used for comparison. Alternatively, the expression level of the genes targeted by the probes can be analyzed in normal RNA samples equivalent to the test sample. Another embodiment is the use of a standard concentration curve that gives absolute copy numbers of the mRNA of the gene being assayed; this might obviate the need for a normalization control because the expression levels would be given in terms of standard concentration units. Those of skill in the art will recognize that many such controls can be used in the methods of the invention.

The methods comprise diagnosing whether the subject is likely to have IBD, IBS, or neither based on the gene expression of the nucleic acid targets. As used herein, "likely to have" means a statistically significant likelihood that the diagnosis is correct. In various embodiments, the method results in an accurate diagnosis in at least 70% of cases; more preferably of at least 75%, 80%, 85%, 90%, or more of the cases.

The methods of the present invention may apply weights, derived by various means in the art, to the number of hybridization complexes formed for each nucleic acid target. Such means can be any suitable for defining the classification rules for use of the

biomarkers of the invention in diagnosing IBD or IBS. Such classification rules can be generated via any suitable means known in the art, including but not limited to supervised or unsupervised classification techniques. In a preferred embodiment, classification rules are generated by use of supervised classification techniques. As used herein, "supervised classification" is a computer-implemented process through which each measurement vector is assigned to a class according to a specified decision rule, where the possible classes have been defined on the basis of representative training samples of known identity. Examples of such supervised classification include, but are not limited to, classification trees, neural networks, k-nearest neighbor algorithms, linear discriminant analysis (LDA), quadratic discriminant analysis (QDA), and support vector machines.

In one non-limiting example, a weighted combination of the genes is arrived at by, for example, a supervised classification technique which uses the expression data from all of the genes within individual patients. The expression level of each gene in a patient is multiplied by the weighting factor for that gene, and those weighted values for each gene's expression are summed for each individual patient, and, optionally, a separate coefficient specific for that comparison is added to the sum which gives a final score. Each comparison set may result in its own specific set of gene weightings; as discussed further below, the IBD v Normal has different gene expression weightings than IBS v normal. Weightings can also have either a positive-sign or a negative-sign. Not all patients in one classification will have the same Gene 1 up, Gene 2 down, etc. (See examples below).

In various embodiments of this third aspect of the invention, the two or more probe sets comprise or consist of at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 probe sets, and wherein none of the 3-14 probe sets selectively hybridize to the same nucleic acid. These embodiments of probe sets are further discussed in the first and second aspects of the invention; all other embodiments of the probe sets and polynucleotides of the first and second aspect can be used in the methods of the invention.

In one preferred embodiment of the third aspect of the invention, at least 3, 4, or 5 of the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3. As disclosed in more detail below, this method can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from

those subjects suffering from IBS. Examples of such preferred probe sets for use in the methods of the invention are provided in **Table 17.** In one preferred version of this embodiment, is a method for diagnosing irritable bowel syndrome (IBS), comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBS under hybridizing conditions with at least 3 nucleotide probes, wherein a first nucleotide probe, a second nucleotide probe, and a third nucleotide probe each consist of 15 or more contiguous nucleotides of a nucleic acid target selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof, wherein each of the first, second, and third nucleotide probes consist of 15 or more contiguous nucleotides of a different nucleic acid target;

(b) detecting formation of hybridization complexes between the probes and the nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBS based on the measure of gene expression of the nucleic acid targets. In a further preferred version of this embodiment, the nucleic acid targets comprise BLCAP, TH1L, UBE2G1, and HIST1H2BK.In a further preferred version of this embodiment, the subject suffers from one or more of abdominal pain, constipation, diarrhea, and a change in bowel habits. In another version of this embodiment, the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells red blood cell-depleted whole blood. In a further version of this embodiment, the method further comprises analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

In another preferred embodiment of the third aspect of the invention, at least 5 or 6 of the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO. As disclosed in more detail below, such probe sets can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from those subjects suffering from IBD. Examples of such preferred probe sets for use in the methods of the invention are provided in **Table 18.** In one preferred version of this embodiment, the method comprises:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under hybridizing conditions with at least 5 nucleotide probes, wherein a first nucleotide probe, a second nucleotide probe, a third nucleotide probe, a fourth nucleotide probe, and a fifth nucleotide probe each consist of 15 or more contiguous nucleotides of a nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof, wherein each of the first, second, third, fourth, and fifth nucleotide probes consist of 15 or more contiguous nucleotides of a different nucleic acid target;

(b) detecting formation of hybridization complexes between the nucleotide probes and the nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD based on the measure of gene expression of the nucleic acid targets. In a further preferred embodiment, the nucleic acid targets comprise RAP1A, BLCAP, UBE2G1, CALM3, GPX1, and NONO. In another embodiment, the subject may be suffering from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change. In a further embodiment, the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood. In a further embodiment, the method further comprises analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

In a further preferred embodiment of the third aspect of the invention, at least 6 or 7 of the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A. As disclosed in more detail below, such probe sets can be used in preferred embodiments of the methods of the invention for distinguishing those subjects suffering from IBS from those subjects suffering from IBD. Examples of such preferred probe sets for use in the methods of the invention are provided in **Table 19.** In one preferred version, of this embodiment, a method for differentiating between inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS) in a subject, comprises:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under hybridizing conditions with at least 6 nucleotide probes, wherein a first nucleotide probe, a second nucleotide probe, a third nucleotide probe, a fourth nucleotide probe, a fifth nucleotide probe, and a sixth nucleotide probe each consist of 15 or more contiguous nucleotides of a nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof; wherein each of the first, second, third, fourth, fifth, and sixth nucleotide probes consist of 15 or more contiguous nucleotides of a different nucleic acid target;

(b) detecting formation of hybridization complexes between the nucleotide probes and the nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD or IBS based on the measure of gene expression of the nucleic acid targets. In a further preferred embodiment, the nucleic acid targets comprise RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A, and BLCAP. In another embodiment, the subject suffers from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change. In a further embodiment, the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood. In another embodiment, the method further comprises analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

In one specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to BLCAP, a second probe set that selectively hybridizes under high stringency conditions to TH1L, a third probe set that selectively hybridizes under high stringency conditions to CALM3, and a fourth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such methods can be used to distinguish between normal and IBS patients.

In a second specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to BLCAP, a second probe set that selectively hybridizes under high stringency conditions to TH1L, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, and a fourth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such methods can be used to distinguish between normal and IBS patients.

In a third specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to GPX1. As disclosed in more detail below, the inventors have discovered that such methods can be used as probes to distinguish between normal and IBD patients.

In a fourth specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to CALM3, and a fifth probe set that selectively hybridizes under high stringency conditions to GPX1. As disclosed in more detail below, the inventors have discovered that such methods can distinguish between normal and IBD patients.

In a fifth specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to CALM3, a fifth probe set that selectively hybridizes under high stringency conditions to GPX1, and a sixth probe set that selectively hybridizes under high stringency conditions to NONO . As disclosed in more detail below, the

inventors have discovered that such methods can distinguish between normal and IBD patients.

In a sixth specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to BLCAP, a third probe set that selectively hybridizes under high stringency conditions to UBE2G1, a fourth probe set that selectively hybridizes under high stringency conditions to CALM3, a fifth probe set that selectively hybridizes under high stringency conditions to GPX1, a sixth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK, and a seventh probe set that selectively hybridizes under high stringency conditions to PPP2RR5A. As disclosed in more detail below, the inventors have discovered that such methods can distinguish normal and IBS patients from IBD patients.

In a seventh specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to UBE2G1, a third probe set that selectively hybridizes under high stringency conditions to CALM3, a fourth probe set that selectively hybridizes under high stringency conditions to GPX1, a fifth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK1, and a sixth probe set that selectively hybridizes under high stringency conditions to PPP2R5A. As disclosed in more detail below, the inventors have discovered that such methods can be used as probes to distinguish IBS patients from IBD patients.

In an eighth specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to RAP1A, a second probe set that selectively hybridizes under high stringency conditions to UBE2G1, a third probe set that selectively hybridizes under high stringency conditions to CALM3, a fourth probe set that selectively hybridizes under high stringency conditions to GPX1, a fifth probe set that selectively hybridizes under high stringency conditions to HIST1H2BK, a sixth probe set that selectively hybridizes under high stringency conditions to PPP2R5A, and a seventh probe set that selectively hybridizes under high stringency conditions to BLCAP. As disclosed in more detail

below, the inventors have discovered that such methods can be used as probes to distinguish IBS patients from IBD patients.

In a ninth specific embodiment of this third aspect of the invention, the methods comprise use of a first probe set that selectively hybridizes under high stringency conditions to BLCAP, a second probe set that selectively hybridizes under high stringency conditions to CALM3, a third probe set that selectively hybridizes under high stringency conditions to GPX1, a fourth probe set that selectively hybridizes under high stringency conditions to TH1L, a fifth probe set that selectively hybridizes under high stringency conditions to RAP1A, and a sixth probe set that selectively hybridizes under high stringency conditions to NONO. As disclosed in more detail below, the inventors have discovered that such methods can be used as probes to distinguish IBS and IBD patients from normal patients.

In a fourth aspect, the present invention provides methods method for diagnosing IBD and/or IBS comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD or IBS under amplifying conditions with 2 or more primer pairs, wherein at least a first primer pair and a second primer pair are capable of selectively amplifying a detectable portion of a nucleic acid target selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3; wherein the first primer pair and the second primer pair do not selectively amplify the same nucleic acid;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the two or more primer pairs, wherein the amplification products provide a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD, IBS, or neither based on the amplification of the nucleic acid targets.

Definitions of primer pairs as used above apply to this aspect of the invention, as well as all other common terms. All embodiments disclosed above for the other aspects of the invention are also suitable for this fourth aspect.

In these methods, amplification of target nucleic acids using the primer pairs is used instead of hybridization to detect gene expression products. Any suitable

amplification technique can be used, including but not limited to PCR, RT-PCT, qPCR, spPCR, etc. Suitable amplification conditions can be determined by those of skill in the art based on the particular primer pair design and other factors, based on the teachings herein. In various embodiments, the two or more primer pairs comprise at least 3-14 primer pairs, wherein none of the 3-14 primer pairs selectively amplify the same nucleic acid.

In one preferred embodiment of the fourth aspect of the invention, at least 3, 4, or 5 of the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3. As disclosed in more detail below, such primer pairs can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from those subjects suffering from IBS. Examples of such preferred primer pairs are those that amplify a detectable portion of the nucleic acids provided in **Table 17.** In one preferred version of this embodiment, a method for diagnosing irritable bowel syndrome (IBS) comprises:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBS under amplifying conditions with at least three primer pairs, wherein a first primer pair, a second primer pair, and a third primer pair selectively amplify a different nucleic acid target selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof, wherein each primer in each primer pair consists of at least 15 contiguous nucleotides of its respective nucleic acid target;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the at least three primer pairs, wherein a number of such amplification products provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBS based on the measure of gene expression of the nucleic acid targets. In a further version of this embodiment, the nucleic acid targets comprise BLCAP, TH1L, UBE2G1, and HIST1H2BK. In another version, the subject suffers from one or more of abdominal pain, constipation, diarrhea, and a change in bowel habits. The mRNA-derived nucleic acid sample may be obtained from peripheral blood mononuclear cells red blood cell-depleted whole blood. The method may further comprise analyzing gene expression of the nucleic acid targets by

applying a weight to the number of amplification products formed for each nucleic acid target.

In another preferred embodiment of the fourth aspect of the invention, at least 5 or 6 of the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO. As disclosed in more detail below, such primer pairs can be used in preferred embodiments of the methods of the invention for distinguishing normal subjects from those subjects suffering from IBD. Examples of such preferred primer pairs are those that amplify a detectable portion of the nucleic acids provided in **Table 18.** In a preferred embodiment, the method for IBD diagnosis comprises

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under amplifying conditions with at least five primer pairs, wherein a first primer pair, a second primer pair, a third primer, a fourth primer pair, and a fifth primer pair each selectively amplify a different nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof, wherein each primer in each primer pair consists of at least 15 contiguous nucleotides of its respective nucleic acid target;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the at least five primer pairs, wherein a number of such amplification products provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD based on the measure of gene expression of the nucleic acid targets. In a further preferred embodiment, the nucleic acid targets comprise RAP1A, BLCAP, UBE2G1, CALM3, GPX1, and NONO. In another embodiment, the subject suffers from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change. In a further embodiment, the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood. In another embodiment, the method further comprises analyzing gene expression of the nucleic acid targets by applying a weight to the number of amplification products formed for each nucleic acid target.

In a further preferred embodiment of the fourth aspect of the invention, at least 6 or 7 of the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A. As disclosed in more detail below, such primer pairs can be used in preferred embodiments of the methods of the invention for distinguishing those subjects suffering from IBS from those subjects suffering from IBD. Examples of such preferred primer pairs are those that amplify a detectable portion of the nucleic acids provided in **Table 19.** In one preferred version, method for differentiating between inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS) in a subject comprises:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under amplifying conditions with at least six primer pairs, wherein a first primer pair, a second primer pair, a third primer, a fourth primer pair, a fifth primer pair, and a sixth primer pair each selectively amplify a different nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof, wherein each primer in each primer pair consists of at least 15 contiguous nucleotides of its respective nucleic acid target;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the at least six primer pairs, wherein a number of such amplification products provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD or IBS based on the measure of gene expression of the nucleic acid targets. In a preferred embodiment, the nucleic acid targets comprise RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A, and BLCAP. In a further embodiment, the subject suffers from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change. In another embodiment, the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood. In a further embodiment, the method further comprises analyzing gene expression of the nucleic acid targets by applying a weight to the number of amplification products formed for each nucleic acid target.

