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(54) Title: METHODS, SYSTEMS, AND KITS FOR TREATING INFLAMMATORY DISEASE TARGETING IL18R1

FIG. 1A

Populatio n	PHENOT YPE	Marker	dbSNP	p value	AI	n miss	OR Z B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl beta	eqtl p	priorit y
CD	CD vs. Ctrl	imm_2_10230 5468	rs130013 25	3.98E-31	A	94040	0.123564 214	10293903 6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232 4148	rs142010 1	6.93E-31	A	94080	0.123034 419	10295771 6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 5593	rs124792 10	1.16E-30	A	94088	0.122583 046	10294916 1	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 8994	rs950880	5.12E-30	A	94092	0.121212 221	10293256 2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 8258	rs130205 53	6.50E-30	G	94088	0.121288 712	10293182 6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 7254	rs130190 81	2.26E-28	C	91372	0.120586 459	10295082 2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 9499	rs127121 41	1.13E-27	A	94101	0.111190 719	10295306 7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 5460	rs228703 7	2.12E-27	A	90448	0.117902 413	10297902 8	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 5251	rs142010 2	2.63E-27	G	94059	0.110446 109	10294881 9	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 5371	rs124663 80	3.92E-27	A	94097	0.110032 167	10294893 9	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 7505	rs199746 7	4.14E-27	A	94088	0.109983 326	10295107 3	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 7982	rs155861 9	4.35E-27	C	94094	0.109929 235	10293155 0	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10230 5866	rs142008 8	4.47E-27	A	94092	0.109908 721	10293943 4	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 0561	rs129993 64	5.26E-27	A	94085	0.113865 41	10297412 9	intronic	NA	NA	NA	NA

(57) Abstract: Described herein are methods, systems, compositions, and kits useful for the diagnosis and/or treatment of a disease or condition in a subject. The present disclosure relates to methods and systems for identifying and stratifying patients suitable for treatment with an IL18R1 modulator, as described herein.

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METHODS, SYSTEMS, AND KITS FOR TREATING INFLAMMATORY DISEASE TARGETING IL18R1

CROSS-REFERENCE

[001] This application claims the benefit of U.S. Provisional Application No. 62/802,828 filed February 8, 2019 and U.S. Provisional Application No. 62/815,223 filed March 7, 2019, which are incorporated by reference herein in their entirety.

SEQUENCE LISTING

[002] This application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on January 28, 2020, is named 52388-751_601_SL.txt and is 19,985 bytes in size.

SUMMARY

[003] Inflammatory bowel diseases (IBD) is a heterogeneous group of chronic, relapsing inflammatory disorders of the gastrointestinal (GI) tract affecting more than 3 million adults in the United States, according to the most recent Centers for Disease and Prevention (CDC) survey. The two most common manifestations of IBD are Crohn's disease (CD) and ulcerative colitis (UC). Each of these forms of IBD has various subclinical phenotypes that manifest in certain IBD patients. For example, the chronic inflammation of the GI tract caused by CD and UC leads to the formation of scar tissue (fibrosis) and stenosis (fibrostenosis) in the intestinal wall in some IBD patients, that is largely unresponsive to current therapeutic interventions. For these patients endoscopic or surgical treatment is often the only treatment available.

[004] IBD, including CD and UC, is characterized by an uncontrolled activity of the immune response within the intestinal mucosal, which depends on genetic susceptibility to developing the IBD, subclinical phenotypes of IBD, as well as to various stimuli related to IBD pathogenesis (*e.g.*, intestinal microbiome). Genome Wide Association Studies (GWAS) have enabled scientists to identify genetic variants in certain IBD susceptibility gene loci useful for the selection of IBD patients for treatment with targeted therapeutic strategies, and identifying drugable targets in the development of novel therapies.

[005] Few treatment options are available to patients that suffer from IBD. Current therapeutic regimens include one or more of anti-inflammatory medication (*e.g.*, corticosteroids) and immunomodulatory therapy (*e.g.*, anti-TNF therapy). However, nearly half of all patients treated with an anti-TNF therapy do not respond to the induction of the therapy, or experience a loss of response to the treatment after a period of time, during which, disease severity has progressed significantly. Therefore, there remains a significant need for targeted and effective treatment options that respond to the underlying immunopathogenesis of IBD.

[0006] Interleukin 18 (IL18) is a member of the IL-1 cytokine family, which consists of eleven members that play important roles in regulating inflammation, including IL-1 alpha, IL-1 beta, IL-1ra, IL-18, IL-33, IL-36Ra, IL-36 alpha, IL-36 beta, IL-36 gamma, IL-37, and IL-38. While most of these cytokines are biologically active as full-length molecules, activation and secretion of IL-1 beta and IL18 requires inflammasome/Caspase-1-dependent processing. IL18R1 specifically binds IL18, and is essential for IL18 mediated signal transduction. In normal tissues IL-18 can be found in whole blood and in epithelium of the lung and small intestine.

[0007] The IL18 receptor (IL-18R) is composed of two subunits, IL18 receptor alpha (IL-18R α) and IL18R β (or IL-18Rap), both of which consist of three extracellular immunoglobulin-like domains and one intracellular Toll/IL-1 receptor (TIR) domain. Ligand binding triggers receptor heterodimerization and initiates downstream signaling events via the two TIR domains, which recruit MyD88 and signal through IL-1R-associated kinases (IRAK) to initiate p38 MAPK and NF- κ B-mediated responses.

[0008] IL-18 expression is increased in mucosal biopsies of IBD patients compared with those of control patients, and increased in inflamed versus noninflamed intestinal tissues of IBD patients. IL18 in IBD may be found in intestinal epithelial cells, and lamina propria (LP) macrophages and dendritic cells in more severe disease state. High levels of IL18 expression in lymphoid follicles in the LP of CD patients has been found in close association with CD4⁺ T cells.

[0009] IL18 is critical in driving the pathologic breakdown of barrier integrity in a model of colitis. Deletion of IL18 or IL18R1 in intestinal epithelial cells conferred protection from colitis and mucosal damage in mice. In contrast, deletion of the IL18 negative regulator IL18bp resulted in severe colitis associated with loss of mature goblet cells. Colitis and goblet cell loss were rescued in IL18bp(-/-); IL18r(Δ /EC) mice, demonstrating that colitis severity is controlled at the level of IL18 signaling in intestinal epithelial cells. IL18 inhibited goblet cell maturation by regulating the transcriptional program instructing goblet cell development. These results inform on the mechanism of goblet cell dysfunction underlying the pathology of ulcerative colitis.

[0010] IL18 has a pathogenic role in the intestine in murine models of CD4⁺ T cell mediated colitis. In addition, in mice lacking key inflammasome components that regulate the processing and secretion of IL-18, IL-18 may provide a tissue-protective role following injury to the intestinal epithelium, indicating that the role of IL-18 in intestinal immune regulation may be variable.

[0011] IL18R1 expression *in vivo* is enhanced on both effector and regulatory CD4⁺ T cells in the intestinal lamina propria, with Th17 cells exhibiting particularly high levels. During steady state, intestinal epithelial cells (IEC) constitutively secrete IL18 that acts directly on IL18R1-expressing CD4⁺ T cells to limit colonic Th17 cell differentiation, in part by antagonizing IL1R1-signalling. In addition, IL18R1 signaling has been shown to be critical for Foxp3⁺ Treg cell mediated control of intestinal inflammation, where it promotes expression of Treg effector molecules. Thus, IL18R1 may

be a promising target for the treatment of disease or conditions associated with inflammation, and cellular immunity, such as inflammatory bowel disease (*e.g.*, IBD, CD, UC).

[0012] Aspects disclosed herein are practical applications of patient selection criteria useful for the identification and selection of subjects suitable for treatment with a particular therapeutic agent to treat one or more inflammatory diseases or disorders described herein (*e.g.*, inflammatory bowel diseases), or subclinical phenotypes thereof. In some instances, the patient selection criteria are useful for the identification and selection of subjects not suitable for a treatment with a standard therapy (*e.g.*, anti-TNF therapy, corticosteroid, thiopurine). In some instances, the patient selection criteria comprise polymorphisms or aberrations of a gene or gene expression product. In some instances the patient selection criteria comprise single nucleotide variants (SNVs), single nucleotide polymorphisms (SNPs), insertion or deletions (indels), and the like. In some instances, expression of a gene expression product (*e.g.*, a biomarker), alone, or in combination with the polymorphisms are useful as patient selection criteria. In some instances, the polymorphism or aberration is located at a gene or genetic locus encoding at least a part of the target of the therapeutic agent (*e.g.*, IL18R1). In some instances, that polymorphism or aberration is associated with an increase or a decrease in the expression of the target gene expression product. For example, disclosed herein is overlapping eQTL and subclinical phenotype association data suggesting the minor allele for eQTL in UC rectum is associated with upregulation of gene expression. The minor allele is also associated with risk for colonic disease and time to first surgery but is protective for smoking history. This data is consistent with the idea that increased IL18R1 expression is associated with disease in UC.

[0013] Aspects disclosed herein provide methods of treating or preventing a disease or condition in a subject, the method comprising administering a modulator of Interleukin 18 Receptor 1 (IL18R1) activity or expression to the subject, provided a genotype is detected in a sample obtained the subject. In some embodiments, the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide.

In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cirrhosis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within s SEQ ID

NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.

[0014] Aspects disclosed herein provide methods of reducing or ablating activity or expression of Interleukin 18 Receptor 1 (IL18R1) in a subject, the method comprising administering a modulator of IL18R1 to the subject, provided a genotype is detected in a sample obtained from the subject. In some embodiments, the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide

comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cholangitis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a

subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.

[0015] Aspects disclosed herein provide methods of treating or preventing a disease or condition in a subject, the method comprising: obtaining a sample from a subject; detecting a presence or an absence of a genotype in the sample obtained from the subject; and administering to the subject a modulator of Interleukin 18 Receptor 1 (IL18R1) activity or expression to the subject, provided the presence of the genotype is detected in the sample obtained from the subject. In some embodiments, the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at

the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cirrhosis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within s SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} ,

about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.

[0016] Aspects disclosed herein provide methods of reducing, ablating, increasing, or activating, an activity or expression of Interleukin 18 Receptor 1 (IL18R1) in a subject, the method comprising: obtaining a sample from a subject; detecting a presence or an absence of a genotype in the sample obtained from the subject; and administering to the subject a modulator of IL18R1 activity or expression to the subject, provided the presence of the genotype is detected in the sample obtained from the subject. In some embodiments, the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1

activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cirrhosis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within s SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about $1.0 \times$

10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.

[0017] Aspects disclosed herein provide methods of diagnosing a disease or condition in a subject, the method comprising: obtaining a sample from a subject; detecting a presence or an absence of a genotype in the sample obtained from the subject; and diagnosing the disease or condition in the subject, provided the presence of the genotype is detected in the sample obtained from the subject. In some embodiments, the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof. In some embodiments, wherein the methods further comprise administering to the subject a modulator or IL18R1 activity or expression. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator

of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises an inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cirrhosis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the

subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.

[0018] Aspects disclosed herein provide methods of determining whether a subject is at risk for developing a disease or condition, in a subject, the method comprising: obtaining a sample from a subject; detecting a presence or an absence of a genotype in the sample obtained from the subject; and determining the subject is at risk for developing the disease or condition, provided the presence of the genotype is detected in the sample obtained from the subject. In some embodiments, the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof. In some embodiments, wherein the methods further comprise administering to the subject a modulator or IL18R1 activity or expression. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or

an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cholangitis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a

subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.

[0019] Aspects disclosed herein provide methods of determining whether a subject is suitable for treatment of a disease or condition with a modulator of Interleukin 18 Receptor 1 (IL18R1) activity or expression, the method comprising: obtaining a sample from a subject; detecting a presence or an absence of a genotype in the sample obtained from the subject; and determining the subject is suitable for treatment of the disease or condition with a modulator of IL18R1, provided the presence of the genotype is detected in the sample obtained from the subject. In some embodiments, the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof. In some embodiments, wherein the methods further comprise administering to the subject a modulator or IL18R1 activity or expression. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or

an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cholangitis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a

subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.

[0020] Aspects disclosed herein provide methods for processing or analyzing a sample obtained from a subject, the method comprising: obtaining a sample from a subject; subjecting the sample to an assay by sequencing, genotype array, and/or nucleic acid amplification, to yield a data set comprising data corresponding to a presence or an absence of a genotype; in a programmed computer, inputting said data from (b) to a trained algorithm to determine whether the subject is at risk of developing, a disease or disorder, wherein the trained algorithm is trained with a plurality of training samples, and wherein said sample is independent of said plurality of training samples; and electronically outputting a report comprising the determination for the subject. In some embodiments, wherein (c) comprises calculating a polygenic risk score (PRS), and the PRS comprises a normalized weighted sum of a number of risk alleles within the genotype present in the subject with weights proportional to a beta value of association between the genotype with the disease or condition. In some embodiments, the data set of (b) further comprises data corresponding to a presence or an absence of a surrogate genotype, provided an absence of a genotype is detected. In some embodiments, the surrogate genotype is in linkage disequilibrium with the absent genotype as determined by an r^2 value of at least about 0.8, about 0.85, about 0.90, about 0.95, or about 1.0. In some embodiments, the report is configured to display the determination of the subject on a user interface of an electronic device. In some embodiments, the electronic device comprises a personal electronic device belonging to the subject. In some embodiments, the methods comprise administering to the subject a modulator or IL18R1 activity or expression, provided the subject is determined to be at risk of having, or developing, the disease or condition. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the

modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cholangitis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a "G" or a "T" allele. In some embodiments, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at

rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0. In some embodiments, the genotype comprises at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14, single nucleotide polymorphism (SNP) or indels.