In one specific embodiment of this fourth aspect of the invention, the methods comprise use of a first primer pair that selectively amplifies a detectable portion of BLCAP, a second primer pair that selectively amplifies a detectable portion of TH1L, a third primer pair that selectively amplifies a detectable portion of CALM3, and a fourth primer pair that selectively amplifies a detectable portion of HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such methods can distinguish between normal and IBS patients.

In a second specific embodiment of this fourth aspect of the invention, the methods comprise use of a first primer pair that selectively amplifies a detectable portion of BLCAP, a second primer pair that selectively amplifies a detectable portion of TH1L, a third primer pair that selectively amplifies a detectable portion of UBE2G1, and a fourth primer pair that selectively amplifies a detectable portion of HIST1H2BK. As disclosed in more detail below, the inventors have discovered that such methods can distinguish between normal and IBS patients.

In a third specific embodiment of this fourth aspect of the invention, the methods comprise use of a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of BLCAP, a third primer pair that selectively amplifies a detectable portion of UBE2G1, and a fourth primer pair that selectively amplifies a detectable portion of GPX1. As disclosed in more detail below, the inventors have discovered that such methods can be used as probes to distinguish between normal and IBD patients.

In a fourth specific embodiment of this fourth aspect of the invention, the methods comprise use of a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of BLCAP, a third primer pair that selectively amplifies a detectable portion of UBE2G1, a fourth primer pair that selectively amplifies a detectable portion of CALM3, and a fifth primer pair selectively amplifies a detectable portion of GPX1. As disclosed in more detail below, the inventors have discovered that such methods can distinguish between normal and IBD patients.

In a fifth specific embodiment of this fourth aspect of the invention, the methods comprise use of a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of BLCAP, a

third primer pair that selectively amplifies a detectable portion of UBE2G1, a fourth primer pair that selectively amplifies a detectable portion of CALM3, a fifth primer pair selectively amplifies a detectable portion of GPX1, and a sixth primer pair selectively amplifies a detectable portion of NONO. As disclosed in more detail below, the inventors have discovered that such methods can distinguish between normal and IBD patients.

In a sixth specific embodiment of this fourth aspect of the invention, the methods comprise use of a primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of BLCAP, a third primer pair that selectively amplifies a detectable portion of UBE2G1, a fourth primer pair that selectively amplifies a detectable portion of CALM3, a fifth primer pair that selectively amplifies a detectable portion of GPX1, a sixth primer pair that selectively amplifies a detectable portion of HIST1H2BK; and a seventh primer pair selectively that amplifies a detectable portion of PPP2RR5A. As disclosed in more detail below, the inventors have discovered that such methods can distinguish normal and IBS patients from IBD patients.

In a seventh specific embodiment of this fourth aspect of the invention, the methods comprise use of a first primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of UBE2G1, a third primer pair that selectively amplifies a detectable portion of CALM3, a fourth primer pair that selectively amplifies a detectable portion of GPX1, a fifth primer pair selectively amplifies a detectable portion of HIST1H2BK, and a sixth primer pair selectively amplifies a detectable portion of PPP2R5A. As disclosed in more detail below, the inventors have discovered that such methods can be used to distinguish between IBS patients and IBD patients

In an eighth specific embodiment of this fourth aspect of the invention, the methods comprise use of a primer pair that selectively amplifies a detectable portion of RAP1A, a second primer pair that selectively amplifies a detectable portion of UBE2G1, a third primer pair that selectively amplifies a detectable portion of CALM3, a fourth primer pair that selectively amplifies a detectable portion of GPX1, a fifth primer pair that selectively amplifies a detectable portion of HIST1H2BK, a sixth primer pair that selectively amplifies a detectable portion of PPP2R5A, and a seventh primer pair selectively that amplifies a detectable portion of BLCAP. As disclosed in more detail

below, the inventors have discovered that such methods can be used as probes to distinguish IBS patients from IBD patients.

In a ninth specific embodiment of this fourth aspect of the invention, the methods comprise use of a first primer pair that selectively amplifies a detectable portion of BLCAP, a second primer pair that selectively amplifies a detectable portion of CALM3, a third primer pair that selectively amplifies a detectable portion of GPX1, a fourth primer pair that selectively amplifies a detectable portion of TH1L, a fifth primer pair selectively amplifies a detectable portion of RAP1A, and a sixth primer pair selectively amplifies a detectable portion of NONO. As disclosed in more detail below, the inventors have discovered that such methods can be used as probes to distinguish IBS and IBD patients from normal patients.

In various embodiments, the methods may further comprise comparing amplification products to a control.

In a further embodiment of all of the methods of the invention, the methods are automated, and appropriate software is used to conduct some or all stages of the method.

In a further aspect, the present invention provides kits for use in the methods of the invention, comprising the biomarkers and/or primer pair sets of the invention and instructions for their use. In a preferred embodiment, the polynucleotides are detectably labeled, most preferably where the detectable labels on each polynucleotide in a given probe set or primer pair are the same, and differ from the detectable labels on the polynucleotides in other probe sets or primer pairs, as disclosed above. In a further preferred embodiment, the probes/primer pairs are provided in solution, most preferably in a hybridization or amplification buffer to be used in the methods of the invention. In further embodiments, the kit also comprises wash solutions, pre-hybridization solutions, amplification reagents, software for automation of the methods, etc.

Example 1

In an effort to identify gene expression profiles that could discriminate between whole blood samples collected from IBS, IBD, and normal patients, and thus provide the basis for a minimally invasive diagnostic test, we employed a proprietary data mining program to analyze publicly available data collected from Crohn's Disease (CD) and Ulcerative Colitis (UC) patients (Burczynski et al., Molecular Classification of Crohn's Disease and Ulcerative Colitis Patients Using Transcriptional Profiles in Peripheral Blood

Mononuclear Cells, Journal of Molecular Diagnostics 8(1):51-61, February 2006), hereinafter referred to as the "Burczynski data."

The Burczynski data consisted of a set of individual expression level features, each feature being a quantitative fluorescent signal derived from a single microarray spot. As detailed in Burczynski et al (2006), the signals were generated by hybridizing fluorescently-labeled RNA from a single patient to all of the spots on a single DNA-based oligonucleotide microarray. From these data, we identified molecular signatures, comprised of sets of expression level features, that effectively differentiated between IBD patients and unaffected normal control subjects. Expression levels of the genes represented by those array features were then measured in a prospectively ascertained sample of patients (the 'pilot study', described below). The Burczynski discovery dataset consisted of 127 separate Affymetrix microarray hybridization experiments on RNA from 26 Ulcerative Colitis patients, 59 Crohn's Disease patients, and 42 normal controls.

We employed our proprietary data mining program to analyze the publicly available Burczynski data. We randomly divided the patients in the Burczynski dataset for purposes of our analysis into 2 approximately equal groups: a training set for biomarker set discovery and a separate non-overlapping test set for assessment of biomarkers discovered from the training set. The training set consisted of 30 CD patients, 13 UC patients, and 21 normal controls. The test set consisted of 29 CD patients, 13 UC patients, and 21 controls. The CD and UC patients were defined as 'affected', and normal controls were defined as 'unaffected'.

Our proprietary data mining program was then used to perform a genetic-algorithm search of expression level data for combinations across the affected and unaffected patient sets. The number of features constituting a marker set combination was fixed at 4. The Burczynski data set contained 22,283 expression level features; the number of 4-wise combinations of features in that data set are:
(!22,283 / (!4 * !22,279) = 10,269,905,646,716,170.

The proprietary data mining program was run 3 separate times on the Burczynski dataset using three specific sets of parameters. (1) One parameter set used the training and test sets defined above with additional settings that gave computational results weighted towards higher sensitivity (to minimize false negatives), (2) the second set was similarly weighted towards higher specificity (to minimize false positives), and (3) the third set used random cross-validation ('bootstrap') with no weighting towards either

specificity or sensitivity. Each 4-feature combination analyzed was assigned a score that characterized its accuracy in discriminating between the affected and unaffected groups. The score for each combination of expression features ranges from 1.00 for completely accurate to 0.00 for completely inaccurate.

For the set weighted towards higher sensitivity (set 1), the top-scoring 4-feature sets were obtained such that a combination's score on the training set was greater than 0.995, or the combination's score on the test set was greater than 0.92. For the set weighted towards higher specificity (set 2), the top-scoring 4-feature sets were obtained such that a combination's score on the training set was greater than 0.9975, or the combination's score on the test set was greater than 0.92. For the bootstrap result set with equal weighting between sensitivity and specificity (set 3), the top-scoring 4-feature sets were obtained such that a combination's score on the training set was greater than 0.995 (ie: approximately 99.5% accuracy).

Significance of the marker sets was assessed empirically by random iterative relabeling. The affected and unaffected statuses of patients were randomly re-assigned, and the proprietary data mining program was then run to determine the top marker solutions for the randomly labeled set. This was repeated to obtain 100,000 marker sets. In the randomly relabeled sets, the training set scores reached a maximum of 0.927; 95% of solutions (the empirical p=0.05 level) scored at or below 0.882, and 99% of solutions the empirical p=0.01 level) scored at or below 0.893. The test set scores in relabeled solutions reached a maximum of 0.915; 95% of solutions (the empirical p=0.05 level) scored at or below 0.753, and 99% of solutions (the empirical p=0.01 level) scored at or below 0.809.

A total of sixteen sets, each comprised of 4 features (in the Burczynski microarray data, some genes are represented by more than 1 feature and some features hybridize to more than 1 gene), was obtained using a combination of thresholds: the score on the training set was greater than 0.9975 and/or the score on the test set was greater than 0.92.

Table 2 contains the combinations of genes that were identified from the gene expression profile of peripheral blood mononuclear cells that effectively differentiate between IBD patients and unaffected normal control subjects.

Table 2. Top 16 4-gene combinations

Combination	Gene 1	Gene 2	Gene 3	Gene 4
1	HIST1H2BK	NONO	PPP2R5A	BLCAP
2	TH1L	PPP2R5A	PGRMC1	BLCAP
3	TH1L	UBE2G1	PPP2R5A	BLCAP
4	TH1L	PPP2R5A	BLCAP	HMGB1
5	HIST1H2BK	RAP1A	PPP2R5A	BLCAP
6	NONO	PPP2R5A	BLCAP	GPX1
7	HIST1H2AC	RAP1A	PPP2R5A	HMGB1
8	TH1L	TFE3	UBE2G1	BLCAP
9	PCBP1	RAP1A	PPP2R5A	PGRMC1
10	NONO	UBE2G1	PPP2R5A	BLCAP
11	TH1L	HIST1H2AC	PPP2R5A	BLCAP
12	UBE2G1	PPP2R5A	BLCAP	GPX1
13	HIST1H2AC	PPP2R5A	BLCAP	GPX1
14	TH1L	PPP2R5A	BLCAP	CALM3
15	TH1L	RAP1A	PPP2R5A	CALM3
16	TH1L	HIST1H2BK	PPP2R5A	BLCAP

Fourteen individual expression array features constitute those 16 sets. The feature sets and their memberships are indicated in **Table 3** below. Each feature represents the expression level of a transcript from a single gene; the HUGO gene names for each feature are indicated. The average fold-difference in expression between the IBD and normal groups is also shown, computed by dividing the average expression level in IBD patients by the average expression level in Normal patients. A fold-difference greater than 1 indicates the gene has higher expression in IBD patients compared to normal patients, while a fold-difference less than 1 indicates the gene has lower expression in IBD patients compared to normal patients. The row labeled "freq" shows how many times that microarray feature occurs in the top 16 marker sets.

Table 3. Gene frequency in top 16 combinations

HGNC name	PPP2R5A	BLCAP	TH1L	UBE2G1	RAP1A	HIST1 H2AC	HIST1 H2BK	GPX1	NONO	PGRMC1	HMGB1	CALM3	TFE3	PCBP1
IBD/NML fold diff	0.76	0.72	0.70	0.76	1.60	2.13	1.94	1.80	0.78	1.70	0.72	1.42	1.41	1.31
Feature #	20569	21724	2313	13649	20394	7839	12991	22020	12337	21635	22076	22134	10442	14167
freq	15	13	8	4	4	3	3	3	3	2	2	2	1	1
14 genes in 16 sets	X	X					X		X					
	X	X	X							X				
	X	X	X	X										
	X	X	X								X			
	X	X			X		X							
	X	X						X	X					
	X				X	X					X			
		X	X	X									X	
	X				X					X				X
	X	X		X					X					
	X	X	X			X								
	X	X		X				X						
	X	X				X		X						
	X	X	X									X		
	X		X		X							X		
	X	X	X				X							

A gene list (**Table 4**) was derived from an analysis (**Table 3**) of the unique set of genes in these combinations.

Table 4. Gene List

gene name	affy #	Hs.ID	gene description
TH1L	220607_x_at	Hs.517148	TH1-like (Drosophila)
HIST1H2AC	215071_s_at	Hs.484950	histone 1, H2ac
TFE3	212457_at	Hs.274184	Transcription factor binding to IGHM enhancer 3
NONO	210470_x_at	Hs.533282	Non-POU domain containing, octamer-binding
HIST1H2BK	209806_at	Hs.437275	Histone 1, H2bk
UBE2G1	209141_at	Hs.462035	Ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)
PCBP1	208620_at	Hs.2853	Poly(rC) binding protein 1
RAP1A	202362_at	Hs.190334	RAP1A, member of RAS oncogene family
PPP2R5A	202187_s_at	Hs.497684	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform
PGRMC1	201121_s_at	Hs.90061	Progesterone receptor membrane component 1
BLCAP	201032_at	Hs.472651	Bladder cancer associated protein
GPX1	200736_s_at	Hs.76686	Glutathione peroxidase 1
HMGB1	200680_x_at	Hs.434102	High-mobility group box 1
CALM3	200622_x_at	Hs.515487	Calmodulin 3 (phosphorylase kinase, delta)

An example of the diagnostic performance of the discovery biomarker sets on the analyzed dataset is shown in **Figure 1**. A logistic regression was performed with the patient's affected/unaffected status against the quantitative levels of the four features from a discovery marker set. The training set patient data were used to perform the regression analysis. The resulting regression coefficients were then used to calculate a weighted sum of the expression levels of the four features in the test set patients. The resulting weighted-sum regression score for each training set patient was then plotted, with IBD patients having open symbols and Normal patients having filled symbols. In the example shown in the graph below, a regression-score cutoff of approximately 2.75 assigns an 'affected' test result to 40 patients with IBD and to 1 Normal patient. An 'unaffected' result is assigned to 2 patients with IBD and 20 Normal patients. Using standard calculations for medical diagnostics, this gives Sensitivity=40/42=0.952, Specificity=20/21=0.952, Positive Predictive Value=40/41=0.976, and Negative Predictive Value=20/22=0.909.