[0021] Aspects disclosed herein provide methods for processing or analyzing a sample obtained from a subject, the method comprising: obtaining a sample from a subject; subjecting the sample to an assay by sequencing, genotype array, and/or nucleic acid amplification, to yield a data set comprising data corresponding to a presence or an absence of a genotype; in a programmed computer, inputting said data from (b) to a trained algorithm to determine a likelihood that the subject is suitable for treatment of a disease or disorder with an agonist of IL18R1, wherein the trained algorithm is trained with a plurality of training samples, and wherein said sample is independent of said plurality of training samples; and electronically outputting a report comprising the determination for the subject. In some embodiments, wherein (c) comprises calculating a polygenic risk score (PRS), and the PRS comprises a normalized weighted sum of a number of risk alleles within the genotype present in the subject with weights proportional to a beta value of association between the genotype with the disease or condition. In some embodiments, the data set of (b) further comprises data corresponding to a presence or an absence of a surrogate genotype, provided an absence of a genotype is detected. In some embodiments, the surrogate genotype is in linkage disequilibrium with the absent genotype as determined by an r^2 value of at least about, 0.8, about 0.85, about 0.90, about 0.95, or about 1.0. In some embodiments, the report is configured to display the determination of the subject on a user interface of an electronic device. In some embodiments, the electronic device comprises a personal electronic device belonging to the subject. In some embodiments, the methods comprise administering

to the subject a modulator of IL18R1 activity or expression, provided the subject is determined to be at risk of having, or developing, the disease or condition. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1. In some embodiments, the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1. In some embodiments, the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule. In some embodiments, the modulator of IL18R1 activity or expression comprises an inverse agonist. In some embodiments, the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM). In some embodiments, the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9. In some embodiments, the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide. In some embodiments, the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling. In some embodiments, the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding. In some embodiments, the genotype is homozygous or heterozygous. In some embodiments, the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cholangitis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis. In some embodiments, the sample comprises whole blood, plasma, serum, or biopsy tissue. In some embodiments, the subject is mammal. In some embodiments, the subject is human. In some embodiments, the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment. In some embodiments, the inflammatory, fibrostenotic, and/or fibrotic disease is refractory. In some embodiments, the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739,

rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof. In some embodiments, the SNP at rs1921622 comprises an “A” or a “G” on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an “A” or a “G” on a reverse DNA strand encoding the SNP. The method of claim 30, wherein the SNP at rs10213846 comprises a “G” or a “T” allele. In some embodiments, the SNP at rs1974675 comprises a “C” or a “T” on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs2041739 comprises an “A” or a “G” on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs76362690 comprises an “A” or a “G” on a forward DNA strand encoding the SNP. In some embodiments, the SNP at rs2287037 comprises an “A” or a “G” on a reverse DNA strand encoding the SNP. In some embodiments, the SNP at rs80256362 comprises an “A” or a “G” on a forward DNA strand encoding the SNP. In some embodiments, the Indel at rs1921622 is within SEQ ID NO: 1. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 2. In some embodiments, the SNP at rs1974675 is within SEQ ID NO: 3. In some embodiments, the SNP at rs2041739 is within s SEQ ID NO: 4. In some embodiments, the SNP at rs76362690 is within SEQ ID NO: 5. In some embodiments, the SNP at rs2287037 is within SEQ ID NO: 6. In some embodiments, the SNP at rs80256362 is within SEQ ID NO: 7. In some embodiments, LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0. In some embodiments, the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn’s disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} . In some embodiments, the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes. In some embodiments, the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0. In some embodiments, the genotype comprises at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14, single nucleotide polymorphism (SNP) or indels.

[0022] Aspects disclosed herein provide methods of treating a subject in need thereof with a modulator of interleukin 18 receptor 1 (IL18R1) activity or expression, wherein the subject has moderate to severe Crohn’s disease (CD), and wherein the subject has a genotype characterized by the presence of one or more SNPs. In some embodiments, the one or more SNPs comprises a SNP listed in Table 1. In some embodiments, the single nucleotide polymorphism is associated with structuring. In some embodiments, the stricturing is isolated to an ileocolonic region of an intestine. In some

embodiments, the one or more SNPs comprises a SNP listed in Table 2. In some embodiments, the single nucleotide polymorphism is associated with a risk of a subject developing morphological defects in ileal Paneth cells. In some embodiments, the one or more SNPs comprises a SNP listed in Table 3.

[0023] Aspects disclosed herein provide methods of treating a subject in need thereof with a modulator of interleukin 18 receptor 1 (IL18R1) activity or expression, wherein the subject has moderate to severe inflammatory bowel disease (IBD), and wherein the subject has a genotype characterized by the presence of one or more SNPs. In some embodiments, the one or more SNPs comprises a SNP listed in Table 4.

[0024] Aspects disclosed herein provide methods of treating a subject in need thereof with a modulator of interleukin 18 receptor 1 (IL18R1) activity or expression, wherein the subject has moderate to severe ulcerative colitis, and wherein the subject has a genotype characterized by the presence of one or more SNPs. In some embodiments, the one or more SNPs comprises a SNP listed in Table 5.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] FIG. 1A to FIG. 1Q illustrate meta-analysis of IL18R1 single nucleotide polymorphism in association with Crohn's disease (CD), inflammatory bowel disease (IBD), or ulcerative colitis (UC), and various subclinical phenotypes of CD, IBD, and UC.

DETAILED DESCRIPTION OF THE DISCLOSURE

[0026] While preferred embodiments of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

Certain Terminologies

[0027] The terminology used herein is for the purpose of describing particular cases only and is not intended to be limiting. As used herein, the singular forms "a", "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. Furthermore, to the extent that the terms "including", "includes", "having", "has", "with", or variants thereof are used in either the detailed description and/or the claims, such terms are intended to be inclusive in a manner similar to the term "comprising."

[0028] The term "about" or "approximately" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is

measured or determined, e.g., the limitations of the measurement system. For example, “about” can mean within 1 or more than 1 standard deviation, per the practice in the given value. Where particular values are described in the application and claims, unless otherwise stated the term “about” should be assumed to mean an acceptable error range for the particular value.

[0029] As used herein “consisting essentially of” when used to define compositions and methods, shall mean excluding other elements of any essential significance to the combination for the stated purpose. Thus, a composition consisting essentially of the elements as defined herein would not exclude other materials or steps that do not materially affect the basic and novel characteristic(s) of the claimed disclosure, such as compositions for treating skin disorders like acne, eczema, psoriasis, and rosacea.

[0030] The terms “homologous,” “homology,” or “percent homology” are used herein to generally mean an amino acid sequence or a nucleic acid sequence having the same, or similar sequence to a reference sequence. Percent homology of sequences can be determined using the most recent version of BLAST, as of the filing date of this application.

[0031] The terms “increased,” or “increase” are used herein to generally mean an increase by a statically significant amount. In some embodiments, the terms “increased,” or “increase,” mean an increase of at least 10% as compared to a reference level, for example an increase of at least about 10%, at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% increase or any increase between 10-100% as compared to a reference level, standard, or control. Other examples of “increase” include an increase of at least 2-fold, at least 5-fold, at least 10-fold, at least 20-fold, at least 50-fold, at least 100-fold, at least 1000-fold or more as compared to a reference level.

[0032] The terms, “decreased” or “decrease” are used herein generally to mean a decrease by a statistically significant amount. In some embodiments, “decreased” or “decrease” means a reduction by at least 10% as compared to a reference level, for example a decrease by at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% decrease (e.g., absent level or non-detectable level as compared to a reference level), or any decrease between 10-100% as compared to a reference level. In the context of a marker or symptom, by these terms is meant a statistically significant decrease in such level. The decrease can be, for example, at least 10%, at least 20%, at least 30%, at least 40% or more, and is preferably down to a level accepted as within the range of normal for an individual without a given disease.

[0033] The term “subject” encompasses mammals. Non-limiting examples of mammal include, any member of the mammalian class: humans, non-human primates such as chimpanzees, and other apes and monkey species; farm animals such as cattle, horses, sheep, goats, swine; domestic animals such as rabbits, dogs, and cats; laboratory animals including rodents, such as rats, mice and guinea pigs,

and the like. In one aspect, the mammal is a human. The term “animal” as used herein comprises human beings and non-human animals. In one embodiment, a “non-human animal” is a mammal, for example a rodent such as rat or a mouse.

[0034] The term “gene,” as used herein, refers to a segment of nucleic acid that encodes an individual protein or RNA (also referred to as a “coding sequence” or “coding region”), optionally together with associated regulatory region such as promoter, operator, terminator and the like, which may be located upstream or downstream of the coding sequence.

[0035] The term “genetic variant” as used herein refers to an aberration in (e.g., a mutation), or of (e.g., copy number variation), a nucleic acid sequence, as compared to the nucleic acid sequence in a reference population. In some embodiments, the genetic variant is common in the reference population. In some embodiments, the genetic variant is rare in the reference population.

[0036] The term, “genotype” as disclosed herein, refers to the chemical composition of polynucleotide sequences within the genome of an individual. In some embodiments, the genotype comprises a single nucleotide polymorphism (SNP), or and indel (insertion or deletion, of a nucleobase within a polynucleotide sequence). In some embodiments, a genotype for a particular SNP, or indel is heterozygous. In some embodiments, a genotype for a particular SNP, or indel is homozygous.

[0037] The term, “single nucleotide polymorphism” or “SNP,” as disclosed herein, refers to a variation in a single nucleotide within a polynucleotide sequence. The variation of an SNV may have multiple different forms. The usage of the term “single nucleotide polymorphism” or “SNP” should not imply any limit on the frequency with which each variation occurs. A single form of an SNP is referred to as an “allele.” An SNP can be mono-, bi-, tri-, or tetra-allelic. An SNP may include a “risk allele,” a “protective allele,” or neither. By way of example, a reference polynucleotide sequence reading 5’ to 3’ is TTACG. A SNP at allele position 3 (of 5’-TTACG-3’) comprise a substitution of the reference allele, “A” to a non-reference allele, “C.” If the “C” allele of the SNP is associated with an increased probability of developing a phenotypic trait, the allele is considered a “risk” allele. However, the same SNP may also comprise a substitution of the “A” allele to a “T” allele at position 3. If the T allele of the SNP is associated with a decreased probability of developing a phenotypic trait, the allele is considered a “protective” allele. In some embodiments, the SNP is represented by an “rs” number, which refers to the accession of reference cluster of one more submitted SNPs in the dbSNP bioinformatics database as of the filing date of this patent application, and which is included within a sequence that comprises the total number of nucleobases from 5’ to 3’. In some embodiments, a SNP may be further defined by the position of the SNP (nucleobase) within the dbSNP sequence, the position of which is always with reference to 5’ length of the sequence plus 1. In some embodiments, a SNP is defined as the genomic position in a reference genome and the allele change (e.g. chromosome 7 at position 234,123,567 from G allele to A allele in the reference human

genome build 37). In some embodiments, the SNP is defined as the genomic position identified with [brackets] or an “N” in a sequence disclosed herein.

[0038] The term, “indel,” as disclosed herein, refers to an insertion, or a deletion, of a nucleobase within a polynucleotide sequence. An indel can be mono-, bi-, tri-, or tetra-allelic. An indel may be “risk,” a “protective,” or neither, for a phenotypic trait. In some embodiments, the indel is represented by an “rs” number, which refers to the accession of reference cluster of one more submitted indels in the dbSNP bioinformatics database as of the filing date of this patent application, and which is included in a sequence that comprises the total number of nucleobases from 5’ to 3’. In some embodiments, an indel may be further defined by the position of the insertion/deletion within the dbSNP sequence, the position of which is always with reference to the 5’ length of the sequence plus 1. In some embodiments, an indel is defined as the genomic position in a reference genome and the allele change. In some embodiments, the indel is defined as the genomic position identified with [brackets] or an “N” in a sequence disclosed herein.

[0039] “Haplotype” as used herein, encompasses a group of one or more genotypes, SNPs, or indels, which tend to be inherited together in a reference population. In some embodiments, a haplotype comprises particular SNPs, or indels, and any SNP, or indel in linkage disequilibrium therewith.

[0040] “Linkage disequilibrium,” or “LD,” as used herein refers to the non-random association of alleles or indels in different gene loci in a given population. LD may be defined by a D' value corresponding to the difference between an observed and expected allele or indel frequencies in the population ($D = P_{ab} - P_a P_b$), which is scaled by the theoretical maximum value of D . LD may be defined by an r^2 value corresponding to the difference between an observed and expected unit of risk frequencies in the population ($D = P_{ab} - P_a P_b$), which is scaled by the individual frequencies of the different loci. In some embodiments, D' comprises at least 0.20. In some embodiments, r^2 comprises at least 0.70.

[0041] The terms “treat,” “treating,” and “treatment” as used herein refers to alleviating or abrogating a disorder, disease, or condition; or one or more of the symptoms associated with the disorder, disease, or condition; or alleviating or eradicating a cause of the disorder, disease, or condition itself. Desirable effects of treatment can include, but are not limited to, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishing any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state and remission or improved prognosis.

[0042] The term “therapeutically effective amount” refers to the amount of a compound or therapy that, when administered, is sufficient to prevent development of, or alleviate to some extent, one or more of the symptoms of a disorder, disease, or condition of the disease; or the amount of a compound that is sufficient to elicit biological or medical response of a cell, tissue, system, animal, or human that is being sought by a researcher, veterinarian, medical doctor, or clinician.

[0043] The term “pharmaceutically acceptable carrier,” “pharmaceutically acceptable excipient,” “physiologically acceptable carrier,” or “physiologically acceptable excipient” refers to a pharmaceutically-acceptable material, composition, or vehicle, such as a liquid or solid filler, diluent, excipient, solvent, or encapsulating material. A component can be “pharmaceutically acceptable” in the sense of being compatible with the other ingredients of a pharmaceutical formulation. It can also be suitable for use in contact with the tissue or organ of humans and animals without excessive toxicity, irritation, allergic response, immunogenicity, or other problems or complications, commensurate with a reasonable benefit/risk ratio. See, Remington: The Science and Practice of Pharmacy, 21st Edition; Lippincott Williams & Wilkins: Philadelphia, PA, 2005; Handbook of Pharmaceutical Excipients, 5th Edition; Rowe et al., Eds., The Pharmaceutical Press and the American Pharmaceutical Association: 2005; and Handbook of Pharmaceutical Additives, 3rd Edition; Ash and Ash Eds., Gower Publishing Company: 2007; Pharmaceutical Preformulation and Formulation, Gibson Ed., CRC Press LLC: Boca Raton, FL, 2004).