Example 2

Eight of the genes listed in Table 4 that occurred frequently in the top sets shown in Table 3 were evaluated, along with Actin B as a control gene, in a subsequent study on a total of 482 RBC (red blood cell)-depleted whole blood samples from: 98 normal controls, 91 Ulcerative Colitis patients, 98 Crohn's Disease patients, 98 IBS patients and 97 patients with non-gastrointestinal inflammatory disease. Samples were obtained from 7 clinical sites at various geographic locations within the U.S.A. In the analysis there was no distinction made between Crohn's and UC.

The RNA expression levels of eight genes from among the 14 features in the top discovery marker sets were measured by quantitative real-time PCR in the RBC-depleted whole blood of a prospectively ascertained sample of affected patients and unaffected controls. An additional ninth gene was measured to serve as an internal reference standard across patients. Five cohorts of patients had RNA assayed:

- 98 Normal
- 98 Crohn's Disease
- 91 Ulcerative Colitis
- 98 Irritable Bowel Syndrome
- 97 Non-Gastrointestinal Inflammatory Disease

The 9 genes (including 1 control) assayed for RNA expression levels in the 5 cohorts of patients were: (Human Genome Organization (HUGO) Gene Nomenclature Committee names are given)

- RAP1A
- BLCAP
- PPP2R5A
- UBE2G1
- GPX1
- TH1-L
- CALM3
- HIST1H2BK
- ACTB (the internal reference gene)

Whole blood samples and clinical information were obtained from all patients. Each IBD patient was diagnosed by a board-certified gastroenterologist; IBD diagnoses were confirmed by endoscopy. Each IBS patient was diagnosed by a board-certified gastroenterologist using Rome I criteria. All protocols were IRB approved; informed consent was obtained and peripheral blood samples and clinical data were collected from

all patients. RNA was isolated, cDNA was synthesized, and quantitative real-time PCR for each gene was performed on an Applied Biosystems 7300 Real-Time PCR System. Expression levels were output as Ct (cycle or crossing threshold). DeltaCts of each gene for each patient were computed to normalize gene expression levels of the 8 marker genes to the intra-subject reference gene (ACTB also referred to as β-Actin). DeltaCt = Ct[marker gene] – Ct[ACTB]. The DeltaCts were then used for analysis of diagnostic classification performance.

2A. IBD vs. Normal 5-gene combination

An example of biomarker performance is shown in **Figure 2**, the boxplots of the logistic regression scores based on expression levels of 5 of the 8 genes whose combination differentiates between normal and IBD patients (RAP1A, BLCAP, UBE2G1, CALM3, and GPX1). The classification matrix and diagnostic accuracy estimates of the combination for IBD v Normal are shown below the graph (Tables 5a-b).

Table 5a. IBD vs Normal (5-gene) Classification Matrix

	IBD	Normal
test > 0	162	25
test ≤ 0	22	71

Fisher exact OR = 20.57 , $p < 2 \times 10^{-16}$

Table 5b. Performance Measures

	study prevalence
Accuracy	83.2%
Sensitivity	88.0%
Specificity	74.0%
Positive Predictive Value (PPV)	86.6%
Negative Predictive Value (NPV)	76.3%

2B. IBD vs. Normal 4-gene combination

An initial logistic regression model was built using data for all eight genes. The model was trimmed by eliminating genes not statistically significantly contributing to the model. The result of this analysis is a four-gene model incorporating: RAP1A, BLCAP, UBE2G1, and GPX1. The accuracy of this model in distinguishing IBD samples from normal samples is 80.4%, as shown in Table 6b, below, along with the other performance measures of this 4-gene combination.

Table 6a. IBD vs Normal (4-gene) Classification Matrix

	IBD	Normal
test > 0	159	30
test ≤ 0	25	66

Fisher exact OR = 13.81 , $p < 2 \times 10^{-16}$

Table 6b. Performance Measures

	study prevalence
Acc	80.4%
Sens	86.4%
Spec	68.8%
PPV	84.1%
NPV	72.5%

2C. Normal & IBS vs. IBD 7 Gene Combination

An example of biomarker performance is shown in **Figure 3**, boxplots of the logistic regression scores based on expression levels of 7 of the 8 genes whose combination differentiates between normal/IBS and IBD patients (RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, AND PPP2R5A). The classification matrix and diagnostic accuracy estimates (Tables 7a-b) of the combination for IBD v Normal/IBS are shown below the graph.

Table 7a. IBS&Normal vs IBD (7-gene) Classification Matrix

	IBD	IBS+Normal
test > 0	141	44
test ≤ 0	43	150

Fisher exact OR = 11.09 , $p < 2 \times 10^{-16}$

Table 7b. Performance measures

	study prevalence
Acc	77.0%
Sens	76.6%
Spec	77.3%
PPV	76.2%
NPV	77.7%

2D. IBS vs. Normal 4-gene combination

An initial logistic regression model was built using data for all eight genes. The model was trimmed by eliminating genes not statistically significantly contributing to the model. The result of this analysis is a four-gene model incorporating: BLCAP, TH1L, CALM3, and HIST1H2BK. The accuracy of this model in distinguishing IBS samples from normal samples is 84.7%.

The biomarker performance is in **Figure 4**, boxplots of the logistic regression scores based on expression levels of 4 of the 8 genes whose combination differentiates between Normal and IBS patients. The classification matrix and diagnostic accuracy estimates of the combination for Normal versus IBS are shown in Tables 8a-b, below the graph.

Table 8a. IBS vs Normal (4-gene) Classification Matrix

	IBS	Normal
test > 0	83	16
test ≤ 0	15	82

Fisher exact OR = 27.62 , $p < 2 \times 10^{-16}$

Table 8b. Performance measures

	study prevalence
Acc	84.2%
Sens	84.7%
Spec	83.7%
PPV	83.8%
NPV	84.5%

2E. IBD vs. IBS 6-gene combination

As above, an initial logistic regression model was built using data for all eight genes. The model was trimmed by eliminating genes not statistically significantly contributing to the model. The result of this analysis is a six-gene model incorporating: RAP1A, UBE2G1, CALM3, GPX1, HISTH2BK, and PPP2R5A. The accuracy of this model in distinguishing IBS samples from IBD samples is 83.0%.

Table 9a. IBD vs IBS differentiation

	IBD	IBS
test > 0	163	27
test ≤ 0	21	71

Fisher exact OR = 20.09 , $p < 2 \times 10^{-16}$

Table 9b. Performance measures

	study prevalence
Acc	83.0%
Sens	88.6%
Spec	72.4%
PPV	85.8%
NPV	77.2%

Summary: The ability of the expression levels of these genes, as measured by RT-PCR and normalized by Actin B expression, to individually distinguish between IBD and normal controls; IBD from IBS; IBD from Normal & IBS; and IBS from Normal are shown in Table 10, (below). The p values for significant differences in expression levels for each gene, between each pair of cohorts are shown. To the right of each p-value, the experimental values (the ΔCt) are shown as "+" (or "-") to indicate a higher (or lower) ΔCt for one member of the subject pair relative to the other (see legend to Table 10). The ΔCt is inversely proportional to the expression level.

Table 10. Significantly different expression levels of individual genes

p values (Wilcoxon rank sum test)								
Probe	**IBD vs normal**		**IBD vs IBS**		**IBD vs norm&IBS**		**IBS vs normal**	
RAP1A	$4.22x10^{-16}$	+	$5.24x10^{-5}$	+	$1.62x10^{-13}$	+	$6.25x10^{-7}$	+
BLCAP	$3.62x10^{-15}$	+	0.78	na	$3.59x10^{-6}$	+	$9.45x10^{-16}$	+
TH1L	$6.78x10^{-7}$	+	0.69	na	$1.0x10^{-3}$	+	$7.86x10^{-6}$	+
UBE2G1	$8.34x10^{-12}$	+	0.003	-	0.018	+	$<2.2x10^{-16}$	+
CALM3	$3.57x10^{-10}$	+	0.24	na	$5.53x10^{-6}$	+	$9.79x10^{-7}$	+
GPX1	0.099	na	0.007	-	$7.59x10^{-3}$	-	0.34	na
HIST1H2BK	0.069	na	$1.02x10^{-6}$	-	0.061	na	$3.85x10^{-9}$	+
PPP2R5A	$5.13x10^{-6}$	+	$7.73x10^{-3}$	-	0.25	na	$7.25x10^{-12}$	+

Legend:
IBD vs normal: + = higher ΔCt in IBD relative to normal; - = lower ΔCt in IBD relative to normal
IBD vs IBS: + = higher ΔCt in IBD relative to IBS; - = lower ΔCt in IBD
IBD vs normal&IBS: + = higher ΔCt in IBD relative to normal&IBS; - = lower ΔCt in IBD
IBS vs normal: + = higher ΔCt in IBS relative to normal; - = lower ΔCt in IBS
All: na = not applicable because p-value is not significant
In all cases, the ΔCt is inversely proportional to expression level. Therefore a lower ΔCt represents a higher level of gene expression and a higher ΔCt represents a lower level of gene expression.

While all eight genes were found to be statistically significantly associated with IBD or IBS, the individual genes are not highly accurate in discriminating the various subgroups. We investigated if combinations of genes selected from the eight might enable clinically useful marker accuracies.

For each of the data subsets: IBD vs. normal control, IBS vs. normal control, IBS and Normal vs. IBD, and IBD vs. IBS, we evaluated the accuracy of gene combinations using logistic regression. One skilled in the art will understand that given a set of measurements, such as the gene expression values for a particular set of genes, and given these measurements across a particular set of samples, such as a group of IBD samples and a group of 'normal' samples, there are many techniques for deriving from that data a 'set of rules' for classifying a sample as, e.g., IBD or normal. Those skilled in the art will understand that an algorithm, including a weighting for each gene expression level, will follow from the logistic regression analysis, according to one method of the body of knowledge known as 'supervised learning', which is a sub-field of 'machine learning', which itself can be considered sub-field of 'data mining'. Supervised learning encompasses techniques for deriving algorithms, or rules, from data. One skilled in the art will understand that there are no clear boundaries between a standard statistical approach, and a 'supervised learning' approach, and that the classification formulas presented below

could be considered as being derived from a supervised learning approach, but could also be termed a standard statistical approach.

The boxplots in the examples above are a visual display of the distribution of the individual scores within each cohort for the weightings that were optimized for a given comparison. The threshold for the classification score is zero in all cases. For IBD v Normal, IBD is greater than zero and Normal is less than zero; the IBS and Other categories are included as informational, but they were not used in determining the gene expression weightings. Similarly for IBD v Normal & IBS, IBD is greater than zero and Normal & IBS are less than zero, and the Other category was not used in deriving the weightings. And the same for IBS v Normal: IBS is greater than zero and Normal is less than zero, and the IBD and Other categories weren't used to derive expression weightings. Thus, the specific ups and downs of the expression levels of individual genes in the marker set do matter in the classifier, but not in a direct always-up or always-down manner. What matters is whether the sum of the weighted expression values is greater than or less than zero. A specific gene may have increased expression in one correctly classified patient, and that same gene may have a decreased expression in another correctly classified patient if the score is "compensated" by appropriately weighted changes in the expression of other genes in the marker set.

By way of non-limiting example, in one specific measurement, the following gene weightings were applied:

IBS vs Normal

4 gene BLCAP, TH1L, CALM3, HIST1H2BK

If(-16.6856+11.2898(BLCAP)-4.9722(TH1L)-3.7663(CALM3)+2.5060(HIST1H2BK))>0

Then IBS

Else Normal

For IBS versus Normal and given the gene weightings above and a threshold of zero with IBS greater than zero and Normal less than or equal to zero, a hypothetical patient with expression levels of BLCAP = 2.0, TH1L=1.0, CALM3=1.0, and HIST1H2BK=2.0 would have a weighted score of (-16.6856+11.2898(2.0)-4.9722(1.0)-3.7663(1.0)+2.5060(2.0) = 2.1675, resulting in a classification of IBS.

Other non-limiting examples of such weightings are as follows:

IBS & Normal vs IBD

7-gene RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A:

If (-.1602+4.487(RAP1A)+2.5746(BLCAP)-2.8938(UBE2G1)+3.8415(CALM3)
-2.3682(GPX1)-1.5623(HIST1H2BK)-1.4927(PPP2RR5A))>0
Then IBD
Else IBS or Normal

IBD vs Normal

4-gene RAP1A, BLCAP, UBE2G1, GPX1

If (-10.8729+3.3467(RAP1A)+5.1866(BLCAP)-3.4559(UBE2G1)+3.237(CALM3)
-3.225(GPX1))>0
Then IBD
Else Normal

IBD vs Normal

5-gene RAP1A, BLCAP, UBE2G1, CALM3, GPX1:

Formula: (-10.7716 + ΔCt_{RAP1A}*3.2485 + ΔCt_{BLCAP}*5.4360 - ΔCt_{UBE2G1}*3.4723 + ΔCt_{CALM3}*3.3511 - ΔCt_{GPX1}*3.4642)

If (-10.7716 + ΔCt_{RAP1A}*3.2485 + ΔCt_{BLCAP}*5.4360 - ΔCt_{UBE2G1}*3.4723 + ΔCt_{CALM3}*3.3511 - ΔCt_{GPX1}*3.4642) >0
Then IBD
Else Normal

IBS vs IBD

6-gene RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A:

Formula: (16.6895 + ΔCt_{RAP1A}*5.1550 - ΔCt_{UBE2G1}*2.5462 + ΔCt_{CALM3}*4.8674 - ΔCt_{GPX1}*2.3979 – $\Delta Ct_{HIST1H2BK}$*2.8183 – $\Delta Ct_{PPP2R5A}$*2.9778)

If 16.6895 + ΔCt_{RAP1A}*5.1550 - ΔCt_{UBE2G1}*2.5462 + ΔCt_{CALM3}*4.8674 - ΔCt_{GPX1}*2.3979 – $\Delta Ct_{HIST1H2BK}$*2.8183 – $\Delta Ct_{PPP2R5A}$*2.9778> **0.0**

Then IBD

ELSE NORMAL

One exemplary classification rule derived from logistic regression analysis of the Burczynski et al (2006) data for classifying IBD vs. Normal using the 5–gene IBD vs Normal biomarker would be:

IF

-1.1704 - .2815*RAP1A + 0.7027*BLCAP + 0.3143*UBE2G1 + 0.1089*CALM3 – 0.4782*GPX1 is less than 0

THEN IBD

ELSE NORMAL

	actual	
predicted	IBD	Normal
IBD	82	1
Normal	3	41

Accuracy	96.9%
Sensitivity	96.5%
Specificity	97.6%
PPV	98.8%
NPV	93.2%

Figure 5 shows the box plots of the regression scores based on expression levels of 5 genes whose combination differentiates IBD from normal (RAP1A, BLCAP, UBE2G1, CALM3, and GPX1).

The weightings disclosed above are optimal examples; as will be clear to those of skill in the art, the weightings can vary widely based on, for example, the use of a different classifier to generate the weightings, or the use of modified weightings that may

provide lower accuracy but improved specificity (or some other change to the assay of interest to a user).

Example 3.

In a separate study, ten of the genes listed in Table 4 that occurred most frequently in the top sets shown in Table 3 were evaluated, along with Actin B as a control gene, in a subsequent study on a total of 482 RBC-depleted whole blood samples from: 98 normal controls, 91 Ulcerative Colitis patients, 98 Crohn's Disease patients, 98 IBS patients and 97 patients with non-gastrointestinal inflammatory disease. Samples were obtained from 7 clinical sites at various geographic locations within the U.S.A.; in the analysis there was no distinction made between Crohn's and UC.

The RNA expression levels of ten genes from among the 15 features in the top discovery marker sets were measured by quantitative real-time PCR in the RBC-depleted whole blood of a prospectively ascertained sample of affected patients and unaffected controls. An additional eleventh gene was measured to serve as an internal reference standard across patients. Five cohorts of patients had RNA assayed:

- 98 Normal
- 98 Crohn's Disease
- 91 Ulcerative Colitis
- 98 Irritable Bowel Syndrome
- 97 Non-Gastrointestinal Inflammatory Disease

The 11 genes (including 1 control) assayed for RNA expression levels in the 5 cohorts of patients were: (Human Genome Organization (HUGO) Gene Nomenclature Committee names are given)

- RAP1A
- BLCAP
- PPP2R5A
- UBE2G1
- GPX1
- TH1-L
- CALM3
- HIST1H2BK
- NONO
- HMGB1
- ACTB (the internal reference gene)

Whole blood samples and clinical information were obtained from all patients. Each IBD patient was diagnosed by a board-certified gastroenterologist; IBD diagnoses were confirmed by endoscopy. Each IBS patient was diagnosed by a board-certified gastroenterologist using Rome I criteria. All protocols were IRB approved; informed consent was obtained and peripheral blood samples and clinical data were collected from all patients. Expression data were obtained from peripheral whole blood samples (with no mononuclear enrichment) by isolating total mRNAs, synthesizing cDNAs, and performing real-time quantitative PCR on an Applied Biosystems 7300 Real-Time PCR System. Expression levels were output as Ct (cycle or crossing threshold). DeltaCts of each gene for each patient were computed to normalize gene expression levels of the10 marker genes to the intra-subject reference gene (ACTB also referred to as β-Actin). DeltaCt = Ct[marker gene] – Ct[ACTB]. The DeltaCts were then used for analysis of diagnostic classification performance.

3A IBD vs Normal (6-gene)

An optimal scoring algorithm for classification of patients as IBD or normal was derived based on 6 of the 10 tested genes (RAP1A, BLCAP, UBE2G1, CALM3, GPX1, NONO). The classification matrix and diagnostic performance measures for this biomarker are given in Table 11a and 11b, respectively.

Table 11a. IBD vs Normal (6-gene) Classification Matrix

		Clinical Diagnosis	
		IBD	Normal
Biomarker Classification	IBD	168	25
	Normal	21	73
Fisher's exact Odds Ratio (2-sided) = 23.0, p < 2 x 10-16			

Table 11b. Diagnostic Performance Measures

accuracy*	84%
sensitivity	89%

specificity	75%
positive predictive value*	87%
negative predictive value*	78%
AUC-ROC	0.91

*result based on study prevalences.

The NPV for an adjusted 25% prior probability of IBD (a rule-out scenario) is 95%. The PPV for an adjusted 75% prior probability of IBD (a rule-in scenario) is 91%.

5

3B. IBS vs Normal (4-gene)

An optimal scoring algorithm for classification of patients as IBS or normal was derived based on 4 of the 10 tested genes (BLCAP, UBE2G1, TH1L, HIST1H2BK). The classification of patients by clinical diagnosis and test result is given in Table 12a. The
10 diagnostic performance of the classification is summarized in Table 12b.

Table 12a. IBS vs Normal (4-gene) Classification Matrix

		Clinical Diagnosis	
		IBS	Normal
Biomarker Classification	IBS	87	21
	Normal	11	77
Fisher's exact Odds Ratio (2-sided) = 28.3, $p < 2 \times 10^{-16}$			

15 **Table 12b. Diagnostic Performance Measures**

accuracy*	84%
sensitivity	89%
specificity	79%
positive predictive value*	81%
negative predictive value*	88%
AUC-ROC	0.92

* result based on study prevalences

The NPV for an adjusted 25% prior probability of IBS (a rule-out scenario) is

96%. The PPV for an adjusted 75% prior probability of IBS (a rule-in scenario) is 93%.

3C. IBS vs IBD (7 gene)

An optimal scoring algorithm for classification of patients as IBS or IBD was derived based on 7 of the 10 tested genes (RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A, BLCAP). The classification of patients by clinical diagnosis and test result is given in Table 13a. The diagnostic performance of the classification is summarized in Table 13b.

Table 13a. IBS vs IBD (7-gene) Classification Matrix

	IBD	IBS
test > 0	163	26
test ⩽ 0	21	72

Fisher's exact OR=21.14, $p < 2 \times 10^{-16}$

Table 13b. Clinical Performance Measures

	study prevalence
Acc	83.3%
Sens	88.6%
Spec	73.5%
PPV	86.2%
NPV	77.4%

The PPV for an adjusted 75% prior probability of IBD (a rule-in IBD scenario) is 90.9%. The NPV for an adjusted 25% prior probability of IBD (a rule-out IBD scenario) is 95.1%.

3D (IBX vs normal)

An optimal scoring algorithm for classification of patients as either IBS or IBD vs normal was derived based on 6 of the 10 tested genes (6-gene BLCAP, CALM3, GPX1, TH1L, RAP1A, NONO IBX vs Normal). The classification of patients by clinical diagnosis and test result is given in Table 14a. The diagnostic performance of the classification is summarized in Table 14b.

Table 14a. IBX vs Normal (6-gene) Classification Matrix

	IBX	norm
test > 0	269	45
test ≤ 0	18	53

Fisher's exact OR=17.4, $p < 2 \times 10^{-16}$

Table 14b. Clinical Performance Measures

	at study prevalence
Acc	83.6%
Sens	93.7%
Spec	54.1%
PPV	85.7%
NPV	74.6%

3E Shared Biology of Genes in Biomarkers

Expression levels of the 10 candidate biomarker genes in Example 3 were assayed on each patient specimen and normalized to a within-patient reference gene. Optimal scoring algorithms for classification of patients as IBD versus normal and IBS versus normal were derived separately using the expression levels of the 10 genes assayed in these pilot study patients. The optimal gene set for each test and each set's performance is indicated in Table 15. The classification results had odds ratios of 23.0 and 28.3, respectively, with both p-values < $2x10^{-16}$. Two genes were common to both diagnostic marker sets. The genes identified as diagnostic for the comparisons reveal an overlap between IBD and IBS patients. This overlap of highly statistically significant biomarkers suggests a shared biology between the two disease states. The commonality of the two genes could indicate that genes have a causative role or that they are part of a common response mechanism.

Table 15. Highly significant expression biomarker sets in IBD and IBS*

Cohort sub set odds ratio and p-value	IBD vs Normal OR=23.0, $p=2x10^{-16}$ (Fisher's 2-sided exact)	IBS vs Normal OR=28.3, $p=2x10^{-16}$ (Fisher's 2-sided exact)
genes in marker sets	Expression level*	Expression level*
BLCAP	+	+
UBE2G1	+	+
TH1L		+
CALM3	+	
HIST1H2BK		+

GPX1	n.a.	
NONO	+	
RAP1A	+	

* univariate ΔCt (inversely proportional to expression level) difference relative to Normal: "+" increased; "-" decreased; "+/-" no difference; n.a. = not significantly different

Summary: The ability of the expression levels of these 10 genes, as measured by RT-PCR and normalized by Actin B expression, to individually distinguish between IBD and normal controls; IBD from IBS; IBS from Normal; and IBS&IBD from normal are shown in Table 16 (below). The p values for significant differences in expression levels for each gene, between each pair of subjects are shown. To the right of each p-value, the experimental values (the ΔCt) are shown as "+" (or "-") to indicate a higher (or lower) ΔCt for one member of the subject pair relative to the other (see legend to Table 16). The ΔCt is inversely proportional to the expression level.

Table 16. Significantly different expression levels of individual genes

Probe	IBD vs normal		IBD vs IBS		IBS vs normal		IBS&IBD vs normal	
RAP1A	$4.22x10^{-16}$	+	$5.24x10^{-5}$	+	$6.25x10^{-7}$	+	$8.24x10^{-15}$	+
BLCAP	$3.62x10^{-15}$	+	0.78	na	$9.45x10^{-16}$	+	$< 2.2x10^{-16}$	+
TH1L	$6.78x10^{-7}$	+	0.69	na	$7.86x10^{-6}$	+	$8.89x10^{-8}$	+
UBE2G1	$8.34x10^{-12}$	+	0.003	-	$<2.2x10^{-16}$	+	$<2.2x10^{-16}$	+
CALM3	$3.57x10^{-10}$	+	0.24	na	$9.79x10^{-7}$	+	$1.19x10^{-10}$	+
GPX1	0.099	na	0.007	-	0.34	na	0.45	na
HIST1H2BK	0.069	na	$1.02x10^{-6}$	-	$3.85x10^{-9}$	+	$1.89x10^{-4}$	+
PPP2R5A	$5.13x10^{-6}$	+	$7.73x10^{-3}$	-	$7.25x10^{-12}$	+	$1.38x10^{-9}$	+
NONO	$6.70x10^{-5}$	+	0.053	na	0.08	na	$4.50x10^{-4}$	+
HMGB1	$4.61x10^{-10}$	+	0.47	na	0.16	na	$4.24x10^{-10}$	+

Legend:
IBD vs normal: + = higher ΔCt in IBD relative to normal; - = lower ΔCt in IBD relative to normal
IBD vs IBS: + = higher ΔCt in IBD relative to IBS; - = lower ΔCt in IBD
IBS vs normal: + = higher ΔCt in IBS relative to normal; - = lower ΔCt in IBS
IBS&IBD vs normal: + = higher ΔCt in IBS&IBD relative to normal; - = lower ΔCt in IBS&IBD
All: na = not applicable because p-value is not significant
In all cases, the ΔCt is inversely proportional to expression level. Therefore a lower ΔCt represents a higher level of gene expression and a higher ΔCt represents a lower level of gene expression.

While all ten genes were found to be statistically significantly associated with IBD or IBS, the individual genes are not highly accurate in discriminating the various subgroups. We investigated whether combinations of genes selected from the ten might enable clinically useful marker accuracies.

For each of the data subsets: IBD vs. normal control, IBS vs. normal control, IBS vs. IBD, and IBD& IBS vs. normal, we evaluated the accuracy of gene combinations using logistic regression. One skilled in the art will understand that given a set of measurements, such as the gene expression values for a particular set of genes, and given these measurements across a particular set of samples, such as a group of IBD samples and a group of 'normal' samples, there are many techniques for deriving from that data a 'set of rules' for classifying a sample as eg IBD or normal. Those skilled in the art will understand that an algorithm, including a weighting for each gene expression level, will follow from the logistic regression analysis, according to one method of the body of knowledge known as 'supervised learning', which is a sub-field of 'machine learning', which itself can be considered a sub-field of 'data mining'. Supervised learning encompasses techniques for deriving algorithms, or rules, from data. One skilled in the art will understand that there are no clear boundaries between a standard statistical approach, and a 'supervised learning' approach, and that the classification formulas presented below could be considered as being derived from a supervised learning approach, but could also be termed a standard statistical approach.