[0044] The term “pharmaceutical composition” refers to a mixture of a compound disclosed herein with other chemical components, such as diluents or carriers. The pharmaceutical composition can facilitate administration of the compound to an organism. Multiple techniques of administering a compound exist in the art including, but not limited to, oral, injection, aerosol, parenteral, and topical administration.

[0045] The term “inflammatory bowel disease” or “IBD” as used herein refers to gastrointestinal disorders of the gastrointestinal tract. Non-limiting examples of IBD include, Crohn's disease (CD), ulcerative colitis (UC), indeterminate colitis (IC), microscopic colitis, diversion colitis, Behcet's disease, and other inconclusive forms of IBD. In some instances, IBD comprises fibrosis, fibrostenosis, stricturing and/or penetrating disease, obstructive disease, or a disease that is refractory (e.g., mrUC, refractory CD), perianal CD, or other complicated forms of IBD.

[0046] Non-limiting examples of “sample” include any material from which nucleic acids and/or proteins can be obtained. As non-limiting examples, this includes whole blood, peripheral blood, plasma, serum, saliva, mucus, urine, semen, lymph, fecal extract, cheek swab, cells or other bodily fluid or tissue, including but not limited to tissue obtained through surgical biopsy or surgical resection. In various embodiments, the sample comprises tissue from the large and/or small intestine. In various embodiments, the large intestine sample comprises the cecum, colon (the ascending colon, the transverse colon, the descending colon, and the sigmoid colon), rectum and/or the anal canal. In some embodiments, the small intestine sample comprises the duodenum, jejunum, and/or the ileum. Alternatively, a sample can be obtained through primary patient derived cell lines, or archived patient samples in the form of preserved samples, or fresh frozen samples.

[0047] The term “biomarker” comprises a measurable substance in a subject whose presence, level, or activity, is indicative of a phenomenon (e.g., phenotypic expression or activity; disease, condition, subclinical phenotype of a disease or condition, infection; or environmental stimuli). In some

embodiments, a biomarker comprises a gene, or gene expression product. In some embodiments, a biomarker comprises a cytokine (e.g., IL-1 α , IL-1 β , IL-2, IL-3, IL-4, IL-5, IL-6, IL-8, IL-9, IL-10, IL-13, IL-17, IL-17F, IL-22, TNF- α , TNF- β , IFN- α 1/- α 2, IFN- β , IFN- γ , TNFSF superfamily: TNF, TL1A, FasL, LIGHT, TRAIL, and TWEAK). In some embodiments, a biomarker comprises a cell type (e.g., Natural Killer (NK) cells, T cells, Effector T cells (Teff), Regulatory T cells (Treg) B cells, T helper (Th) cells, cluster of differentiation (CD) cells, innate lymphoid cells (ILC), antigen-presenting cells (APC), monocytes Paneth cells, granulocytes, dendritic cells, and macrophages).

[0048] The term “serological marker,” as used herein refers to a type of biomarker representing an antigenic response in a subject that may be detected in the serum of the subject. In some embodiments, a serological comprises an antibody against various fungal antigens. Non-limiting examples of a serological marker comprise anti-Saccharomyces cerevisiae antibody (ASCA), an anti-neutrophil cytoplasmic antibody (ANCA), E.coli outer membrane porin protein C (OmpC), anti-Malassezia restricta antibody, anti-Malassezia pachydermatis antibody, anti-Malassezia furfur antibody, anti-Malassezia globosa antibody, anti-Cladosporium albicans antibody, anti-laminaribiose antibody (ALCA), anti-chitobioside antibody (ACCA), anti-laminarin antibody, anti-chitin antibody, pANCA antibody, anit-I2 antibody, and anti-Cbir1 flagellin antibody.

[0049] The term “microbiome” and its variation used herein describe the populations and interactions of the bacteria, fungi, protists, and virus that align the gastrointestinal tract of a subject. A subject afflicted with IBD may possess presence, absence, excess, diminished, or a combination thereof of a microbiome s compared to a healthy subject. Non-limiting examples of bacteria associated with IBD includes strains, sub-strains, and enterotypes of enterobacteriaceae, pasteurellaceae, fusobacteriaceae, neisseriaceae, veillonellaceae, gemellaceae, bacteroidales, clostridales, erysipelotrichaceae, bifidobacteriaceae bacteroides, faecalibacterium, roseburia, blautia, ruminococcus, coprococcus, streptococcus, dorea, blautia, ruminococcus, lactobacillus, enterococcus, streptococcus, escherichia coli, fusobacterium nucleatum, haemophilus parainfluenzae (pasteurellaceae), veillonella parvula, eikenella corrodens (neisseriaceae), and gemella moribillum, bacteroides vulgatus, bacteroides caccae, bifidobacterium bifidum, bifidobacterium longum, bifidobacterium adolescentis, bifidobacterium dentum, blautia hansenii, ruminococcus gnavus, clostridium nexile, faecalibacterium prausnitzii, ruminococcus torques, clostridium bolteae, eubacterium rectale, roseburia intestinalis, coprococcus comes, actinomyces, lactococcus, roseburia, streptococcus, blautia, dialister, desulfovibrio, escherichia, lactobacillus, coprococcus, clostridium, bifidobacterium, klebsiella, granulicatella, eubacterium, anaerostipes, parabacteroides, coprobacillus, gordonibacter, collinsella, bacteroides, , faecalibacterium, , anaerotruncus, alistipes, haemophilus, anaerococcus, veillonella, arevotella, akkermansia, bilophila, sutterella, eggerthella, holdemania, gemella, peptoniphilus, rothia, enterococcus, pediococcus, citrobacter, odoribacter, enterobacteria, fusobacterium, and proteus. Non-limiting examples of viruses associated with IBD include picovirinae, lactococcus phage, cellulophaga phage, bacteroides phage, C2 like virus, enterococcus

phage, caudivirales, cellulophaga phage, phiCD119 like virus, croceibacter phage, clostridium phage, spounavirinae, riemerella phage, lambda like virus, bacillus phage, terenvirinae, lactobacillus phage, enterobacteria phage, thermoanaerobacterium phage, streptococcus phage, and pseudomonas phage.

Non-limiting examples of fungi genera associated with IBD includes *Malassezia*, *Cladosporium*, *Aureobasidium*, *Fusarium*, *Candida*, *Pichia*, *Saccharomyces*, and *Escherichia*.

[0050] The term “medically refractory,” or “refractory,” as used herein, refers to the failure of a standard treatment to induce remission of a disease. In some embodiments, the disease comprises an inflammatory disease disclosed herein. A non-limiting example of refractory inflammatory disease includes refractory Crohn’s disease, and refractory ulcerative colitis (*e.g.*, mrUC). Non-limiting examples of standard treatment include glucocorticosteroids, anti-TNF therapy, anti-a4-b7 therapy (vedolizumab), anti-IL12p40 therapy (ustekinumab), Thalidomide, and Cytosin.

[0051] The term “anti-tumor necrosis factor (TNF) non-response,” or “anti-TNF non-response,” as used herein, refers to a subject not responding to the induction of an anti-TNF therapy (primary non-response), or loss of response during maintenance after a successful induction of the anti-TNF therapy (secondary loss of response). In some embodiments, the induction of the anti-TNF therapy comprises 1, 2, 3, 4, or 5, doses of the therapy. In some embodiments, loss of response is characterized by a reappearance of symptoms consistent with a flare after an initial response to the anti-TNF therapy.

METHODS

[0052] Disease or Condition

[0053] Aspects disclosed herein provide methods of treating, diagnosing, prognosing, or monitoring, a disease or condition. In some cases, the disease or condition comprises an inflammatory disease, fibrostenotic disease, and/or fibrotic disease. Non-limiting examples of inflammatory diseases include diseases of the gastrointestinal (GI) tract, liver, gallbladder, and joints. In some cases, the inflammatory disease inflammatory bowel disease (IBD), Crohn’s disease (CD), or ulcerative colitis, systemic lupus erythematosus (SLE), multiple sclerosis (MS), asthma, celiac disease, primary biliary cirrhosis (PBC), or rheumatoid arthritis. A subject may suffer from fibrosis, fibrostenosis, or a fibrotic disease, either isolated or in combination with an inflammatory disease. An exemplary fibrotic disease is primary sclerosing cholangitis (PSC).

[0054] In some instances, the disease or condition is refractory, which refers a quality of the disease or condition such that there is an observed failure of a standard treatment to induce remission of a disease or condition. Non-limiting examples of refractory inflammatory disease include refractory Crohn’s disease, and medically refractory ulcerative colitis (*e.g.*, mrUC). Non-limiting examples of standard treatment include glucocorticosteroids, anti-TNF therapy, anti-a4-b7 therapy (vedolizumab), anti-IL12p40 therapy (ustekinumab), Thalidomide, and Cytosin. In some instances, the refractory disease or condition is characterized by an increase in colitis, inflammation, fibrosis, fibrostenosis, stricturing, penetrating, obstructive, or otherwise complicated, disease of the GI tract.

[0055] Subject

[0056] Disclosed herein, in some embodiments, are methods of treating, diagnosing, prognosing, or monitoring, a disease or condition in a subject. In some instances, the subject is a mammal. In some embodiments, the subject comprises a mouse, rat, guinea pig, rabbit, chimpanzee, or farm animal. In some instances, the subject is human. In some instances, the subject is diagnosed with the disease or condition disclosed herein. Non-limiting methods for diagnosis using existing indices and scoring systems include Crohn's Disease Activity Index (CDAI), Ulcerative Colitis Disease Activity Index (UCDAI), guidelines from American College of Gastroenterology (ACG) and European Crohn's and Colitis Organization (ECCO), patient-reported outcomes (PRO-2), Harvey-Bradshaw Index, Van Hess Index, Perianal Disease Activity Index (PDAI), Rachmilewitz score, Mayo score, Powell-Tuck index, Patient Simple Clinical Colitis Activity Index (P-SCCAI), Lichtiger index, Seo index, Inflammatory Bowel Disease Questionnaire (IBDQ), Manitoba IBD Index, Crohn's Disease Endoscopic Index of Severity (CDEIS), Simple Endoscopic Score for Crohn Disease (SES-CD), Lewis score (capsule endoscopy), Rutgeert's Score, and the Montreal Classification, and IBD questionnaire. In some instances, the subject is not diagnosed with the disease or condition. In some instances, the subject is suffering from a symptom related to a disease or condition disclosed herein (e.g., abdominal pain, cramping, diarrhea, rectal bleeding, fever, weight loss, fatigue, loss of appetite, dehydration, and malnutrition, anemia, or ulcers).

[0057] In some embodiments, the subject is susceptible to, or is inflicted with, thiopurine toxicity, or a disease caused by thiopurine toxicity (such as pancreatitis or leukopenia). In further embodiments provided, the subject is, or is suspected of being, non-responsive to a standard treatment (e.g., anti-TNF alpha therapy, anti-a4-b7 therapy (vedolizumab), anti-IL12p40 therapy (ustekinumab), Thalidomide, or Cytoxin). In some cases, the subject is not responsive to the induction of said therapy. In some cases, the subject loses response to said standard treatment after a period of time during treatment.

[0058] Interleukin 18 Receptor 1 (IL18R1)

[0059] Interleukin 18 Receptor 1 (IL18R1) (UniProtKB: Q13478) is encoded by the gene *IL18R1* (Entrez Gene: 8809), which is a cytokine receptor that belongs to the interleukin 1 receptor family. This receptor specifically binds interleukin 18 (IL18), and is essential for IL18 mediated signal transduction. IFN-alpha and IL12 are reported to induce the expression of this receptor in NK and T cells. This gene along with four other members of the interleukin 1 receptor family, including IL1R2, IL1R1, IL1RL2 (IL-1Rrp2), and IL1RL1 (T1/ST2), form a gene cluster on chromosome 2q.

[0060] Disclosed herein are genotypes comprising one or more single nucleotide polymorphisms (SNPs or indels (insertion/deletion) at the IL18R1 genetic locus (e.g., IL18R1 risk genotype), according to the following embodiments:

1. A IL18R1 risk genotype comprising one or more SNPs and/or indels at the IL18R1 genetic locus.

2. The IL18R1 risk genotype of embodiment 1, comprising one or more SNPs and/or indels at rs13001325, rs1420101, rs12479210, rs950880, rs13020553, rs13019081, rs12712141, rs2287037, rs1420102, rs12466380, rs1997467, rs1558619, rs1420088, rs12999364, rs4142132, rs12987977, rs11690443, rs1362350, rs12996505, rs873022, rs974389, rs3771177, rs3732129, rs17026974, rs6706844, rs13020793, rs11685480, rs1558622, rs10183388, rs12712135, rs10189711, rs11685424, rs10189202, rs10191914, rs11123918, rs1968171, rs6733174, rs59247511, rs1558620, rs1921622, rs12998521, rs13017455, rs1362349, rs11123923, rs10190555, rs1035127, rs17027087, rs2080289, rs4851570, rs17027060, rs12712145, rs1420098, rs3732123, rs2287034, rs3860444, rs3821203, rs56258475, rs2270298, rs4851006, rs6710885, rs1568681, rs2241117, rs17027037, rs2270297, rs6753717, rs3755274, rs17027071, rs6750020, rs17027006, rs11683700, rs2058622, rs4851007, rs3732126, rs1807782, rs12469506, rs4851575, rs3771172, rs11465633, rs1135354, rs1558627, rs55927292, rs3771171, rs13015714, rs2160202, rs55883125, rs2041740, rs1035130, rs1420103, rs67723747, rs6543116, rs55664618, rs4851005, rs17027056, rs1420089, rs62152661, rs1420095, rs56030066, rs62152714, rs17696376, rs12105808, rs78248680, rs56151044, rs62152662, rs17651485, rs3771170, rs11123926, rs76721133, rs4988955, rs9807962, rs9808453, rs13424006, rs11695627, rs3771166, rs10173193, rs11465575, rs4851566, rs9308857, rs1974675, rs6751967, rs3771162, rs56386507, rs1997466, rs12712140, and rs1362348, or a SNP and/or indel in linkage disequilibrium therewith, or a combination thereof.
3. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs13001325.
4. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1420101.
5. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12479210.
6. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs950880.
7. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs13020553.
8. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs13019081.
9. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12712141.
10. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2287037.
11. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1420102.

12. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12466380.
13. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1997467.
14. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1558619.
15. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1420088.
16. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12999364.
17. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4142132.
18. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12987977.
19. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11690443.
20. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1362350.
21. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12996505.
22. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs873022.
23. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs974389.
24. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3771177.
25. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3732129.
26. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17026974.
27. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs6706844.
28. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs13020793.
29. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11685480.

30. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1558622.
31. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs10183388.
32. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12712135.
33. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs10189711.
34. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11685424.
35. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs10189202.
36. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs10191914.
37. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11123918.
38. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1968171.
39. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs6733174.
40. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs59247511.
41. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1558620.
42. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1921622.
43. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12998521.
44. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs13017455.
45. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1362349.
46. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11123923.
47. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs10190555.

48. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1035127.
49. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17027087.
50. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2080289.
51. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4851570.
52. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17027060.
53. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12712145.
54. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1420098.
55. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3732123.
56. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2287034.
57. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3860444.
58. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3821203.
59. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs56258475.
60. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2270298.
61. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4851006.
62. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs6710885.
63. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1568681.
64. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2241117.
65. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17027037.

66. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2270297.
67. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs6753717.
68. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3755274.
69. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17027071.
70. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs6750020.
71. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17027006.
72. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11683700.
73. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2058622.
74. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4851007.
75. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3732126.
76. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1807782.
77. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12469506.
78. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4851575.
79. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3771172.
80. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11465633.
81. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1135354.
82. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1558627.
83. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs55927292.

84. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3771171.
85. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs13015714.
86. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2160202.
87. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs55883125.
88. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs2041740.
89. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1035130.
90. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1420103.
91. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs67723747.
92. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs6543116.
93. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs55664618.
94. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4851005.
95. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17027056.
96. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1420089.
97. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs62152661.
98. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1420095.
99. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs56030066.
100. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs62152714.
101. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17696376.

102. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12105808.
103. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs78248680.
104. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs56151044.
105. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs62152662.
106. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs17651485.
107. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3771170.
108. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11123926.
109. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs76721133.
110. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4988955.
111. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs9807962.
112. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs9808453.
113. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs13424006.
114. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11695627.
115. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3771166.
116. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs10173193.
117. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs11465575.
118. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs4851566.
119. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs9308857.

120. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1974675.
121. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs6751967.
122. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs3771162.
123. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs56386507.
124. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1997466.
125. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs12712140.
126. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at rs1362348.
127. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at a SNP listed in Table 1.
128. The IL18R1 risk genotype of embodiment 127, wherein the one or more SNP and/or indels is associated with stricturing.
129. The IL18R1 risk genotype of embodiment 128, wherein the stricturing is isolated to an ileocolonic region of an intestine.
130. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at a SNP listed in Table 2.
131. The IL18R1 risk genotype of embodiment 130, wherein the one or more SNPs and/or indels is associated with a risk of a subject developing morphological defects in ileal Paneth cells.
132. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at a SNP listed in Table 3.
133. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at a SNP listed in Table 4.
134. The IL18R1 risk genotype of any previous embodiment, comprising one or more SNPs and/or indels at a SNP listed in Table 5.
135. The IL18R1 risk genotype of any previous embodiments, comprising one or more SNPs and/or indels at a SNP listed in FIG. 1A to FIG. 1Q.
136. The IL18R1 risk genotype of any previous embodiments, comprising one or more SNPs or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith.
137. The IL18R1 risk genotype of any previous embodiment, wherein the SNP at rs1921622 comprises an “A” or a “G” on a forward DNA strand encoding the SNP.

138. The IL18R1 risk genotype of any previous embodiments, wherein the SNP at rs2287037 comprises an “A” or a “G” on a reverse DNA strand encoding the SNP.
139. The IL18R1 risk genotype of any previous embodiments, wherein the SNP at rs1974675 comprises a “C” or a “T” on a reverse DNA strand encoding the SNP.
140. The IL18R1 risk genotype of any previous embodiments, wherein the SNP at rs2041739 comprises an “A” or a “G” on a reverse DNA strand encoding the SNP.
141. The IL18R1 risk genotype of any previous embodiments, wherein the SNP at rs76362690 comprises an “A” or a “G” on a forward DNA strand encoding the SNP.
142. The IL18R1 risk genotype of any previous embodiments, wherein the SNP at rs2287037 comprises an “A” or a “G” on a reverse DNA strand encoding the SNP.
143. The IL18R1 risk genotype of any previous embodiments, wherein the SNP at rs80256362 comprises an “A” or a “G” on a forward DNA strand encoding the SNP.
144. The IL18R1 risk genotype of any previous embodiments, comprising 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 SNPs and/or indels.
145. The IL18R1 risk genotype of any previous embodiments, wherein the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn’s disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
146. The IL18R1 risk genotype of any previous embodiments, wherein the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
147. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises one or more SNPs and/or indels in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0
148. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises SEQ ID NO: 1.
149. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises SEQ ID NO: 2.
150. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises SEQ ID NO: 3.
151. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises SEQ ID NO: 4.

152. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises SEQ ID NO: 5.
153. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises SEQ ID NO: 6.
154. The IL18R1 risk genotype of any previous embodiments, wherein the genotype comprises SEQ ID NO: 7.
155. The IL18R1 risk genotype of embodiment 1498, wherein the “N” within SEQ ID NO: 1 comprises an “A” or a “G.”
156. The IL18R1 risk genotype of embodiment 149, wherein the “N” within SEQ ID NO: 2 comprises an “A” or a “G.”
157. The IL18R1 risk genotype of embodiment 150, wherein the “N” within SEQ ID NO: 3 comprises a “C” or a “T.”
158. The IL18R1 risk genotype of embodiment 151, wherein the “N” within SEQ ID NO: 4 comprises an “A” or a “G.”
159. The IL18R1 risk genotype of embodiment 152, wherein the “N” within SEQ ID NO: 5 comprises an “A” or a “G.”
160. The IL18R1 risk genotype of embodiment 153, wherein the “N” within SEQ ID NO: 6 comprises an “A” or a “G.”
161. The IL18R1 risk genotype of embodiment 154, wherein the “N” within SEQ ID NO: 7 comprises an “A” or a “G.”

[0061] Clinical and Subclinical Phenotype Associations

[0062] In some instances, a presence or an absence of a SNP and/or indel in a subject is associated with a particular phenotype (*e.g.*, disease or condition), or subclinical phenotype, such as those described herein. In some embodiments, the method comprises determining whether the subject has an allele associated with the disease or condition (“risk allele”). Non-limiting examples of clinical phenotypes include inflammatory bowel disease (IBD), Crohn’s disease (CD), ulcerative colitis (UC), multiple sclerosis (MS), primary sclerosing cholangitis (PSC), Pancolitis (*e.g.*, UC which affects the entire large intestine), Proctitis (*e.g.*, inflammation of the rectum), Iritis (*e.g.*, inflammation of the iris), Thrombosis (*e.g.*, formation of blood clot inside a blood vessel), Uveitis (*e.g.*, inflammation of the eye, of the uvea), Spondylitis (*e.g.*, inflammation of the spine), arthralgias (*e.g.*, inflammation of the joints), nodosum, perianal Crohn’s disease (pCD), Psoriasis (*e.g.*, inflammation of the skin), asthma, Celiac disease, primary biliary cirrhosis, and oral ulcers. In some instances, a SNP disclosed herein is associated with IBD. In some instances, a SNP disclosed herein is associated with CD. In some instances, a SNP disclosed herein is associated with UC. In some instances, the SNP disclosed herein is associated with MS. In some instances, the SNP disclosed herein is associated with PSC. In some instances, the SNP disclosed herein is associated with Pancolitis. In some instances, the SNP

disclosed herein is associated with Proctitis. In some instances, the SNP disclosed herein is associated with Iritis. In some instances, the SNP disclosed herein is associated with Thrombosis. In some instances, the SNP disclosed herein is associated with Uveitis. In some instances, the SNP disclosed herein is associated with Spondylitis. In some instances, the SNP disclosed herein is associated with arthralgias. In some instances, the althralgia comprises rheumatoid arthritis (RA). In some instances, the SNP disclosed herein is associated with nodosum. In some instances, the SNP disclosed herein is associated with pCD. In some instances, the SNP disclosed herein is associated with Psoriasis. In some instances, the SNP disclosed herein is associated with oral ulcers. In some instances, a SNP is associated with clinical phenotype (*e.g.*, one or the diseases disclosed herein) in a particular location of the intestine. In some instances, the location comprises the ileal, ileocolonic, or colonic region of the intestine, or a combination thereof.

[0063] Disclosed herein are SNPs associated with a subclinical phenotype of a disease or disorder disclosed herein. A subclinical phenotype may be a specific diagnosable disease or condition, or metric to measure disease progression that is characteristic of severe or unusual forms of disease. Non-limiting examples of IBD subclinical phenotypes include, but are not limited to, non-stricturing disease, stricturing disease, stricturing and penetrating disease, a time to first surgery, a time to a second surgery, Paneth cell morphologies, and non-response or loss of response to one or more standard therapies. Non-limiting examples of standard therapy of inflammatory disease include glucocorticosteroids, anti-TNF therapy, anti-a4-b7 therapy (vedolizumab), anti-IL12p40 therapy (ustekinumab), Thalidomide, and Cytosin. In some instances, a SNP is associated with non-response or loss of response to anti-TNF therapy. In some embodiments, a presence of one or more SNPs in a sample obtained from a subject is indicative that the subject has, or will develop, non-response or loss of response to an anti-TNF therapy. Paneth cell morphological phenotypes were determined using the classification set forth in VanDussen *et al.*, “Genetic Variants Synthesize the Produce Paneth Cell Phenotypes That Define Subtypes of Crohn’s Disease,” *Gastroenterology* 2014; 146:200-209.

[0064] Disclosed herein, in some embodiments, are SNPs associated with a time to a first surgery and/or time to a second surgery. Time to a first surgery, and time to second surgery, are subclinical phenotypes used to identify subjects at risk for severe forms of disease. In the context of inflammatory bowel disease, a time to first surgery may be a time from a symptom of the inflammatory bowel disease to a surgery. The time to first surgery may be a time from first diagnosis of the IBD to a time of a first surgery. The time to second surgery may be a time from a first surgery to the time of a second surgery. The first and/or second surgery may comprise surgery on at least a portion of the gastrointestinal tract of the subject. Non-limiting surgeries include an intestinal resection, colectomy, perianal surgery, and stricturoplasty. The symptom may be a symptom described herein. The portion of the gastrointestinal tract may be selected from the anus, the colon, the large intestine, the small intestine, the stomach, and the esophagus.

[0065] Disclosed herein, in some embodiments, are SNPs that are associated with a faster progression to surgery, as compared to an individual who does not carry the SNP. A faster progression to surgery is indicative of complicated disease, often resistant to therapy. In some embodiments, a presence of one or more SNPs in a sample obtained from a subject is indicative that the subject has, or will develop, complicated disease behavior characterized by a faster progression to a first and/or second surgery. A “first surgery,” as disclosed herein, refers to the first surgical treatment (*e.g.*, colectomy or resection) of a disease or disorder described herein in a subject. A “second surgery,” as used here, refers to the second surgical treatment of the same disease or disorder in the subject. In some instances, a SNP disclosed herein is associated with a first time from a first symptom of the inflammatory bowel disease to a first surgery. In some instances, a SNP disclosed herein is associated with a first time from a diagnosis of the inflammatory bowel disease to a first surgery. In some instances, a SNP disclosed herein is associated with a time from an age to a first surgery. The first time may be about one year to about fifteen years. The first time may be about two years to about twelve years. The first time may be about four years to about ten years. The first time may be about four years to about eight years. In some instances, the time to a first colectomy for a subject with mrUC comprises less than 60 months.

[0066] In some instances, a SNP disclosed herein is associated with a second time from a first surgery to a second surgery. The second time may be about one year to about fifteen years. The second time may be about two years to about twelve years. The second time may be about four years to about ten years. The second time may be about four years to about eight years. The time to first surgery for patients carrying a risk allele may be about three years to about nine years. The time to first surgery for patients carrying a risk allele may be about four years to about eight years. The time to first surgery for patients for a risk allele may be about three years to about seven years. The time to first surgery for patients for a risk allele may be about seven years. The time to first surgery for patients homozygous for a non-risk minor allele may be about ten years. The time to first surgery for patients homozygous for a non-risk minor allele may be greater than about ten years. The time to first surgery for patients homozygous for a non-risk minor allele may be at least about ten years.