The threshold for the classification score is zero in all cases. For IBD v Normal, IBD is greater than zero and Normal is less than zero; the IBS and Other were not used in determining the gene expression weightings. Similarly for IBS vs. Normal, IBS is greater than zero and Normal is less than zero, and the Other categories were not used in deriving the weightings. In the case of IBD vs. IBS, IBD is greater than zero and IBS is less than zero and the Normal and Other categories were not used to derive expression weightings. Finally, in the case of IBD and IBS vs. normal, a score greater than zero indicates either IBD or IBS; a score less than zero indicates Normal, and the Other category was not used to derive the weightings. Thus, the specific ups and downs of the expression levels of individual genes in the marker set do matter in the classifier, but not in a direct always-up or always-down manner with respect to the disease or non-disease status patient. Of more importance is whether the sum of the weighted expression values is greater than or less than zero. A specific gene may have increased expression in one correctly classified patient, and that same gene may have a decreased expression in another correctly classified patient if the score is "compensated" by appropriately weighted changes in the expression of other genes in the marker set.

The following exemplary gene weightings were applied:

IBD vs Normal

6-gene RAP1A, BLCAP, UBE2G1, CALM3, GPX1, NONO:

IBD Diagnostic Index: = (-16.5312 + 4.7721[dCt_{BLCAP}] - 3.3249[dCt_{GPX1}] + 3.6521[dCt_{RAP1A}] - 3.0221[dCt_{UBE2G1}] + 3.0669[dCt_{CALM3}] + 0.8405[dCt_{NONO}])

If (-16.5312 + 4.7721[dCt_{BLCAP}] - 3.3249[dCt_{GPX1}] + 3.6521[dCt_{RAP1A}] - 3.0221[dCt_{UBE2G1}] + 3.0669[dCt_{CALM3}] + 0.8405[dCt_{NONO}]) >0

Then IBD

Else Normal

IBS vs Normal

4-gene BLCAP, TH1L, UBE2G1, HIST1H2BK:

Formula: = -22.1323 + 5.4337 [dCt_{BLCAP}] + 3.3187[dCt_{UBE2G1}] - 4.1747 [dCt_{TH1L}] + 1.6902[$dCt_{HIST1H2BK}$]

If [-22.1323 + 5.4337 [dCt_{BLCAP}] + 3.3187[dCt_{UBE2G1}] - 4.1747 [dCt_{TH1L}] + 1.6902[$dCt_{HIST1H2BK}$] >0

Then IBS

Else Normal

IBD vs IBS

7-gene RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A, BLCAP:

Formula: (17.6564 + ΔCt_{RAP1A}*5.7988 - ΔCt_{UBE2G1}*5.6479 + ΔCt_{CALM3}*3.4257 - ΔCt_{GPX1}*2.5535 - $\Delta Ct_{HIST1H2BK}$*2.1366 - $\Delta Ct_{PPP2R5A}$*2.4503 + ΔCt_{BLCAP}*3.0325)

IF (17.6564 + ΔCt_{RAP1A}*5.7988 - ΔCt_{UBE2G1}*5.6479 + ΔCt_{CALM3}*3.4257 - ΔCt_{GPX1}*2.5535 - $\Delta Ct_{HIST1H2BK}$*2.1366 - $\Delta Ct_{PPP2R5A}$*2.4503 + ΔCt_{BLCAP}*3.0325)>0

Then IBD

Else IBS

IBX vs Normal

6-gene BLCAP, CALM3, GPX1, TH1L, RAP1A, NONO:

Formula: $(-13.5528 + \Delta Ct_{BLCAP}*4.9346 + \Delta Ct_{CALM3}*2.8244 - \Delta Ct_{GPX1}*1.8043 - \Delta Ct_{TH1L}*2.8452 + \Delta Ct_{RAP1A}*1.2203 + \Delta Ct_{NONO}*1.04)$

IF $(-13.5528 + \Delta Ct_{BLCAP}*4.9346 + \Delta Ct_{CALM3}*2.8244 - \Delta Ct_{GPX1}*1.8043 - \Delta Ct_{TH1L}*2.8452 + \Delta Ct_{RAP1A}*1.2203 + \Delta Ct_{NONO}*1.04)>0$

Then IBD or IBS

Else Normal

We subsequently analyzed the biomarker performance based on expression levels of combinations of 3 of the 5 genes tested above (Examples 2D and 3B), whose combination differentiates between normal and IBS patients (BLCAP, TH1L, CALM3, HIST1H2BK, and UBE2G1).The classification matrix and diagnostic accuracy estimates of the combination for IBS v Normal, as well as exemplary gene weightings, are shown in **Table 17.**

Table 17

combination	2x2 table			fisher's	accuracy	sensitivity	specificity	PPV	NPV
BLCAP TH1L CALM3		IBS	Normal	OR=19.39 $p< 2 \times 10^{-16}$	81.6%	82.7%	80.6%	81.0%	82.3%
	test > 0	81	19						
	test ? 0	17	79						
equation: -10.0504 + 8.4473* ΔCt_{BLCAP} - 5.4222* ΔCt_{TH1L} + 2.4570 * ΔCt_{CALM3}									
BLCAP TH1L UBE2G1		IBS	Normal	OR=33.38 $p< 2 \times 10^{-16}$	84.7%	89.8%	79.6%	81.5%	88.6%
	test > 0	88	20						
	test ? 0	10	78						
equation: -16.4275 + 5.0435* ΔCt_{BLCAP} - 4.4467* ΔCt_{TH1L} + 4.1683 * ΔCt_{UBE2G1}									
BLCAP TH1L HIST1H2BK		IBS	Normal	OR=27.62 $p< 2 \times 10^{-16}$	84.2%	84.5%	83.8%	83.7%	84.7%
	test > 0	82	16						
	test ? 0	15	83						
equation: -17.5471 + 8.2126* ΔCt_{BLCAP} - 4.2986* ΔCt_{TH1L} + 2.1835* $\Delta Ct_{HIST1H2BK}$									
BLCAP CALM3 UBE2G1		IBS	Normal	OR=17.68 $p< 2 \times 10^{-16}$	80.6%	84.7%	76.5%	78.3%	83.3%
	test > 0	83	23						
	test ? 0	15	75						
equation: -21.741 + 0.6081*ΔCt_{BLCAP} - 0.5865*ΔCt_{CALM3} + 3.933*ΔCt_{UBE2G1}									
BLCAP CALM3 HIST1H2BK		IBS	Normal	OR=15.86 $p< 2 \times 10^{-16}$	79.6%	84.7%	74.5%	76.9%	83.0%
	test > 0	83	25						
	test ? 0	15	73						
equation: -24.6537 + 4.4848* ΔCt_{BLCAP} - 2.1685* ΔCt_{CALM3} + 2.9207* $\Delta Ct_{HIST1H2BK}$									
BLCAP UBE2G1 HIST1H2BK		IBS	Normal	OR=14.30 $p=3.0 \times 10^{-16}$	78.6%	84.7%	72.4%	75.5%	82.6%
	test > 0	83	27						
	test ? 0	15	71						
equation: -27.6040 + 1.2774* ΔCt_{BLCAP} + 2.8181* ΔCt_{UBE2G1} + 1.7602* $\Delta Ct_{HIST1H2BK}$									
TH1L CALM3 UBE2G1		IBS	Normal	OR=14.43 $p< 2 \times 10^{-16}$	79.1%	82.7%	75.5%	77.1%	81.3%
	test > 0	81	24						
	test ? 0	17	74						
equation: -19.4675 - 2.5799* ΔCt_{TH1L} + 0.9379* ΔCt_{CALM3} + 6.1263* ΔCt_{UBE2G1}									
TH1L CALM3 HIST1H2BK		IBS	Normal	OR=4.94 $p=1.7 \times 10^{-7}$	68.9%	73.5%	64.3%	67.3%	70.8%
	test > 0	72	35						
	test ? 0	26	63						
equation: -17.0992 - 1.3345* ΔCt_{TH1L} - 0.1432* ΔCt_{CALM3} + 2.3132* $\Delta Ct_{HIST1H2BK}$									
TH1L UBE2G1 HIST1H2BK		IBS	Normal	OR=18.13 $p< 2 \times 10^{-16}$	80.6%	85.7%	75.5%	77.8%	84.1%
	test > 0	84	24						
	test ? 0	14	74						
equation: -23.9436 - 2.0622* ΔCt_{TH1L} + 5.8134* ΔCt_{UBE2G1} + 1.4056* $\Delta Ct_{HIST1H2BK}$									
CALM3 UBE2G1 HIST1H2BK		IBS	Normal	OR=14.70 $p< 2 \times 10^{-16}$	79.1%	83.7%	74.5%	76.6%	82.0%
	test > 0	82	25						
	test ? 0	16	73						
equation: -26.9573 - 1.7284* ΔCt_{CALM3} + 4.4926 ΔCt_{UBE2G1} + 2.016* $\Delta Ct_{HIST1H2BK}$									

We subsequently analyzed the biomarker performance based on expression levels of combinations of 5 of the 6 genes tested above (Examples 2A, 2B, and 3A), whose combination differentiates between normal and IBD patients (RAP1A, BLCAP, UBE2G1, CALM3, GPX1, and NONO).The classification matrix and diagnostic accuracy estimates of the combination for IBD v Normal, as well as exemplary gene weightings, are shown in **Table 18.** The equation and weightings for the 5-gene IBD vs Normal combination taught above (RAP1A, BLCAP, UBE2G1, CALM3, and GPX1, Example 2A) are identical to the first combination listed in Table 18. The performance measures in Tables 5a and 5b for set RAP1A, BLCAP, UBE2G1, CALM3, and GPX1) are slightly

different because additional patients were included in the Table 18 data: Table 5a summarizes results from 280 patients, and Table 18 summarizes results from 287 patients.

Table 18

combination	2x2 table			fisher's	accuracy	sensitivity	specificity	PPV	NPV
RAP1A BLCAP UBE2G1 GPX1 CALM3		IBD	Normal	OR=17.27 $p< 2 \times 10^{-16}$	81.9%	85.7%	74.5%	86.6%	73.0 %
	test > 0	162	25						
	test ? 0	27	73						
equation: -10.7716 + 3.2485* ΔCt_{RAP1A} + 5.4360* ΔCt_{BLCAP} – 3.4723*ΔCt_{UBE2G1} – 3.4642* ΔCt_{GPX1} + 3.3511* ΔCt_{CALM3}									
RAP1A UBE2G1 GPX1 CALM3 NONO		IBD	Normal	OR= 12.78 $p< 2 \times 10^{-16}$	79.8%	86.2%	67.3%	83.6%	71.7%
	test > 0	163	32						
	test ? 0	26	66						
equation: -24.3638 + 3.2362* ΔCt_{RAP1A} + 0.4716*ΔCt_{UBE2G1} – 2.2953* ΔCt_{GPX1} + 2.3207* ΔCt_{CALM3} + 2.3578* ΔCt_{NONO}									
RAP1A BLCAP GPX1 CALM3 NONO		IBD	Normal	OR=14.03 $p< 2 \times 10^{-16}$	80.5%	86.2%	69.4%	84.5%	72.3%
	test > 0	163	30						
	test ? 0	26	68						
equation: -22.0546 + 2.9300* ΔCt_{RAP1A} + 1.8471*ΔCt_{BLCAP} – 2.5939* ΔCt_{GPX1} + 2.0732* ΔCt_{CALM3} + 1.5925* ΔCt_{NONO}									
RAP1A BLCAP UBE2G1 CALM3 NONO		IBD	Normal	OR=9.40 $p=4.3x10^{-16}$	77.4%	84.7%	63.3%	81.6%	68.1%
	test > 0	160	36						
	test ? 0	29	62						
equation: -26.4580 + 4.3570* ΔCt_{RAP1A} + 2.2414*ΔCt_{BLCAP} – 1.0652* ΔCt_{UBE2G1}+ 0.2504* ΔCt_{CALM3} + 1.2175* ΔCt_{NONO}									
RAP1A BLCAP UBE2G1 GPX1 NONO		IBD	Normal	OR=15.28 $p< 2 \times 10^{-16}$	80.8%	84.1%	74.5%	86.4%	70.9%
	test > 0	159	25						
	test ? 0	30	73						
equation: -21.1203 + 4.7113* ΔCt_{RAP1A} + 3.8401*ΔCt_{BLCAP} – 1.7575* ΔCt_{UBE2G1} – 2.2260* ΔCt_{GPX1} + 1.2861* ΔCt_{NONO}									
BLCAP UBE2G1 GPX1 CALM3 NONO		IBD	Normal	OR=14.67 $p< 2 \times 10^{-16}$	80.8%	87.3%	68.4%	84.2%	73.6%
	test > 0	165	31						
	test ? 0	24	67						
equation: -9.0048 + 3.6181*ΔCt_{BLCAP} – 1.6280* ΔCt_{UBE2G1} – 3.6336* ΔCt_{GPX1} + 4.4814* ΔCt_{CALM3} + 0.8072* ΔCt_{NONO}									

5

We subsequently analyzed the biomarker performance based on expression levels of combinations of 6 of the 7 genes tested above (Examples 2E and 3C), whose combination differentiates between IBS and IBD patients (RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK1, PPP2R5A, and BLCAP).The classification matrix and diagnostic accuracy estimates of the combination for IBS v IBD, as well as exemplary gene weightings, are shown in **Table 19.**

Table 19

combination	2x2 table	fisher's	accuracy	sensitivity	specificity	PPV	NPV
RAP1A UBE2G1 CALM3 GPX1 HIST1H2BK PPP2R5A	IBD / IBS test > 0: 168 / 27 test ? 0: 21 / 71	OR=16.26 $p < 2 \times 10^{-16}$	81.5%	86.2%	72.4%	85.8%	73.2%
equation: $16.6895 + 5.155^* \Delta Ct_{RAP1A} - 2.5462^* \Delta Ct_{UBE2G1} + 4.8674^* \Delta Ct_{CALM3} - 2.3979^* \Delta Ct_{GPX1} - 2.8183^* \Delta Ct_{HIST1H2BK} - 2.9778^* \Delta Ct_{PPP2R5A}$							
RAP1A CALM3 GPX1 HIST1H2BK PPP2R5A BLCAP	IBD / IBS test > 0: 167 / 29 test ? 0: 22 / 69	OR= 17.80 $p < 2 \times 10^{-16}$	82.2%	88.4%	70.4%	85.2%	75.8%
equation: $13.2115 + 4.4136^* \Delta Ct_{RAP1A} + 4.8119^* \Delta Ct_{CALM3} - 2.1923^* \Delta Ct_{GPX1} - 3.0788^* \Delta Ct_{HIST1H2BK} - 3.2874^* \Delta Ct_{PPP2R5A} - 1.3537^* \Delta Ct_{BLCAP}$							
RAP1A UBE2G1 GPX1 HIST1H2BK PPP2R5A BLCAP	IBD / IBS test > 0: 168 / 29 test ? 0: 21 / 69	OR=18.75 $p < 2 \times 10^{-16}$	82.6%	88.9%	70.4%	85.3%	76.7%
equation: $14.9114 + 6.8342^* \Delta Ct_{RAP1A} - 6.6508^* \Delta Ct_{UBE2G1} - 1.5818^* \Delta Ct_{GPX1} - 1.3437^* \Delta Ct_{HIST1H2BK} - 2.0964^* \Delta Ct_{PPP2R5A} + 4.3897^* \Delta Ct_{BLCAP}$							
RAP1A UBE2G1 CALM3 HIST1H2BK PPP2R5A BLCAP	IBD / IBS test > 0: 171 / 31 test ? 0: 18 / 67	OR=20.22 $p < 2 \times 10^{-16}$	82.9%	90.5%	68.4%	84.7%	78.8%
equation: $6.224 + 7.0296^* \Delta Ct_{RAP1A} - 5.2346^* \Delta Ct_{UBE2G1} + 1.0171^* \Delta Ct_{CALM3} - 1.8810^* \Delta Ct_{HIST1H2BK} - 2.1413^* \Delta Ct_{PPP2R5A} + 2.7922^* \Delta Ct_{BLCAP}$							
RAP1A UBE2G1 CALM3 GPX1 PPP2R5A BLCAP	IBD / IBS test > 0: 166 / 29 test ? 0: 23 / 69	OR=16.93 $p < 2 \times 10^{-16}$	81.9%	87.8%	70.4%	85.1%	75.0%
equation: $14.1274 + 5.8613^* \Delta Ct_{RAP1A} - 7.1962^* \Delta Ct_{UBE2G1} + 1.1262^* \Delta Ct_{CALM3} - 2.1478^* \Delta Ct_{GPX1} - 2.2727^* \Delta Ct_{PPP2R5A} + 4.7122^* \Delta Ct_{BLCAP}$							
UBE2G1 CALM3 GPX1 HIST1H2BK PPP2R5A BLCAP	IBD / IBS test > 0: 165 / 39 test ? 0: 24 / 59	OR=10.29 $p < 2 \times 10^{-16}$	78.0%	87.3%	60.2%	80.9%	71.1%
equation: $21.6433 - 3.1122^* \Delta Ct_{UBE2G1} + 5.9519^* \Delta Ct_{CALM3} - 3.2758^* \Delta Ct_{GPX1} - 2.2307^* \Delta Ct_{HIST1H2BK} - 1.2969^* \Delta Ct_{PPP2R5A} + 1.5055^* \Delta Ct_{BLCAP}$							
RAP1A UBE2G1 CALM3 GPX1 HIST1H2BK BLCAP	IBD / IBS test > 0: 164 / 29 test ? 0: 25 / 69	OR=15.40 $p < 2 \times 10^{-16}$	81.2%	86.8%	70.4%	85.0%	73.4%
equation: $12.5376 + 4.5779^* \Delta Ct_{RAP1A} - 6.7553^* \Delta Ct_{UBE2G1} + 2.5618^* \Delta Ct_{CALM3} - 2.1679^* \Delta Ct_{GPX1} - 1.9711^* \Delta Ct$							

We claim:

1. A biomarker consisting of between 2 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3); and

(b) a second probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:11 (HIST1H2AC), SEQ ID NO:12 (TFE3), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:13 (NONO), SEQ ID NO:14 (PCBP1), SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:10 (PPP2R5A), SEQ ID NO:15 (PGRMC1), SEQ ID NO:3 (BLCAP), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:16 (HMGB1), and SEQ ID NO:6 (CALM3),

wherein the first probe set and the second probe set do not selectively hybridize to the same nucleic acid.

2. The biomarker of claim 1, wherein a third probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first probe set, the second probe set, and the third probe set selectively hybridize to the same nucleic acid.

3. The biomarker of claim 2, wherein a fourth probe set that selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first probe set, the second probe set, the third probe set, and the fourth probe set selectively hybridize to the same nucleic acid.

4. The biomarker of claim 3, wherein a fifth probe set selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of TH1L,

HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3; and

wherein none of the first probe set, the second probe set, the third probe set, the fourth probe set and the fifth probe set selectively hybridize to the same nucleic acid.

5. The biomarker of claim 4, wherein a sixth probe set selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first probe set, the second probe set, the third probe, the fourth probe set, the fifth probe set, and the sixth probe set selectively hybridize to the same nucleic acid.

6. The biomarker of claim 5, wherein a seventh probe set selectively hybridizes under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first probe set, the second probe set, the third probe, the fourth probe set, the fifth probe set, the sixth probe set, and the seventh probe set selectively hybridize to the same nucleic acid.

7. The biomarker of any one of claims 2-4, wherein the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3.

8. The biomarker of claim 3 wherein the first probe set selectively hybridizes under high stringency conditions to BLCAP, the second probe set selectively hybridizes under high stringency conditions to TH1L, the third probe set selectively hybridizes under high stringency conditions to UBE2G1, and the fourth probe set selectively hybridizes under high stringency conditions to HIST1H2BK.

9. The biomarker of claim 4 or 5, wherein the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO.

10. The biomarker of claim 5 wherein the first probe set selectively hybridizes under high stringency conditions to RAP1A, the second probe set selectively hybridizes under high stringency conditions to BLCAP, the third probe set selectively hybridizes under high stringency conditions to UBE2G1, the fourth probe set selectively hybridizes under

high stringency conditions to CALM3, the fifth probe set selectively hybridizes under high stringency conditions to GPX1, and the sixth probe set selectively hybridizes to NONO.

11. The biomarker of claim 5 or 6, wherein the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A.

12. The biomarker of claim 6 wherein the first probe set selectively hybridizes under high stringency conditions to RAP1A, the second probe set selectively hybridizes under high stringency conditions to BLCAP, the third probe set selectively hybridizes under high stringency conditions to UBE2G1, the fourth probe set selectively hybridizes under high stringency conditions to CALM3, the fifth probe set selectively hybridizes under high stringency conditions to GPX1, the sixth probe set selectively hybridizes under high stringency conditions to HIST1H2BK, and the seventh probe set selectively hybridizes under high stringency conditions to PPP2RR5A.

13. A biomarker, comprising:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3; and

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein the first primer pair and the second primer pair do not selectively amplify the same nucleic acid.

14. The biomarker of claim 13, further comprising a third primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first primer pair, the second primer pair, and the third primer pair selectively amplify the same nucleic acid.

15. The biomarker of claim 14, further comprising a fourth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group

consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first primer pair, the second primer pair, the third primer pair, and the fourth primer pair selectively amplify the same nucleic acid.

16. The biomarker of claim 15, further comprising a fifth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first primer pair, the second primer pair, the third primer pair the fourth primer pair, and the fifth primer pair selectively amplify the same nucleic acid.

17. The biomarker of claim 16, further comprising a sixth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first primer pair, the second primer pair, the third primer pair the fourth primer pair, the fifth primer pair, and the sixth primer pair selectively amplify the same nucleic acid.

18. The biomarker of claim 17, further comprising a seventh primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3,

wherein none of the first primer pair, the second primer pair, the third primer pair the fourth primer pair, the fifth primer pair, the sixth primer pair, and the seventh primer pair selectively amplify the same nucleic acid.

19. The biomarker of any one of claims 14-16, wherein the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3.

20. The biomarker of claim 15 wherein the first primer pair selectively amplifies a detectable portion of BLCAP, the second primer pair selectively amplifies a detectable portion of TH1L, the third primer pair selectively amplifies a detectable portion of UBE2G1, and the fourth primer pair selectively amplifies a detectable portion of HIST1H2BK.

21. The biomarker of any one of claims 16-17 wherein the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO.

22. The biomarker of claim 17 wherein the first primer pair selectively amplifies a detectable portion of RAP1A, the second primer pair selectively amplifies a detectable portion of BLCAP, the third primer pair selectively amplifies a detectable portion of UBE2G1, the fourth primer pair selectively amplifies a detectable portion of CALM3, the fifth primer pair selectively amplifies a detectable portion of GPX1, and the sixth primer pair selectively amplifies a detectable portion of NONO

23. The biomarker of any one of claims 17-18 wherein the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A.

24. The biomarker of claim 18 wherein the primer pair selectively amplifies a detectable portion of RAP1A, the second primer pair selectively amplifies a detectable portion of BLCAP, the third probe set primer pair selectively amplifies a detectable portion of UBE2G1, the fourth primer pair selectively amplifies a detectable portion of CALM3, the fifth primer pair selectively amplifies a detectable portion of GPX1; the sixth primer pair selectively amplifies a detectable portion of HIST1H2BK, and the seventh primer pair selectively amplifies a detectable portion of PPP2RR5A.

25. A method for diagnosing IBD and/or IBS comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD or IBS under hybridizing conditions with 2 or more probes sets, wherein at least a first probe set and a second probe set selectively hybridize under high stringency conditions to a nucleic acid target selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3; wherein the first probe set and the second probe set do not selectively hybridize to the same nucleic acid;

(b) detecting formation of hybridization complexes between the 2 or more probe sets and nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD, IBS, or neither based on the gene expression of the nucleic acid targets.

26. The method of claim 25, wherein the two or more probe sets comprise at least 3 probe sets, and wherein none of the first probe set, the second probe set, and the third probe set selectively hybridize to the same nucleic acid.

27. The method of claim 26, wherein the two or more probe sets comprise at least 4 probe sets, and wherein none of the first probe set, the second probe set, the third probe set, and the fourth probe set selectively hybridize to the same nucleic acid.

28. The method of claim 27, wherein the two or more probe sets comprise at least 5 probe sets, and wherein none of the first probe set, the second probe set, the third probe set, the fourth probe set, and the fifth probe set selectively hybridize to the same nucleic acid.

29. The method of claim 28, wherein the two or more probe sets comprise at least 6 probe sets, and wherein none of the first probe set, the second probe set, the third probe set, the fourth probe set, fifth probe set, and the sixth probe set selectively hybridize to the same nucleic acid.

30. The method of claim 29, wherein the two or more probe sets comprise at least 7 probe sets, and wherein none of the first probe set, the second probe set, the third probe set, the fourth probe set, fifth probe set, the sixth probe set, and the seventh probe set selectively hybridize to the same nucleic acid.

31. The method of any one of claims 26-28, wherein the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3, wherein the method distinguishes normal subjects from those subjects suffering from IBS.

32. The method of claim 27 wherein the first probe set selectively hybridizes under high stringency conditions to BLCAP, the second probe set selectively hybridizes under high stringency conditions to TH1L, the third probe set selectively hybridizes under high stringency conditions to UBE2G1, and the fourth probe set selectively hybridizes under high stringency conditions to HIST1H2BK, and wherein the method distinguishes normal subjects from those subjects suffering from IBS.

33. The method of claim 28 or 29 wherein the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO, wherein the method distinguishes normal subjects from those subjects suffering from IBD.

33. The method of claim 29 wherein the first probe set selectively hybridizes under high stringency conditions to RAP1A, the second probe set selectively hybridizes under high stringency conditions to BLCAP, the third probe set selectively hybridizes under high stringency conditions to UBE2G1, the fourth probe set selectively hybridizes under high stringency conditions to CALM3, the fifth probe set selectively hybridizes under high stringency conditions to GPX1, and the fifth probe set selectively hybridizes under high stringency conditions to NONO, wherein the method distinguishes normal subjects from those subjects suffering from IBD.

34. The method of claim 28 or 29 wherein the probe sets selectively hybridize under high stringency conditions to a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A, wherein the method distinguishes those subjects suffering from IBS from those subjects suffering from IBD.

35. The method of claim 29 wherein the first probe set selectively hybridizes under high stringency conditions to RAP1A, the second probe set selectively hybridizes under high stringency conditions to BLCAP, the third probe set selectively hybridizes under high stringency conditions to UBE2G1, the fourth probe set selectively hybridizes under high stringency conditions to CALM3, the fifth probe set selectively hybridizes under high stringency conditions to GPX1, the sixth probe set selectively hybridizes under high stringency conditions to HIST1H2BK, and the seventh probe set selectively hybridizes under high stringency conditions to PPP2RR5A.

36. A method for diagnosing IBD and/or IBS comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD or IBS under amplifying conditions with 2 or more primer pairs, wherein at least a first primer pair and a second primer pair are capable of selectively amplifying a detectable portion of a nucleic acid target selected from the group consisting of TH1L, HIST1H2AC, TFE3, HIST1H2BK, UBE2G1, NONO, PCBP1, RAP1A, PPP2R5A, PGRMC1, BLCAP, GPX1, HMGB1, and CALM3; wherein the first primer pair and the second primer pair do not selectively amplify the same nucleic acid;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the two or more primer pairs, wherein the amplification products provide a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD, IBS, or neither based on the gene expression of the nucleic acid targets.

37. The method of claim 36, wherein the two or more primer pairs comprise at least three primer pairs, wherein none of the first primer pair, the second primer pair, and the third primer pair selectively amplify the same nucleic acid.

38. The method of claim 37, wherein the two or more primer pairs comprise at least four primer pairs, wherein none of the first primer pair, the second primer pair, the third primer pair, and the fourth primer pair selectively amplify the same nucleic acid.