[0067] Serological Marker Association

[0068] Disclosed herein, in some embodiments are SNP is associated with the expression of serological markers. In some instances, a presence of one or more SNPs in a sample obtained from a subject is indicative that the subject has, or will develop, a disease or condition or subtype of the disease or condition, associated with a presence of a microbiome. Non-limiting examples of serological markers include anti-*Saccharomyces cerevisiae* (ASCA) anti-laminaribioside (ALCA), anti-chitobioside (ACCA), anti-mannobioside (AMCA), anti-laminarin (anti-L) and anti-chitin (anti-C), anti-outer membrane porin C (anti-OmpC), anti-Cbir1 flagellin and anti-I2 antibody, and anti-neutrophil cytoplasmic autoantibodies (ANCA). In some instances, the association between a SNP and associated serological marker with an inflammatory disease or condition disclosed herein is

stronger than the association between the SNP alone. In some instances, the presence of a serological marker in combination with the SNP is predictive of the inflammatory disease or condition.

[0069] In some instances, a SNP disclosed herein is associated with stricturing disease, penetrating disease, or a combination of stricturing and penetrating disease. Stricturing may be described as the presence of a stricture or narrowed region of the intestine. The stricture may comprise scar tissue. In some instances, a SNP disclosed herein is associated with penetrating. Penetrating may be described as the presence of a fistula. Fistulae may occur between sections of the bowel or between the bowel and skin. In some instances, the SNP is associated with stricturing, penetrating, and/or stricturing and penetrating disease is localized in the ileum, colon, or ileocolonic region of the intestine. In some instances, the SNP is associated with medically refractory disease, characterized by the failure of a standard treatment to induce remission of a disease in a subject. In some embodiments, the disease comprises an inflammatory disease disclosed herein. A non-limiting example of refractory inflammatory disease includes refractory Crohn's disease, and refractory ulcerative colitis (mrUC).

[0070] Expression Quantitative Trait Loci

[0071] Disclosed herein, in some embodiments, are genotypes comprising one or more SNPs associated with an increase or a decrease in eQTL expression. In some instances, the SNP occurs in an expression quantitative trait locus (eQTL). Expression quantitative trait loci are genomic loci that affect expression of an mRNA or protein. In some instances, a SNP in an eQTL results in increased IL18R1 expression. In some instances, a SNP in an eQTL results in decreased IL18R1 expression. In some instances, the eQTL is a local eQTL, *e.g.*, within the gene locus. In some instances, the eQTL is a distant eQTL, *e.g.*, outside of the gene locus. In some instances, the eQTL is on a different chromosome than the IL18R1 locus, referred to herein as a trans eQTL. In some instances, the eQTL is on the same chromosome as the IL18R1 locus, referred to herein as a cis eQTL. In some instances, the cis gene comprises a gene listed in FIG. 1A to FIG. 1Q. Q. Q. Q. Q. Q. Q. Q. Q.

[0072] In some instances, the cis gene comprises one or more of Mitogen-Activated Protein Kinase Kinase Kinase 4 (*MAP4K4*), Interleukin 1 Receptor Like 1 (*IL1RL1*), Transmembrane Protein 182 (*TMEM182*), and Interleukin 18 Receptor Accessory Protein (*IL18RAP*). In some instances, the SNP is associated with an increase in expression of MAP4K4. In some instances, the SNP is associated with an increase in expression of IL1RL1. In some instances, the SNP is associated with an increase in expression of TMEM182. In some instances, the SNP is associated with an increase in expression of IL18RAP. In some instances, the SNP is associated with a decrease in expression of MAP4K4. In some instances, the SNP is associated with a decrease in expression of IL1RL1. In some instances, the SNP is associated with a decrease in expression of TMEM182. In some instances, the SNP is associated with a decrease in expression of IL18RAP. In some instances the "increase" or the "decrease" is with reference to a level of the cis gene in a reference population. In some instances, the reference population is a "control" group of individuals who are not diseased.

[0073] In some instances, the eQTL is tissue-independent. In some instances, the eQTL is tissue-dependent. In some instances, methods disclosed herein comprise assaying for or detecting a SNP in an eQTL of rectum tissue. In some instances, methods disclosed herein comprise assaying for or detecting a SNP in an eQTL of anal tissue. In some instances, methods disclosed herein comprise assaying for or detecting a SNP in an eQTL of colon tissue. In some instances, methods disclosed herein comprising assaying for or detecting a SNP in an eQTL of the small intestine tissue. In some instances, methods disclosed herein comprise assaying for or detecting a SNP in an eQTL of intestinal tissue. In some instances, methods disclosed herein comprise assaying for or detecting a SNP in an eQTL of stomach tissue. In some instances, methods disclosed herein comprise assaying for or detecting a SNP in an eQTL of esophageal tissue. QTL mapping may be performed by analysis of variance (ANOVA), standard interval mapping, composite interval mapping, and family-based pedigree mapping. In some instances, the SNP is associated with an increase in expression of IL1RL1 in the small intestine tissue. In some instances, the SNP is associated with an increase in expression of MAP4K4 in the small intestine tissue. In some instances, the SNP is associated with an increase in expression of TMEM182 in the small intestine tissue. In some instances, the SNP is associated with an increase in expression of IL18RAP in the small intestine tissue. In some instances, the SNP is associated with a decrease in expression of IL1RL1 in the small intestine tissue. In some instances, the SNP is associated with a decrease in expression of MAP4K4 in the small intestine tissue in the small intestine tissue. In some instances, the SNP is associated with a decrease in expression of TMEM182 in the small intestine tissue. In some instances, the SNP is associated with a decrease in expression of IL18RAP in the small intestine tissue. In some instances, the SNP is associated with an increase in expression of IL1RL1 in the colon tissue. In some instances, the SNP is associated with an increase in expression of MAP4K4 in the colon tissue. In some instances, the SNP is associated with an increase in expression of TMEM182 in the colon tissue. In some instances, the SNP is associated with an increase in expression of IL18RAP in the colon tissue. In some instances, the SNP is associated with a decrease in expression of IL1RL1 in the colon tissue. In some instances, the SNP is associated with a decrease in expression of MAP4K4 in the colon tissue in the colon tissue. In some instances, the SNP is associated with a decrease in expression of TMEM182 in the colon tissue. In some instances, the SNP is associated with a decrease in expression of IL18RAP in the colon tissue.

[0074] The combination of an eQTL and an association between a SNP and an IBD may allow one to determine how gene expression is related to risk of disease. By way of non-limiting example, rs1921622 has both eQTL and an association with stricturing disease with evidence of penetrating disease in the colon of subjects with CD. eQTL shows that the major allele is associated with an upregulation (Cis_Beta = 0.04961; eqtl_p value = 0.01669) of the MAP4K4 mRNA in small bowel tissue and the association shows that major allele is associated with a risk of stricturing disease with evidence of penetrating disease in the colon of subjects with CD. In other cases the major or minor allele may code for downregulation of the gene and the minor allele might be the risk allele.

[0075] Method of Detection

[0076] Disclosed herein, in some embodiments, are methods of detecting a presence, absence, or level, of a genotype (*e.g.*, IL18R1 risk genotype) or biomarker in a sample obtained from a subject. In some instances, the methods of detection disclosed herein are useful for the diagnosis, prognosis, monitoring of disease progression, selection for treatment, monitoring of treatment, and/or treatment of inflammatory bowel disease (*e.g.*, Crohn's disease, ulcerative colitis, and the like) disclosed herein.

[0077] In some embodiments, methods of detecting a presence, absence, or level of a genotype or biomarker in the sample obtained from the subject involve detecting a nucleic acid sequence. In some cases, the nucleic acid sequence comprises deoxyribonucleic acid (DNA). In some instances, the nucleic acid sequence comprises a denatured DNA molecule or fragment thereof. In some instances, the nucleic acid sequence comprises DNA selected from: genomic DNA, viral DNA, mitochondrial DNA, plasmid DNA, amplified DNA, circular DNA, circulating DNA, cell-free DNA, or exosomal DNA. In some instances, the DNA is single-stranded DNA (ssDNA), double-stranded DNA, denaturing double-stranded DNA, synthetic DNA, and combinations thereof. The circular DNA may be cleaved or fragmented. In some instances, the nucleic acid sequence comprises ribonucleic acid (RNA). In some instances, the nucleic acid sequence comprises fragmented RNA. In some instances, the nucleic acid sequence comprises partially degraded RNA. In some instances, the nucleic acid sequence comprises a microRNA or portion thereof. In some instances, the nucleic acid sequence comprises an RNA molecule or a fragmented RNA molecule (RNA fragments) selected from: a microRNA (miRNA), a pre-miRNA, a pri-miRNA, a mRNA, a pre-mRNA, a viral RNA, a viroid RNA, a virusoid RNA, circular RNA (circRNA), a ribosomal RNA (rRNA), a transfer RNA (tRNA), a pre-tRNA, a long non-coding RNA (lncRNA), a small nuclear RNA (snRNA), a circulating RNA, a cell-free RNA, an exosomal RNA, a vector-expressed RNA, an RNA transcript, a synthetic RNA, and combinations thereof.

[0078] Disclosed herein, in some embodiments, the genotype or biomarker is detected by subjecting a sample obtained from the subject to a nucleic acid-based detection assay. In some instances, the nucleic acid-based detection assay comprises quantitative polymerase chain reaction (qPCR), gel electrophoresis (including for *e.g.*, Northern or Southern blot), immunochemistry, *in situ* hybridization such as fluorescent *in situ* hybridization (FISH), cytochemistry, or sequencing. In some embodiments, the sequencing technique comprises next generation sequencing. In some embodiments, the methods involve a hybridization assay such as fluorogenic qPCR (*e.g.*, TaqMan™, SYBR green, SYBR green I, SYBR green II, SYBR gold, ethidium bromide, methylene blue, Pyronin Y, DAPI, acridine orange, Blue View or phycoerythrin), which involves a nucleic acid amplification reaction with a specific primer pair, and hybridization of the amplified nucleic acid probes comprising a detectable moiety or molecule that is specific to a target nucleic acid sequence. In some instances, a number of amplification cycles for detecting a target nucleic acid in a qPCR assay is about 5 to about 30 cycles. In some instances, the number of amplification cycles for detecting a target nucleic acid is

at least about 5 cycles. In some instances, the number of amplification cycles for detecting a target nucleic acid is at most about 30 cycles. In some instances, the number of amplification cycles for detecting a target nucleic acid is about 5 to about 10, about 5 to about 15, about 5 to about 20, about 5 to about 25, about 5 to about 30, about 10 to about 15, about 10 to about 20, about 10 to about 25, about 10 to about 30, about 15 to about 20, about 15 to about 25, about 15 to about 30, about 20 to about 25, about 20 to about 30, or about 25 to about 30 cycles. For TaqMan™ methods, the probe may be a hydrolysable probe comprising a fluorophore and quencher that is hydrolyzed by DNA polymerase when hybridized to a target nucleic acid. In some cases, the presence of a target nucleic acid is determined when the number of amplification cycles to reach a threshold value is less than 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, or 20 cycles. In some instances, hybridization may occur at standard hybridization temperatures, e.g., between about 35 °C and about 65 °C in a standard PCR buffer.

[0079] An additional exemplary nucleic acid-based detection assay comprises the use of nucleic acid probes conjugated or otherwise immobilized on a bead, multi-well plate, or other substrate, wherein the nucleic acid probes are configured to hybridize with a target nucleic acid sequence. In some instances, the nucleic acid probe is specific to one or more genetic variants disclosed herein is used. In some instances, the nucleic acid probe specific to a SNP or SNV comprises a nucleic acid probe sequence sufficiently complementary to a risk or protective allele of interest, such that hybridization is specific to the risk or protective allele. In some instances, the nucleic acid probe specific to an indel comprises a nucleic acid probe sequence sufficiently complementary to an insertion of a nucleobase within a polynucleotide sequence flanking the insertion, such that hybridization is specific to the indel. In some instances, the nucleic acid probe specific to an indel comprises a probe sequence sufficiently complementary to a polynucleotide sequence flanking a deletion of a nucleobase within the polynucleotide sequence, such that hybridization is specific to the indel. In some instances, the nucleic acid probe specific to a biomarker comprises a nucleic acid probe sequence sufficiently complementary to the polynucleotide sequence of the biomarker. In some instances, the biomarker comprises a transcribed polynucleotide sequence (e.g., RNA, cDNA). In some embodiments, the nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least about 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, or 50 nucleotides in length and sufficient to specifically hybridize under standard hybridization conditions to the target nucleic acid sequence. In some embodiments, the target nucleic acid sequence is immobilized on a solid surface and contacted with a probe, for example by running the isolated target nucleic acid sequence on an agarose gel and transferring the target nucleic acid sequence from the gel to a membrane, such as nitrocellulose. In some embodiments, the probe(s) are immobilized on a solid surface, for example, in an Affymetrix gene chip array, and the probe(s) are contacted with the target nucleic acid sequence. The present disclosure provides exemplary probes that are hybridizable to a target nucleic acid sequence comprising one or more single nucleotide polymorphisms (SNPS) at rs13001325, rs1420101, rs12479210, rs950880, rs13020553, rs13019081,

rs12712141, rs2287037, rs1420102, rs12466380, rs1997467, rs1558619, rs1420088, rs12999364, rs4142132, rs12987977, rs11690443, rs1362350, rs12996505, rs873022, rs974389, rs3771177, rs3732129, rs17026974, rs6706844, rs13020793, rs11685480, rs1558622, rs10183388, rs12712135, rs10189711, rs11685424, rs10189202, rs10191914, rs11123918, rs1968171, rs6733174, rs59247511, rs1558620, rs1921622, rs12998521, rs13017455, rs1362349, rs11123923, rs10190555, rs1035127, rs17027087, rs2080289, rs4851570, rs17027060, rs12712145, rs1420098, rs3732123, rs2287034, rs3860444, rs3821203, rs56258475, rs2270298, rs4851006, rs6710885, rs1568681, rs2241117, rs17027037, rs2270297, rs6753717, rs3755274, rs17027071, rs6750020, rs17027006, rs11683700, rs2058622, rs4851007, rs3732126, rs1807782, rs12469506, rs4851575, rs3771172, rs11465633, rs1135354, rs1558627, rs55927292, rs3771171, rs13015714, rs2160202, rs55883125, rs2041740, rs1035130, rs1420103, rs67723747, rs6543116, rs55664618, rs4851005, rs17027056, rs1420089, rs62152661, rs1420095, rs56030066, rs62152714, rs17696376, rs12105808, rs78248680, rs56151044, rs62152662, rs17651485, rs3771170, rs11123926, rs76721133, rs4988955, rs9807962, rs9808453, rs13424006, rs11695627, rs3771166, rs10173193, rs11465575, rs4851566, rs9308857, rs1974675, rs6751967, rs3771162, rs56386507, rs1997466, rs12712140, and/or rs1362348. In some instances, the probe comprises at least about 10 nucleic acids within SEQ ID NOS: 1-7, or reverse complement thereof, including the nucleobase indicated with an "N". In some embodiments, the "N" within SEQ ID NO: 1 comprises an "A" or a "G." In some embodiments, the "N" within SEQ ID NO: 2 comprises an "A" or a "G." In some embodiments, the "N" within SEQ ID NO: 3 comprises a "C" or a "T." In some embodiments, the "N" within SEQ ID NO: 4 comprises an "A" or a "G." In some embodiments, the "N" within SEQ ID NO: 5 comprises an "A" or a "G." In some embodiments, the "N" within SEQ ID NO: 6 comprises an "A" or a "G." In some embodiments, the "N" within SEQ ID NO: 7 comprises an "A" or a "G."