39. The method of claim 38, wherein the two or more primer pairs comprise at least five primer pairs, wherein none of the first primer pair, the second primer pair, the third primer pair, the fourth primer pair, and the fifth primer pair selectively amplify the same nucleic acid.

40. The method of claim 39, wherein the two or more primer pairs comprise at least six primer pairs, wherein none of the first primer pair, the second primer pair, the third primer pair, the fourth primer pair, the fifth primer pair, and the sixth primer pair selectively amplify the same nucleic acid.

41. The method of claim 40, wherein the two or more primer pairs comprise at least seven primer pairs, wherein none of the first primer pair, the second primer pair, the third primer pair, the fourth primer pair, the fifth primer pair, the sixth primer pair, and the seventh primer pair selectively amplify the same nucleic acid.

42. The method of any one of claims 37-39 wherein the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of TH1L, HIST1H2BK, UBE2G1, BLCAP, and CALM3, wherein the method distinguishes normal subjects from those subjects suffering from IBS.

43. The method of claim 38 wherein the first primer pair selectively amplifies a detectable portion of BLCAP, the second primer pair selectively amplifies a detectable portion of TH1L, the third primer pair selectively amplifies a detectable portion of UBE2G1 and the fourth primer pair selectively amplifies a detectable portion of HIST1H2BK.

44. The method of claim 39 or 40 wherein the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, GPX1, CALM3, and NONO, wherein the method distinguishes normal subjects from those subjects suffering from IBD

45. The method of claim 40 wherein the first primer pair selectively amplifies a detectable portion of RAP1A, the second primer pair selectively amplifies a detectable portion of BLCAP, the third primer pair selectively amplifies a detectable portion of UBE2G1, the fourth primer pair selectively amplifies a detectable portion of CALM3, the fifth primer pair selectively amplifies a detectable portion of GPX1, and the sixth primer pair selectively amplifies a detectable portion of NONO.

46. The method of claim 40 or 41 wherein the primer pairs selectively amplify a detectable portion of a nucleic acid selected from the group consisting of RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, and PPP2R5A, wherein the method distinguishes those subjects suffering from IBS from those subjects suffering from IBD.

47. The method of claim 41 wherein the primer pair selectively amplifies a detectable portion of RAP1A, the second primer pair selectively amplifies a detectable portion of BLCAP, the third probe set primer pair selectively amplifies a detectable portion of UBE2G1, the fourth primer pair selectively amplifies a detectable portion of CALM3, the fifth primer pair selectively amplifies a detectable portion of GPX1, the sixth primer pair selectively amplifies a detectable portion of HIST1H2BK, and the seventh primer pair selectively amplifies a detectable portion of PPP2RR5A.

48. The method of any one of claims 25-35, wherein diagnosing whether the subject is likely to have IBD, IBS, or neither based on the amplification of the nucleic acid targets comprises analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

49. The method of any one of claims 36-47, wherein diagnosing whether the subject is likely to have IBD, IBS, or neither based on the amplification of the nucleic acid targets comprises analyzing the amplification products by applying a weight to the number of amplification products formed for each nucleic acid target.

50. A biomarker consisting of between 3 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

(b) a second probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting

of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof; and

(c) a third probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

wherein each of the between 3 and 35 different probe sets consists of one or more probes of 15 or more contiguous nucleotides, or full complements thereof, of a single mRNA different from that of the other probe sets, and wherein each of the different probe sets is optionally detectably labeled.

51. The biomarker of claim 50, wherein the first probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; the second probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of TH1L, or a full complement thereof; the third probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; and a fourth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof.

52. A biomarker consisting of between 3 and 35 different nucleic acid primer pairs, wherein:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), wherein each primer in the second primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof; and

(c) a third primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), wherein each primer in the third primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

wherein each of the between 3 and 35 different primer pairs consists of one or more primer pairs of 15 or more contiguous nucleotides, or full complements thereof, for a single mRNA different from that of the other primer pairs, and wherein each of the different primer pairs is optionally detectably labeled.

53. The biomarker of claim 52, wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; each primer in the second primer pair consists of 15 or more contiguous nucleotides of TH1L, or a full complement thereof; each primer in the third primer pair consists of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; and each primer in a fourth primer pair consists of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof.

54. A method for diagnosing irritable bowel syndrome (IBS), comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBS under hybridizing conditions with at least 3 nucleotide probes, wherein a first nucleotide probe, a second nucleotide probe, and a third nucleotide probe each consist of 15 or more contiguous nucleotides of a nucleic acid target selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof, wherein each of the first, second, and third nucleotide probes consist of 15 or more contiguous nucleotides of a different nucleic acid target;

(b) detecting formation of hybridization complexes between the probes and the nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBS based on the measure of gene expression of the nucleic acid targets.

55. The method of claim 54, wherein the nucleic acid targets comprise BLCAP, TH1L, UBE2G1, and HIST1H2BK.

56. The method of claim 54 or 55, wherein the subject suffers from one or more of abdominal pain, constipation, diarrhea, and a change in bowel habits.

57. The method of any one of claims 54-56, wherein the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells red blood cell-depleted whole blood.

58. The method of any one of claims 54-57, further comprising analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

59. A method for diagnosing irritable bowel syndrome (IBS), comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBS under amplifying conditions with at least three primer pairs, wherein a first primer pair, a second primer pair, and a third primer pair selectively amplify a different nucleic acid target selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof, wherein each primer in each primer pair consists of at least 15 contiguous nucleotides of its respective nucleic acid target;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the at least three primer pairs, wherein a number of such amplification products provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBS based on the measure of gene expression of the nucleic acid targets.

60. The method of claim 59, wherein the nucleic acid targets comprise BLCAP, TH1L, UBE2G1, and HIST1H2BK.

61. The method of claim 59 or 60, wherein the subject suffers from one or more of abdominal pain, constipation, diarrhea, and a change in bowel habits.

62. The method of any one of claims 59-61, wherein the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells red blood cell-depleted whole blood.

63. The method of any one of claims 59-62, further comprising analyzing gene expression of the nucleic acid targets by applying a weight to the number of amplification products formed for each nucleic acid target.

64. A biomarker consisting of between 5 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(b) a second probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(c) a third probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(d) a fourth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof; and

(e) a fifth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

wherein each of the between 5 and 35 different probe sets consists of one or more probes of 15 or more contiguous nucleotides, or full complements thereof, of a single

mRNA different from that of the other probe sets, and wherein each of the different probe sets is optionally detectably labeled.

65. The biomarker of claim 64, wherein the first probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; the second probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; the third probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; the fourth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; the fifth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of GPX1, or a full complement thereof; and a sixth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of NONO or a full complement thereof.

66. A biomarker consisting of between 5 and 35 different nucleic acid primer pairs, wherein:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO)), wherein each primer in the second primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:4 (TH1L), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:5 (UBE2G1), SEQ ID NO:3 (BLCAP), and SEQ ID NO:6 (CALM3), or a full complement thereof;

(c) a third primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A),

SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the third primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

(d) a fourth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof; and

(e) a fifth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), wherein each primer in the fifth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof;

wherein each of the between 5 and 35 different primer pairs consists of one or more primer pairs of 15 or more contiguous nucleotides, or full complements thereof, for a single mRNA different from that of the other primer pairs, and wherein each of the different primer pairs is optionally detectably labeled.

67. The biomarker of claim 66, wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; each primer in the second primer pair consists of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof; each primer in the third primer pair consists of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; each primer in the fifth primer pair consists of 15 or more

contiguous nucleotides of GPX1, or a full complement thereof; and each primer in a sixth primer pair consists of 15 or more contiguous nucleotides of NONO, or a full complement thereof.

68. A method for diagnosing inflammatory bowel disease (IBD), comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under hybridizing conditions with at least 5 nucleotide probes, wherein a first nucleotide probe, a second nucleotide probe, a third nucleotide probe, a fourth nucleotide probe, and a fifth nucleotide probe each consist of 15 or more contiguous nucleotides of a nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof, wherein each of the first, second, third, fourth, and fifth nucleotide probes consist of 15 or more contiguous nucleotides of a different nucleic acid target;

(b) detecting formation of hybridization complexes between the nucleotide probes and the nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD based on the measure of gene expression of the nucleic acid targets.

69. The method of claim 168, wherein the nucleic acid targets comprise RAP1A, BLCAP, UBE2G1, CALM3, GPX1, and NONO.

70. The method of claim 68 or 69, wherein the subject suffers from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change.

71. The method of any one of claims 68-70, wherein the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood.

72. The method of any one of claims 68-71, further comprising analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

73. A method for diagnosing inflammatory bowel disease (IBD), comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under amplifying conditions with at least five primer pairs,

wherein a first primer pair, a second primer pair, a third primer, a fourth primer pair, and a fifth primer pair each selectively amplify a different nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:3 (BLCAP), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), and SEQ ID NO:13 (NONO), or a full complement thereof, wherein each primer in each primer pair consists of at least 15 contiguous nucleotides of its respective nucleic acid target;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the at least five primer pairs, wherein a number of such amplification products provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD based on the measure of gene expression of the nucleic acid targets.

74. The method of claim 73, wherein the nucleic acid targets comprise RAP1A, BLCAP, UBE2G1, CALM3, GPX1, and NONO.

75. The method of claim 73 or 74, wherein the subject suffers from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change.

76. The method of any one of claims 73-75, wherein the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood.

77. The method of any one of claims 73-76, further comprising analyzing gene expression of the nucleic acid targets by applying a weight to the number of amplification products formed for each nucleic acid target.

78. A biomarker consisting of between 6 and 35 different nucleic acid probe sets, wherein:

(a) a first probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(b) a second probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3),

SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(c) a third probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(d) a fourth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(e) a fifth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof; and

(f) a sixth probe set consisting of one or more nucleotide probes consisting of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

wherein each of the between 6 and 35 different probe sets consists of one or more probes of 15 or more contiguous nucleotides, or full complements thereof, of a single mRNA different from that of the other probe sets, and wherein each of the different probe sets is optionally detectably labeled.

79. The biomarker of claim 78, wherein the first probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; the second probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; the third probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; the fourth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of GPX1, or a full complement

thereof; the fifth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof; the sixth probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of PPP2R5A, or a full complement thereof; and a seventh probe set consists of one or more nucleotide probes of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof.

80. A biomarker consisting of between 6 and 35 different nucleic acid primer pairs, wherein:

(a) a first primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(b) a second primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the second primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(c) a third primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the third primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8

(GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(d) a fourth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

(e) a fifth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the fifth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof; and

(f) a sixth primer pair capable of selectively amplifying a detectable portion of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), wherein each primer in the sixth primer pair consists of 15 or more contiguous nucleotides of a nucleic acid selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof;

wherein each of the between 6 and 35 different primer pairs consists of one or more primer pairs of 15 or more contiguous nucleotides, or full complements thereof, for a single mRNA different from that of the other primer pairs, and wherein each of the different primer pairs is optionally detectably labeled.

81. The biomarker of claim 80, wherein each primer in the first primer pair consists of 15 or more contiguous nucleotides of RAP1A, or a full complement thereof; each primer in the second primer pair consists of 15 or more contiguous nucleotides of UBE2G1, or a full complement thereof; each primer in the third primer pair consists of 15 or more contiguous nucleotides of CALM3, or a full complement thereof; each primer in the fourth primer pair consists of 15 or more contiguous nucleotides of GPX1, or a full complement thereof; each primer in the fifth primer pair consists of 15 or more contiguous nucleotides of HIST1H2BK, or a full complement thereof; each primer in the sixth primer pair consists of 15 or more contiguous nucleotides of PPP2R5A, or a full complement thereof; and wherein each primer in a seventh primer pair consists of 15 or more contiguous nucleotides of BLCAP, or a full complement thereof.

82. A method for differentiating between inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS) in a subject, comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under hybridizing conditions with at least 6 nucleotide probes, wherein a first nucleotide probe, a second nucleotide probe, a third nucleotide probe, a fourth nucleotide probe, a fifth nucleotide probe, and a sixth nucleotide probe each consist of 15 or more contiguous nucleotides of a nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof; wherein each of the first, second, third, fourth, fifth, and sixth nucleotide probes consist of 15 or more contiguous nucleotides of a different nucleic acid target;

(b) detecting formation of hybridization complexes between the nucleotide probes and the nucleic acid targets in the nucleic acid sample, wherein a number of such hybridization complexes provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD or IBS based on the measure of gene expression of the nucleic acid targets.

83. The method of claim 82, wherein the nucleic acid targets comprise RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A, and BLCAP.

84. The method of claim 82 or 83, wherein the subject suffers from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change.

85. The method of any one of claims 82-84, wherein the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood.

86. The method of any one of claims 82-85, further comprising analyzing gene expression of the nucleic acid targets by applying a weight to the number of hybridization complexes formed for each nucleic acid target.

87. A method for differentiating between inflammatory bowel disease (IBD) and irritable bowel syndrome (IBS) in a subject, comprising:

(a) contacting a mRNA-derived nucleic acid sample obtained from a subject suspected of having IBD under amplifying conditions with at least six primer pairs, wherein a first primer pair, a second primer pair, a third primer, a fourth primer pair, a fifth primer pair, and a sixth primer pair each selectively amplify a different nucleic acid target selected from the group consisting of SEQ ID NO:1 and/or 2 (RAP1A), SEQ ID NO:5 (UBE2G1), SEQ ID NO:6 (CALM3), SEQ ID NO:7 and/or 8 (GPX1), SEQ ID NO:9 (HIST1H2BK), SEQ ID NO:10 (PPP2R5A), and SEQ ID NO:3 (BLCAP), or a full complement thereof, wherein each primer in each primer pair consists of at least 15 contiguous nucleotides of its respective nucleic acid target;

(b) detecting amplification products generated by amplification of nucleic acid targets in the nucleic acid sample by the at least six primer pairs, wherein a number of such amplification products provides a measure of gene expression of the nucleic acid targets; and

(c) diagnosing whether the subject is likely to have IBD or IBS based on the measure of gene expression of the nucleic acid targets.