[0080] In some embodiments, the term "probe" with regards to nucleic acids, refers to any nucleic acid molecule that is capable of selectively binding to a specifically intended target nucleic acid sequence. In some instances, probes are specifically designed to be labeled, for example, with a radioactive label, a fluorescent label, an enzyme, a chemiluminescent tag, a colorimetric tag, or other labels or tags that are known in the art. In some instances, the fluorescent label comprises a fluorophore. In some instances, the fluorophore is an aromatic or heteroaromatic compound. In some instances, the fluorophore is a pyrene, anthracene, naphthalene, acridine, stilbene, benzoxazole, indole, benzindole, oxazole, thiazole, benzothiazole, canine, carbocyanine, salicylate, anthranilate, xanthenes dye, coumarin. Exemplary xanthene dyes include, e.g., fluorescein and rhodamine dyes. Fluorescein and rhodamine dyes include, but are not limited to 6-carboxyfluorescein (FAM), 2'/7'-dimethoxy-4'/5'-dichloro-6-carboxyfluorescein (JOE), tetrachlorofluorescein (TET), 6-carboxyrhodamine (R6G), N,N,N,N'-tetramethyl-6-carboxyrhodamine (TAMRA), 6-carboxy-X-rhodamine (ROX). Suitable fluorescent probes also include the naphthylamine dyes that have an amino group in the alpha or beta position. For example, naphthylamino compounds include 1-

dimethylaminonaphthyl-5-sulfonate, 1-anilino-8-naphthalene sulfonate and 2-p-toluidinyl-6-naphthalene sulfonate, 5-(2'-aminoethyl)aminonaphthalene-1-sulfonic acid (EDANS). Exemplary coumarins include, e.g., 3-phenyl-7-isocyanatocoumarin; acridines, such as 9-isothiocyanatoacridine and acridine orange; N-(p-(2-benzoxazolyl)phenyl) maleimide; cyanines, such as, e.g., indodicarbocyanine 3 (Cy3), indodicarbocyanine 5 (Cy5), indodicarbocyanine 5.5 (Cy5.5), 3-(-carboxy-pentyl)-3'-ethyl-5,5'-dimethyloxacarboxyanine (CyA); 1H, 5H, 11H, 15H-Xantheno[2,3, 4-ij:5,6, 7-i'j']diquinolizin-18-ium, 9-[2 (or 4)-[[[6-[2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]amino]sulfonyl]-4 (or 2)-sulfophenyl]-2,3, 6,7, 12,13, 16,17-octahydro-inner salt (TR or Texas Red); or BODIPY™ dyes. In some cases, the probe comprises FAM as the dye label.

[0081] Disclosed herein, in some embodiments, a genotype or biomarker is detected by subjecting a sample obtained from the subject to a nucleic acid amplification assay. In some instances, the amplification assay comprises polymerase chain reaction (PCR), qPCR, self-sustained sequence replication, transcriptional amplification system, Q-Beta Replicase, rolling circle replication, or any suitable other nucleic acid amplification technique. A suitable nucleic acid amplification technique is configured to amplify a region of a nucleic acid sequence comprising one or more genetic risk variants disclosed herein. In some instances, the amplification assays requires primers. The nucleic acid sequence for the genetic risk variants and/or genes known or provided herein is sufficient to enable one of skill in the art to select primers to amplify any portion of the gene or genetic variants. A DNA sample suitable as a primer may be obtained, e.g., by polymerase chain reaction (PCR) amplification of genomic DNA, fragments of genomic DNA, fragments of genomic DNA ligated to adaptor sequences or cloned sequences. A person of skill in the art would utilize computer programs to design of primers with the desired specificity and optimal amplification properties, such as Oligo version 7.0 (National Biosciences). Controlled robotic systems are useful for isolating and amplifying nucleic acids and can be used.

[0082] In some embodiments, detecting the biomarker or genotype of the subject comprises sequencing genetic material obtained from a biological sample from the subject. Sequencing can be performed with any appropriate sequencing technology, including but not limited to single-molecule real-time (SMRT) sequencing, Polony sequencing, sequencing by ligation, reversible terminator sequencing, proton detection sequencing, ion semiconductor sequencing, nanopore sequencing, electronic sequencing, pyrosequencing, Maxam-Gilbert sequencing, chain termination (e.g., Sanger) sequencing, +S sequencing, or sequencing by synthesis. Sequencing methods also include next-generation sequencing, e.g., modern sequencing technologies such as Illumina sequencing (e.g., Solexa), Roche 454 sequencing, Ion torrent sequencing, and SOLiD sequencing. In some cases, next-generation sequencing involves high-throughput sequencing methods. Additional sequencing methods available to one of skill in the art may also be employed.

[0083] In some instances, a number of nucleotides that are sequenced are at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 100, 150, 200, 300, 400, 500, 2000, 4000, 6000, 8000, 10000, 20000, 50000, 100000,

or more than 100000 nucleotides. In some instances, the number of nucleotides sequenced is in a range of about 1 to about 100000 nucleotides, about 1 to about 10000 nucleotides, about 1 to about 1000 nucleotides, about 1 to about 500 nucleotides, about 1 to about 300 nucleotides, about 1 to about 200 nucleotides, about 1 to about 100 nucleotides, about 5 to about 100000 nucleotides, about 5 to about 10000 nucleotides, about 5 to about 1000 nucleotides, about 5 to about 500 nucleotides, about 5 to about 300 nucleotides, about 5 to about 200 nucleotides, about 5 to about 100 nucleotides, about 10 to about 100000 nucleotides, about 10 to about 10000 nucleotides, about 10 to about 1000 nucleotides, about 10 to about 500 nucleotides, about 10 to about 300 nucleotides, about 10 to about 200 nucleotides, about 10 to about 100 nucleotides, about 20 to about 100000 nucleotides, about 20 to about 10000 nucleotides, about 20 to about 1000 nucleotides, about 20 to about 500 nucleotides, about 20 to about 300 nucleotides, about 20 to about 200 nucleotides, about 20 to about 100 nucleotides, about 30 to about 100000 nucleotides, about 30 to about 10000 nucleotides, about 30 to about 1000 nucleotides, about 30 to about 500 nucleotides, about 30 to about 300 nucleotides, about 30 to about 200 nucleotides, about 30 to about 100 nucleotides, about 50 to about 100000 nucleotides, about 50 to about 10000 nucleotides, about 50 to about 1000 nucleotides, about 50 to about 500 nucleotides, about 50 to about 300 nucleotides, about 50 to about 200 nucleotides, or about 50 to about 100 nucleotides.

[0084] Disclosed herein, in some embodiments, are methods for detecting a transcriptomic risk signature or transcriptomic risk profile in a sample obtained from the subject. In some embodiments, the presence, level, or activity of two or more biomarkers in a sample is determined by detecting a transcribed or reverse transcribed polynucleotide, or portion thereof (e.g., mRNA, or cDNA), of a target gene making up the transcriptomic risk signature or transcriptomic risk profile. Any suitable method of detecting a biomarker, such as those disclosed herein, may be utilized to detect a transcriptomic risk signature or transcriptomic risk profile, such as those disclosed herein. A transcriptomic risk signature or transcriptomic risk profile can also be detected at the protein level, using a detection reagent that detects the protein product encoded by the mRNA of the biomarker, directly or indirectly, such the detection reagents disclosed herein.

[0085] Disclosed herein, in some embodiments, genetic material is extracted from a sample obtained from a subject, e.g., a sample of blood or serum. In certain embodiments where nucleic acids are extracted, the nucleic acids are extracted using any technique that does not interfere with subsequent analysis. In certain embodiments, this technique uses alcohol precipitation using ethanol, methanol or isopropyl alcohol. In certain embodiments, this technique uses phenol, chloroform, or any combination thereof. In certain embodiments, this technique uses cesium chloride. In certain embodiments, this technique uses sodium, potassium or ammonium acetate or any other salt commonly used to precipitate DNA. In certain embodiments, this technique utilizes a column or resin based nucleic acid purification scheme such as those commonly sold commercially, one non-limiting example would be the GenElute Bacterial Genomic DNA Kit available from Sigma Aldrich. In certain

embodiments, after extraction the nucleic acid is stored in water, Tris buffer, or Tris-EDTA buffer before subsequent analysis. In an exemplary embodiment, the nucleic acid material is extracted in water. In some cases, extraction does not comprise nucleic acid purification. In certain embodiments, RNA may be extracted from cells using RNA extraction techniques including, for example, using acid phenol/guanidine isothiocyanate extraction (RNAzol B; Biogenesis), RNeasy RNA preparation kits (Qiagen) or PAXgene (PreAnalytix, Switzerland).

[0086] In some embodiments, methods of detecting a presence, absence, or level of a target protein (e.g., biomarker) in the sample obtained from the subject involve detecting protein activity or expression. A target protein may be detected by use of an antibody-based assay, where an antibody specific to the target protein is utilized. In some embodiments, antibody-based detection methods utilize an antibody that binds to any region of target protein. An exemplary method of analysis comprises performing an enzyme-linked immunosorbent assay (ELISA). The ELISA assay may be a sandwich ELISA or a direct ELISA. Another exemplary method of analysis comprises a single molecule array, e.g., Simoa. Other exemplary methods of detection include immunohistochemistry and lateral flow assay. Additional exemplary methods for detecting target protein include, but are not limited to, gel electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, and the like, or various immunological methods such as fluid or gel precipitation reactions, immunodiffusion (single or double), immunoelectrophoresis, radioimmunoassay (RIA), immunofluorescent assays, and Western blotting. In some embodiments, antibodies, or antibody fragments, are used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. The antibody or protein can be immobilized on a solid support for Western blots and immunofluorescence techniques. Suitable solid phase supports or carriers include any support capable of binding an antigen or an antibody. Exemplary supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

[0087] In some cases, a target protein may be detected by detecting binding between the target protein and a binding partner of the target protein. In some cases, the target protein comprises IL18R1. Non-limiting examples of binding partners of IL18R1 include IL18. Exemplary methods of analysis of protein-protein binding comprise performing an assay *in vivo* or *in vitro*, or *ex vivo*. In some instances, the method of analysis comprises an assay such as a co-immunoprecipitation (co-IP), pull-down, crosslinking protein interaction analysis, labeled transfer protein interaction analysis, or Far-western blot analysis, FRET based assay, including, for example FRET-FLIM, a yeast two-hybrid assay, BiFC, or split luciferase assay.

[0088] Disclosed herein, in some embodiments, are methods of detecting a presence or a level of one or more serological markers in a sample obtained from a subject. In some embodiments, the one or more serological markers comprises anti-Saccharomyces cerevisiae antibody (ASCA), an anti-neutrophil cytoplasmic antibody (ANCA), E.coli outer membrane porin protein C (OmpC), anti-

Malassezia restricta antibody, anti-Malassezia pachydermatis antibody, anti-Malassezia furfur antibody, anti-Malassezia globosa antibody, anti-Cladosporium albicans antibody, anti-laminaribiose antibody (ALCA), anti-chitobioside antibody (ACCA), anti-laminarin antibody, anti-chitin antibody, pANCA antibody, anti-I2 antibody, and anti-Cbir1 flagellin antibody. In some embodiments, the antibodies comprises immunoglobulin A (IgA), immunoglobulin G (IgG), immunoglobulin E (IgE), or immunoglobulin M (IgM), immunoglobulin D (IgD), or a combination thereof. Any suitable method for detecting a target protein or biomarker disclosed herein may be used to detect a presence, absence, or level of a serological marker. In some embodiments, the presence or the level of the one or more serological markers is detected using an enzyme-linked immunosorbent assay (ELISA), a single molecule array (Simoa), immunohistochemistry, internal transcribed spacer (ITS) sequencing, or any combination thereof. In some embodiments, the ELISA is a fixed leukocyte ELISA. In some embodiments, the ELISA is a fixed neutrophil ELISA. A fixed leukocyte or neutrophil ELISA may be useful for the detection of certain serological markers, such as those described in Saxon *et al.*, A distinct subset of antineutrophil cytoplasmic antibodies is associated with inflammatory bowel disease, *J. Allergy Clin. Immuno.* 86:2; 202-210 (August 1990). In some embodiments, ELISA units (EU) are used to measure positivity of a presence or level of a serological marker (e.g., seropositivity), which reflects a percentage of a standard or reference value. In some embodiments, the standard comprises pooled sera obtained from well-characterized patient population (e.g., diagnosed with the same disease or condition the subject has, or is suspected of having) reported as being seropositive for the serological marker of interest. In some embodiments, the control or reference value comprises 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 EU. In some instances, a quartile sum scores are calculated using, for example, the methods reported in Landers C J, Cohavy O, Misra R. *et al.*, Selected loss of tolerance evidenced by Crohn's disease-associated immune responses to auto- and microbial antigens. *Gastroenterology* (2002)123:689–699.

[0089] Methods of Diagnosis and Prognosis

[0090] Disclosed herein, in some embodiments, are methods of diagnosing a disease or condition in a subject. In some cases, the disease or condition comprises an inflammatory disease, fibrostenotic disease, and/or fibrotic disease. Non-limiting examples of inflammatory diseases include diseases of the GI tract, liver, gallbladder, and joints. In some cases, the inflammatory disease IBD, CD, UC, systemic lupus erythematosus (SLE), or rheumatoid arthritis. In some embodiments, the disease or condition comprises fibrosis, fibrostenosis, or a fibrotic disease, either isolated or in combination with an inflammatory disease. An exemplary fibrotic disease is PSC. In some embodiments, a subtype of the disease or condition is diagnosed in the subject. Non-limiting examples of subtypes of IBD include, stricturing disease, penetrating disease, stricturing and penetrating disease, obstructive disease, refractory disease, or another complicated form of IBD. In some instances, the subject is diagnosed with, or predicted to develop, one disease or condition, two disease or conditions, three disease or conditions, or more.

[0091] Disclosed herein, in some embodiments, are methods of diagnosing a disease or condition in a subject comprising: (a) obtaining a sample from a subject; (b) subjecting the sample to an assay configured to detect a presence, absence, or level, of one or more IL18R1 risk genotypes; (c) diagnosing the subject with the disease or condition, provided the presence, absence, or level of one or more IL18R1 risk genotypes is detected in the sample obtained from the subject. In some embodiments, the one or more IL18R1 risk genotypes is detected using one or more methods of detection, kits and/or compositions disclosed herein. In some embodiments, the subject is treated by administering a therapeutically effective amount of a therapeutic agent and/or additional agent disclosed herein to the subject, provided the subject is diagnosed with the disease or condition. In some embodiments, the therapeutic agent comprises an antagonist of IL18R1. In some embodiments, the one or more IL18R1 risk genotypes is associated with Crohn's disease. In some embodiments, the one or more IL18R1 risk genotypes is associated with inflammatory bowel disease. In some embodiments, the one or more IL18R1 risk genotypes is associated with ulcerative colitis.

[0092] Disclosed herein, in some embodiments, are methods of predicting whether a subject will develop a disease or condition, the method comprising: (a) obtaining a sample from a subject; (b) subjecting the sample to an assay configured to detect a presence, absence, or level, of one or more IL18R1 risk genotypes; (c) predicting that the subject will develop the disease or condition, provided the presence, absence, or level of the one or more IL18R1 risk genotypes is detected in the sample obtained from the subject. In some embodiments, the one or more IL18R1 risk genotypes is detected using one or more methods of detection, kits and/or compositions disclosed herein. In some embodiments, the subject is treated by administering a therapeutically effective amount of a therapeutic agent and/or additional agent disclosed herein to the subject, provided the subject is predicted to develop the disease or condition. In some embodiments, the therapeutic agent comprises an antagonist of IL18R1. In some embodiments, the one or more IL18R1 risk genotypes is associated with Crohn's disease. In some embodiments, the one or more IL18R1 risk genotypes is associated with inflammatory bowel disease. In some embodiments, the one or more IL18R1 risk genotypes is associated with ulcerative colitis.

[0093] In some embodiments, the one or more IL18R1 risk genotypes comprises a SNP provided in FIG. 1A to FIG. 1Q. In some instances, the one or more IL18R1 risk genotypes is provided in Tables 1-5. In some instances, the one or more SNPs of IL18R1 comprise rs13001325, rs1420101, rs12479210, rs950880, rs13020553, rs13019081, rs12712141, rs2287037, rs1420102, rs12466380, rs1997467, rs1558619, rs1420088, rs12999364, rs4142132, rs12987977, rs11690443, rs1362350, rs12996505, rs873022, rs974389, rs3771177, rs3732129, rs17026974, rs6706844, rs13020793, rs11685480, rs1558622, rs10183388, rs12712135, rs10189711, rs11685424, rs10189202, rs10191914, rs11123918, rs1968171, rs6733174, rs59247511, rs1558620, rs1921622, rs12998521, rs13017455, rs1362349, rs11123923, rs10190555, rs1035127, rs17027087, rs2080289, rs4851570, rs17027060, rs12712145, rs1420098, rs3732123, rs2287034, rs3860444, rs3821203, rs56258475,

rs2270298, rs4851006, rs6710885, rs1568681, rs2241117, rs17027037, rs2270297, rs6753717, rs3755274, rs17027071, rs6750020, rs17027006, rs11683700, rs2058622, rs4851007, rs3732126, rs1807782, rs12469506, rs4851575, rs3771172, rs11465633, rs1135354, rs1558627, rs55927292, rs3771171, rs13015714, rs2160202, rs55883125, rs2041740, rs1035130, rs1420103, rs67723747, rs6543116, rs55664618, rs4851005, rs17027056, rs1420089, rs62152661, rs1420095, rs56030066, rs62152714, rs17696376, rs12105808, rs78248680, rs56151044, rs62152662, rs17651485, rs3771170, rs11123926, rs76721133, rs4988955, rs9807962, rs9808453, rs13424006, rs11695627, rs3771166, rs10173193, rs11465575, rs4851566, rs9308857, rs1974675, rs6751967, rs3771162, rs56386507, rs1997466, rs12712140, and/or rs1362348, or a SNP in linkage disequilibrium therewith.

[0094] Methods of Characterizing a Subtype of a Disease or Condition

[0095] Disclosed herein, in some embodiments, are methods of characterizing a disease or condition, or a subtype of a disease or condition. In some cases, the disease or condition comprises an inflammatory disease, fibrostenotic disease, and/or fibrotic disease. Non-limiting examples of inflammatory diseases include diseases of the GI tract, liver, gallbladder, and joints. In some cases, the inflammatory disease IBD, CD, UC, systemic lupus erythematosus (SLE), or rheumatoid arthritis. In some embodiments, the disease or condition comprises fibrosis, fibrostenosis, or a fibrotic disease, either isolated or in combination with an inflammatory disease. An exemplary fibrotic disease is PSC. Non-limiting examples of subtypes of IBD include, stricturing disease, penetrating disease, stricturing and penetrating disease, obstructive disease, refractory disease, or another complicated form of IBD.

[0096] Disclosed herein, in some embodiments, are methods of characterizing a disease or condition, or a subtype of a disease or condition comprising: (a) obtaining a sample from a subject; (b) subjecting the sample to an assay configured to detect a presence, absence, or level, of one or more IL18R1 risk genotypes; (c) characterizing the disease or condition as being associated with at least one of non-stricturing and non-penetrating, stricturing, and penetrating, provided the presence, absence, or level of one or more IL18R1 risk genotypes is detected in the sample obtained from the subject. In some embodiments, the one or more IL18R1 risk genotypes is detected using one or more methods of detection, kits and/or compositions disclosed herein. In some embodiments, the subject is treated by administering a therapeutically effective amount of a therapeutic agent and/or additional agent disclosed herein to the subject, provided the subject is disease or condition is characterized as being associated with at least one of non-stricturing and non-penetrating, stricturing, and penetrating. In some embodiments, the therapeutic agent comprises a modulator of IL18R1.

[0097] Disclosed herein, in some embodiments, are methods of characterizing a disease or condition, or a subtype of a disease or condition comprising: (a) obtaining a sample from a subject; (b) subjecting the sample to an assay configured to detect a presence, absence, or level, of one or more IL18R1 risk genotypes; (c) characterizing the disease or condition as being associated with at least one of non-stricturing and non-penetrating, stricturing, and penetrating that is isolated to an ileum, ileocolonic region of an intestine, or colon, provided the presence, absence, or level of one or more

IL18R1 risk genotypes is detected in the sample obtained from the subject. In some embodiments, the one or more IL18R1 risk genotypes is detected using one or more methods of detection, kits and/or compositions disclosed herein. In some embodiments, the subject is treated by administering a therapeutically effective amount of a therapeutic agent and/or additional agent disclosed herein to the subject, provided the subject is disease or condition is characterized as being associated with the at least one of non-stricturing and non-penetrating, stricturing, and penetrating is isolated to an ileum, ileocolonic region of an intestine, or colon. In some embodiments, the therapeutic agent comprises a modulator of IL18R1.

[0098] Disclosed herein, in some embodiments, are methods of characterizing a disease or condition, or a subtype of a disease or condition comprising: (a) obtaining a sample from a subject; (b) subjecting the sample to an assay configured to detect a presence, absence, or level, of one or more IL18R1 risk genotypes; (c) characterizing the disease or condition as being associated with morphological defects in ileal Paneth cells, provided the presence, absence, or level of one or more IL18R1 risk genotypes is detected in the sample obtained from the subject. In some embodiments, the one or more IL18R1 risk genotypes is detected using one or more methods of detection, kits and/or compositions disclosed herein. In some embodiments, the subject is treated by administering a therapeutically effective amount of a therapeutic agent and/or additional agent disclosed herein to the subject, provided the subject is disease or condition is characterized as being associated with morphological defects in ileal Paneth cells. In some embodiments, the therapeutic agent comprises an modulator of IL18R1.

[0099] In some embodiments, the one or more IL18R1 risk genotypes comprises a SNP provided in FIG. 1A to FIG. 1Q. In some instances, the one or more IL18R1 risk genotypes is provided in Tables 1-5. In some instances, the one or more SNPs of IL18R1 comprise rs13001325, rs1420101, rs12479210, rs950880, rs13020553, rs13019081, rs12712141, rs2287037, rs1420102, rs12466380, rs1997467, rs1558619, rs1420088, rs12999364, rs4142132, rs12987977, rs11690443, rs1362350, rs12996505, rs873022, rs974389, rs3771177, rs3732129, rs17026974, rs6706844, rs13020793, rs11685480, rs1558622, rs10183388, rs12712135, rs10189711, rs11685424, rs10189202, rs10191914, rs11123918, rs1968171, rs6733174, rs59247511, rs1558620, rs1921622, rs12998521, rs13017455, rs1362349, rs11123923, rs10190555, rs1035127, rs17027087, rs2080289, rs4851570, rs17027060, rs12712145, rs1420098, rs3732123, rs2287034, rs3860444, rs3821203, rs56258475, rs2270298, rs4851006, rs6710885, rs1568681, rs2241117, rs17027037, rs2270297, rs6753717, rs3755274, rs17027071, rs6750020, rs17027006, rs11683700, rs2058622, rs4851007, rs3732126, rs1807782, rs12469506, rs4851575, rs3771172, rs11465633, rs1135354, rs1558627, rs55927292, rs3771171, rs13015714, rs2160202, rs55883125, rs2041740, rs1035130, rs1420103, rs67723747, rs6543116, rs55664618, rs4851005, rs17027056, rs1420089, rs62152661, rs1420095, rs56030066, rs62152714, rs17696376, rs12105808, rs78248680, rs56151044, rs62152662, rs17651485, rs3771170, rs11123926, rs76721133, rs4988955, rs9807962, rs9808453, rs13424006, rs11695627,

rs3771166, rs10173193, rs11465575, rs4851566, rs9308857, rs1974675, rs6751967, rs3771162, rs56386507, rs1997466, rs12712140, and/or rs1362348, or a SNP in linkage disequilibrium therewith.

[00100] Methods of Treatment

[00101] Disclosed herein, in some embodiments, are methods of treating a disease or condition, or a symptom of the disease or condition, in a subject, comprising administering of therapeutic effective amount of one or more therapeutic agents to the subject. In some embodiments, the one or more therapeutic agents is administered to the subject alone (e.g., standalone therapy). In some embodiments, the one or more therapeutic agents is administered in combination with an additional agent. In some embodiments, the therapeutic agent is a first-line therapy for the disease or condition. In some embodiments, the therapeutic agent is a second-line, third-line, or fourth-line therapy, for the disease or condition.

[00102] Therapeutic Agent

[00103] Disclosed herein, in some embodiments, are therapeutic agents useful for the treatment of a disease or condition, or symptom of the disease or condition, disclosed herein. In some embodiments, the therapeutic agent comprises a modulator, agonist, and/or antagonist of interleukin 18 receptor 1 (IL18R1).

[00104] Methods disclosed herein may comprise and/or utilize a therapeutic agent or use thereof, wherein the therapeutic agent is effective to modify expression and/or activity of IL18R1 (e.g., modulator of IL18R1). Therapeutic agents that modify expression and/or activity of IL18R1 may also be referred to herein as IL18R1-targeting agents. Alternatively or additionally, compositions, kits and methods disclosed herein may comprise and/or utilize a therapeutic agent or use thereof, wherein the therapeutic agent modifies expression and/or activity of a protein that functions upstream or downstream of a pathway that involves IL18R1. In some embodiments, the modulator of IL18R1 is effective to increase or activate the activity or expression of IL18R1 in the subject (e.g., agonist or partial agonist). In some embodiments, the modulator of IL18R1 is effective to decrease or reduce the activity or expression of IL18R1 (e.g., antagonist or partial antagonist).

[00105] In some embodiments, the IL18R1 modulator is an antibody, an antigen binding fragment, a RNA interfering agent (RNAi), a small interfering RNA (siRNA), a short hairpin RNA (shRNA), a microRNA (miRNA), an antisense oligonucleotide, a peptide, a peptidomimetic, a small molecule, or an aptamer.

[00106]] In some instances, the therapeutic agent is an antagonist of IL18R1. In some instances, the antagonist acts as an inverse agonist. In some instances, the therapeutic agent is an allosteric modulator of IL18R1. Methods disclosed herein may comprise administering IL18R1-targeting agents alone. In other instances, methods disclosed herein may comprise administering IL18R1-targeting agents along with another therapeutic agent disclosed herein, a nutritional-based therapy, a nature-based therapy, a diet-based therapy, or a combination thereof.