88. The method of claim 87, wherein the nucleic acid targets comprise RAP1A, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A, and BLCAP.

89. The method of claim 87 or 88, wherein the subject suffers from one or more of abdominal pain, constipation, diarrhea, a change in bowel habits, vomiting, hematochezia, and weight change.

90. The method of any one of claims 87-89, wherein the mRNA-derived nucleic acid sample is obtained from peripheral blood mononuclear cells or red blood cell-depleted whole blood.

91. The method of any one of claims 87-90, further comprising analyzing gene expression of the nucleic acid targets by applying a weight to the number of amplification products formed for each nucleic acid target.

Figure 1

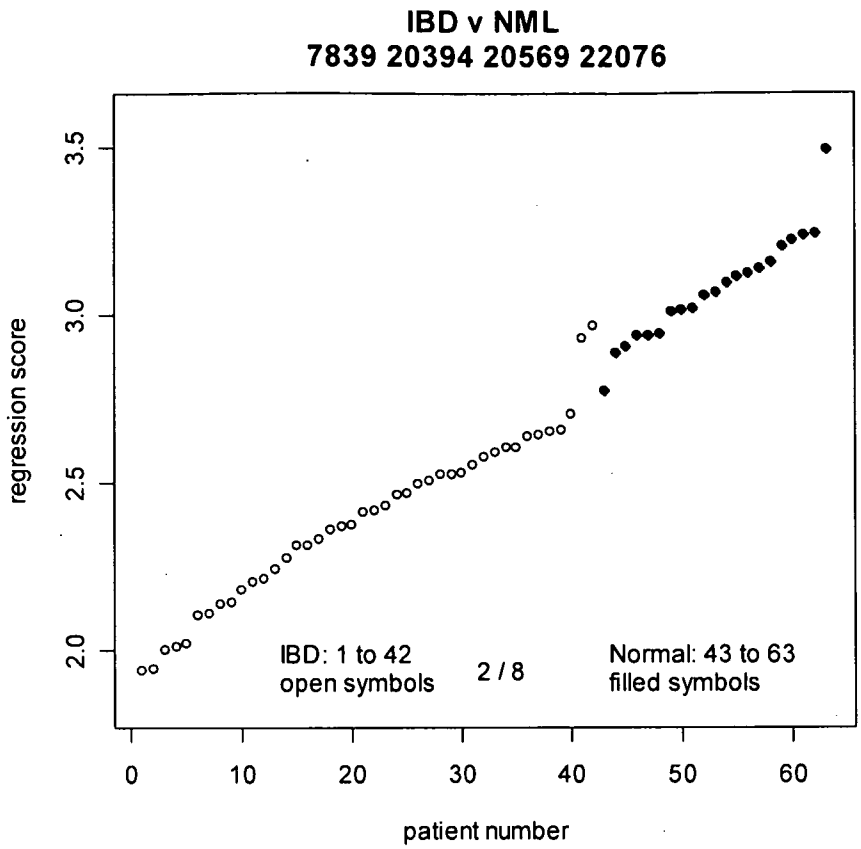
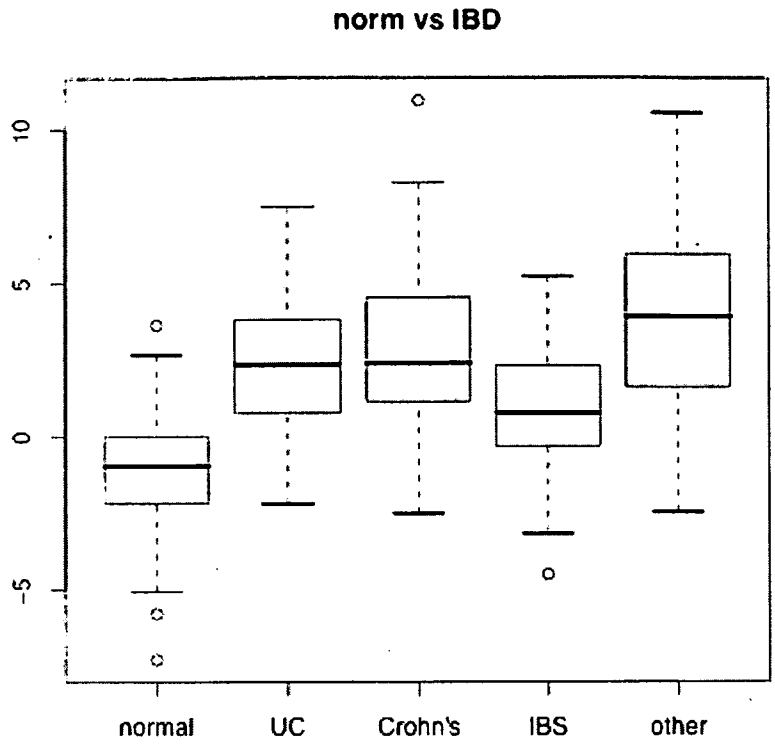
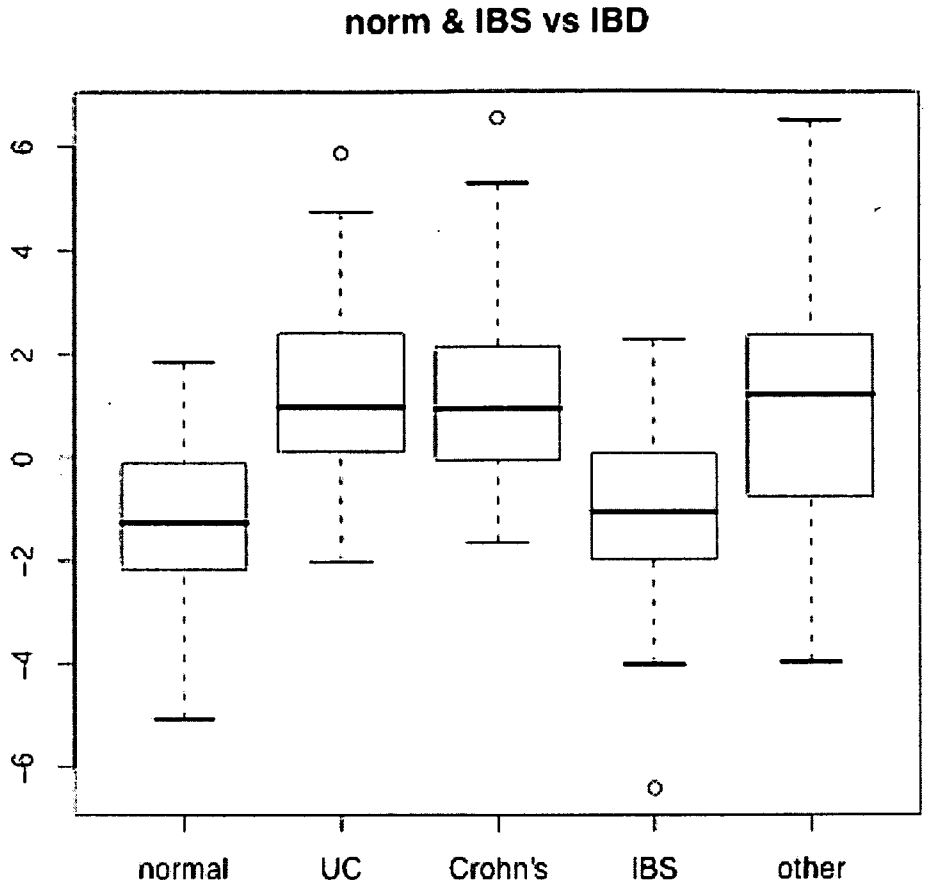

IBD v NML
7839 20394 20569 22076
regression score
2.0
2.5
3.0
3.5
IBD: 1 to 42
open symbols
2 / 8
Normal: 43 to 63
filled symbols
0
10
20
30
40
50
60
patient number

Figure 2



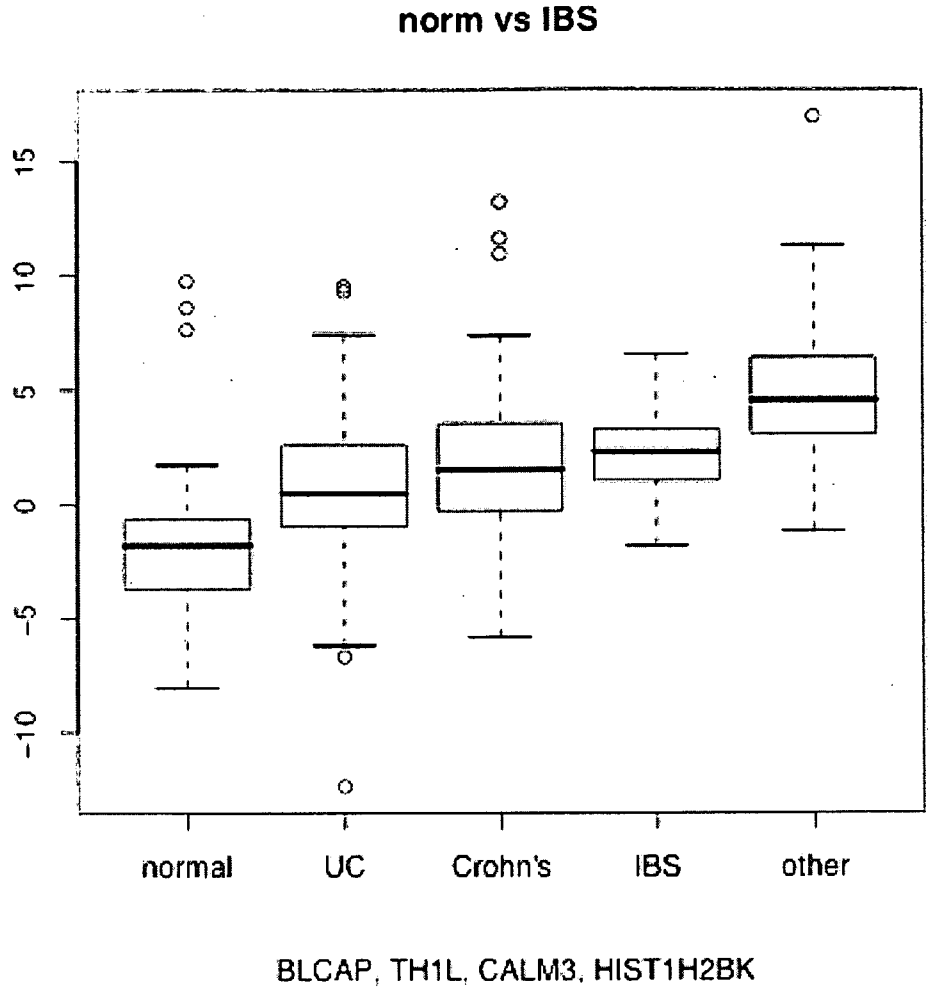
RAP1A, BLCAP, UBE2G1, CALM3, GPX1

Figure 3



RAP1A, BLCAP, UBE2G1, CALM3, GPX1, HIST1H2BK, PPP2R5A

Figure 4


norm vs IBS
15
10
5
0
−5
−10
normal
UC
Crohn's
IBS
other
BLCAP, TH1L, CALM3, HIST1H2BK

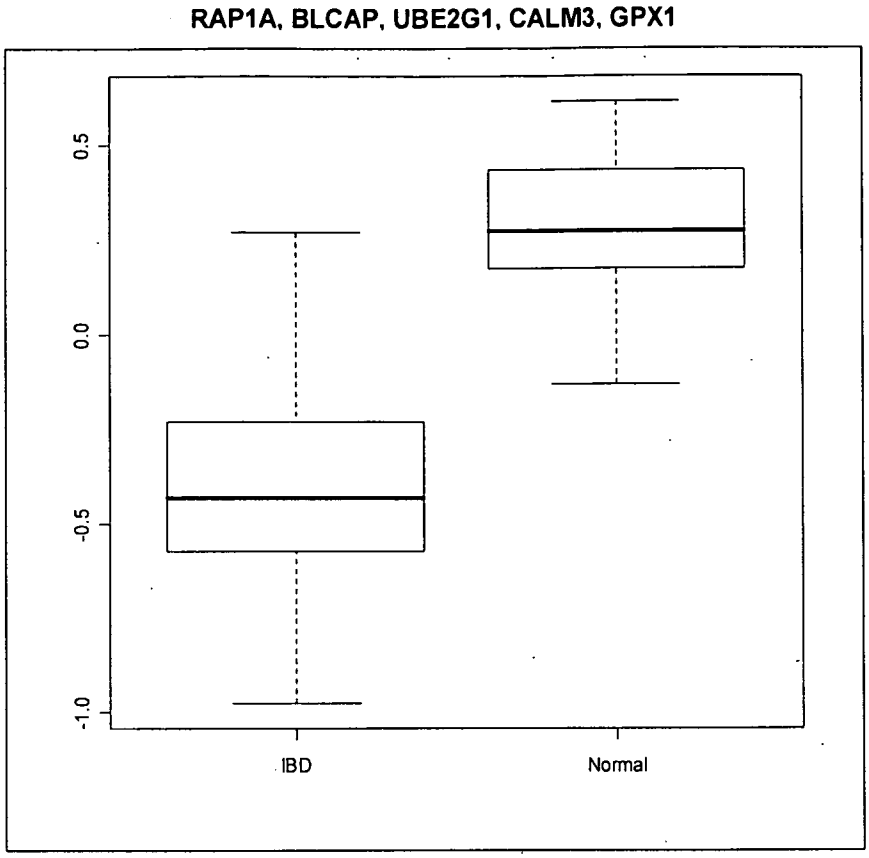



Figure 5