[00107] In some instances, the subject has a SNP that is associated with, or causes, an increased expression of IL18R1. In some instances, the subject has a SNP that is associated with, or causes increased activity of IL18R1. In some instances, the SNP is associated with, or causes and increase expression of IL18R1. In some instances, the SNP is associated with, or causes an increase activity of IL18R1. In these instances, it may be suitable to use an IL18R1 antagonist to bring IL18R1 activity back to a normal level, e.g., that of a person without the IBD of the subject.

[00108] In some instances, the subject has a SNP that is associated with, or causes decreased expression of IL18R1. In some instances, the subject has a SNP is associated with, or causes, decreased activity of IL18R1. In some instances, the SNP is associated with, or causes, a decrease in expression of IL18R1. In some instances, the SNP is associated with, or causes, decreased activity of IL18R1. In these instances, it may be suitable to use an IL18R1 agonist to bring IL18R1 activity back to a normal level, e.g., that of a person without the IBD of the subject.

[00109] In some instances, the therapeutic agent is a small molecule drug. By way of non-limiting example, a small molecule drug may be a chemical compound. In some instances, the therapeutic agent is a large molecule drug. Large molecule drugs generally comprise a peptide or nucleic acid. By way of non-limiting example, the large molecule drug may comprise an antibody or antigen binding antibody fragment. In some instances, the therapeutic agent comprises a small molecule and a large molecule. By way of non-limiting example, the therapeutic agent may comprise an antibody-drug conjugate.

[00110] In some instances, the therapeutic agent is a small molecule that binds IL18R1. In some instances, the small molecule that binds IL18R1 is an IL18R1 agonist. In some instances, the small molecule that binds IL18R1 is an IL18R1 partial agonist. In some instances, the small molecule that binds IL18R1 is an IL18R1 antagonist. In some instances, the small molecule that binds IL18R1 is an IL18R1 partial agonist.

[00111] In some instances, the therapeutic agent is a modulator of IL18R1 binding protein. For example, the therapeutic agent is a modulator of IL18. In some instances, the modulator of IL18 is an antibody, an antigen binding fragment, a RNA interfering agent (RNAi), a small interfering RNA (siRNA), a short hairpin RNA (shRNA), a microRNA (miRNA), an antisense oligonucleotide, a peptide, a peptidomimetic, a small molecule, or an aptamer.

[00112] In some embodiments, the agonist of IL18R1 comprises an IL18R1 polypeptide. In some embodiments, the IL18R1 polypeptide comprises a human IL18R1 protein (huIL18R1), or a homolog thereof. In some instances the polypeptide is an antagonist, agonist or modulator (e.g., allosteric modulator, orthosteric modulator) of IL18R1. In some embodiments, the IL18R1 polypeptide comprises a recombinant IL18R1 polypeptide. In some embodiments, the recombinant huIL18R1 precursor protein comprises SEQ ID NO: 8)(

MNCRELPLTLWVLISVSTAESCTSRPHITVVEGEPFYLKHCSCSLAHEIETTTKSWYKSSGSQE
HVELNPRSSSRIALHDCVLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVT

SKIVEVKKFFQITCENSYYQTLVNSTSLYKNCKKLLLENNKNPTIKKNAEFEDQGYYS CVHFL
HHNGKLFNITKTFNITIVEDRSNIVPVLLGPKLNHVAVELGKNVRLNCSALLNEEDVIYWMFG
EENGSDPNIHEEKEMRIMTPEGKWHASKVLRIENIGESNLNVLYNCTVASTGGTDTKSFILVR
KADMADIPGHVFTRGMIIAVLILVAVVCLVTVCVIYRVDLVLFYRHLTRRDETLDGKTYDA
FVSYLKECRPENGEETHFAVEILPRVLEKHFYKLCIFERDVVPGGAVVDEIHSLEKSRRLIIV
LSKSYMSNEVRYELESGLHEALVERKIKILIEFTPVTDFTLFPQSLKLLKSHRVLKWKADKSL
SYNSRFWKNLLYLMPAKTVKPRDEPEVLPVLSSES), which is the amino acid sequence of
human IL18R1 protein (NCBI Reference Sequence No. NP_003846.1). In some embodiments, the
IL18R1 polypeptide comprises a recombinant IL18R1 polypeptide. In some embodiments, the
huIL18R1 comprises an amino acid sequence about 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%,
91%, or 90% homologous to SEQ ID NO: 8. In some embodiments, the recombinant huIL18R1
precursor protein comprises SEQ ID NO: 9

(MNCKKLLLENNKNPTIKKNAEFEDQGYYS CVHFLHHNGKLFNITKTFNITIVEDRSNIVPVLL
GPKLNHVAVELGKNVRLNCSALLNEEDVIYWMFGEENGSDPNIHEEKEMRIMTPEGKWHAS
KVLRIENIGESNLNVLYNCTVASTGGTDTKSFILVRKDMADIPGHVFTRGMIIAVLILVAVVCL
VTVCVIYRVDLVLFYRHLTRRDETLDGKTYDAFVSYLKECRPENGEETHFAVEILPRVLEK
HFGYKLCIFERDVVPGGAVVDEIHSLEKSRRLIIVLSKSYMSNEVRYELESGLHEALVERKIKI
ILIEFTPVTDFTLFPQSLKLLKSHRVLKWKADKSLSYNSRFWKNLLYLMPAKTVKPRDEPEV
LPVLSSES), which is the amino acid sequence of human IL18R1 (NCBI Reference Sequence No.
NP_001269328). In some embodiments, the huIL18R1 comprises an amino acid sequence about 99%,
98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, or 90% homologous to SEQ ID NO: 9.

[00113] In some instances, the IL18R1 polypeptide is truncated. In some instances, the truncation is
an N-terminal deletion. In other instances, the truncation is a C-terminal deletion. In additional
instances, the truncation comprises both N-terminal and C-terminal deletions. For example, the
truncation can be a deletion of at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, or
more residues from either the N-terminus or the C-terminus, or both termini. In some cases, the
IL18R1 polypeptide comprises an N-terminal deletion of at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,
11, 12, 13, 14, 15, 20, or more residues. In some cases, the IL18R1 polypeptide comprises an N-
terminal deletion of at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 residues. In some cases, the IL18R1
polypeptide comprises an N-terminal deletion of at least or about 2 residues. In some cases, the
IL18R1 polypeptide comprises an N-terminal deletion of at least or about 3 residues. In some cases,
the IL18R1 polypeptide comprises an N-terminal deletion of at least or about 4 residues. In some
cases, the IL18R1 polypeptide comprises an N-terminal deletion of at least or about 5 residues. In
some cases, the IL18R1 polypeptide comprises an N-terminal deletion of at least or about 6 residues.
In some cases, the IL18R1 polypeptide comprises an N-terminal deletion of at least or about 7
residues. In some cases, the IL18R1 polypeptide comprises an N-terminal deletion of at least or about
8 residues. In some cases, the IL18R1 polypeptide comprises an N-terminal deletion of at least or

about 9 residues. In some cases, the IL18R1 polypeptide comprises an N-terminal deletion of at least or about 10 residues.

[00114] In some embodiments, the IL18R1 polypeptide has an enhanced plasma half-life. In some instances, the plasma half-life comprises at least 30 minutes, 45 minutes, 60 minutes, 75 minutes, or 90 minutes, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 18 hours, 24 hours, 36 hours, 48 hours, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 12 days, 14 days, 21 days, 28 days, 30 days, or longer than the plasma half-life of the wild-type IL18R1 protein.

[00115] In some embodiments, the IL18R1 polypeptide is a conjugate. In some embodiments, the IL18R1 conjugate comprises an IL18R1 polypeptide comprising at least one amino acid and a conjugating moiety bound to the at least one amino acid. In some embodiments, the at least one amino acid is located proximal to the N-terminus (e.g., proximal to the N-terminal residue). For example, the at least one amino acid is located optionally within the first 10, 20, 30, 40, or 50 residues from the N-terminus. In some cases, the at least one amino acid is located at the N-terminus (i.e., the at least one amino acid is the N-terminal residue of the IL18R1 polypeptide). In other embodiments, the at least one amino acid is located proximal to the C-terminus (e.g., proximal to the C-terminal residue). For example, the at least one amino acid is located optionally within the first 10, 20, 30, 40, or 50 residues from the C-terminus. In some cases, the at least one amino acid is located at the C-terminus (i.e., the at least one amino acid is the C-terminal residue of the IL18R1 polypeptide). In some instances, the IL18R1 conjugate has an enhanced plasma half-life, such as the half-lives described herein. In some embodiments, the IL18R1 conjugate is functionally active (e.g., retains activity). In some embodiments, the IL18R1 conjugate is not functionally active (e.g., devoid of activity). In some embodiments, the conjugating moiety comprises a polymer comprising Polyethylene glycol (PEG).

[00116] In some embodiments, the IL18R1 polypeptide is fused with a second polypeptide. In some embodiments, the second polypeptide comprises a polypeptide with a long plasma half-life relative to the plasma half-life of the IL18R1 polypeptide. In some embodiments, the second polypeptide comprises an antibody or antibody fragment. In some embodiments, the antibody or antibody fragment comprises an IgG1, IgG2, IgG4, IgG3, or IgE. In some embodiments, the IgG is an Fc. In some embodiments, the IgG Fc is human. In some instances, the long plasma half-life polypeptide comprises HSA, transferrin, IgA monomer, Retinol-binding protein, Factor H, Factor XIII, C-reactive protein, Factor IX, Fibrinogen, IFN-alpha, Pentameric IgM, IL-2, or Thyroglobulin.

[00117] Dosages and Routes of Administration

[00118] In general, methods disclosed herein comprise administering a therapeutic agent by oral administration. However, in some instances, methods comprise administering a therapeutic agent by intraperitoneal injection. In some instances, methods comprise administering a therapeutic agent in the form of an anal suppository. In some instances, methods comprise administering a therapeutic

agent by intravenous (“i.v.”) administration. It is conceivable that one may also administer therapeutic agents disclosed herein by other routes, such as subcutaneous injection, intramuscular injection, intradermal injection, transdermal injection percutaneous administration, intranasal administration, intralymphatic injection, rectal administration intragastric administration, or any other suitable parenteral administration. In some embodiments, routes for local delivery closer to site of injury or inflammation are preferred over systemic routes. Routes, dosage, time points, and duration of administering therapeutics may be adjusted. . In some embodiments, administration of therapeutics is prior to, or after, onset of either, or both, acute and chronic symptoms of the disease or condition.

[00119] An effective dose and dosage of therapeutics to prevent or treat the disease or condition disclosed herein is defined by an observed beneficial response related to the disease or condition, or symptom of the disease or condition. Beneficial response comprises preventing, alleviating, arresting, or curing the disease or condition, or symptom of the disease or condition (e.g., reduced instances of diarrhea, rectal bleeding, weight loss, and size or number of intestinal lesions or strictures, reduced fibrosis or fibrogenesis, reduced fibrostenosis, reduced inflammation). In some embodiments, the beneficial response may be measured by detecting a measurable improvement in the presence, level, or activity, of biomarkers, transcriptomic risk profile, or intestinal microbiome in the subject. An “improvement,” as used herein refers to shift in the presence, level, or activity towards a presence, level, or activity, observed in normal individuals (e.g. individuals who do not suffer from the disease or condition). In instances wherein the therapeutic agent is not therapeutically effective or is not providing a sufficient alleviation of the disease or condition, or symptom of the disease or condition, then the dosage amount and/or route of administration may be changed, or an additional agent may be administered to the subject, along with the therapeutic agent. In some embodiments, as a patient is started on a regimen of a therapeutic agent, the patient is also weaned off (e.g., step-wise decrease in dose) a second treatment regimen.

[00120] Suitable dose and dosage administered to a subject is determined by factors including, but not limited to, the particular therapeutic agent, disease condition and its severity, the identity (e.g., weight, sex, age) of the subject in need of treatment, and can be determined according to the particular circumstances surrounding the case, including, e.g., the specific agent being administered, the route of administration, the condition being treated, and the subject or host being treated. In general, however, doses employed for adult human treatment are typically in the range of 0.01 mg-5000 mg per day. In one aspect, doses employed for adult human treatment are from about 1 mg to about 1000 mg per day. In one embodiment, the desired dose is conveniently presented in a single dose or in divided doses administered simultaneously (or over a short period of time) or at appropriate intervals, for example as two, three, four or more sub-doses per day. Non-limiting examples of effective dosages of for oral delivery of a therapeutic agent include between about 0.1 mg/kg and about 100 mg/kg of body weight per day, and preferably between about 0.5 mg/kg and about 50 mg/kg of body weight per day. In other instances, the oral delivery dosage of effective amount is about 1 mg/kg and about 10 mg/kg of body

weight per day of active material. Non-limiting examples of effective dosages for intravenous administration of the therapeutic agent include at a rate between about 0.01 to 100 pmol/kg body weight/min. In some embodiments, the daily dosage or the amount of active in the dosage form are lower or higher than the ranges indicated herein, based on a number of variables in regard to an individual treatment regime. In various embodiments, the daily and unit dosages are altered depending on a number of variables including, but not limited to, the activity of the therapeutic agent used, the disease or condition to be treated, the mode of administration, the requirements of the individual subject, the severity of the disease or condition being treated, and the judgment of the practitioner.

[00121] In some embodiments, the administration of the therapeutic agent is hourly, once every 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days, 15 days, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, or 5 years, or 10 years. The effective dosage ranges may be adjusted based on subject's response to the treatment. Some routes of administration will require higher concentrations of effective amount of therapeutics than other routes.

[00122] In certain embodiments wherein the patient's condition does not improve, upon the doctor's discretion the administration of therapeutic agent is administered chronically, that is, for an extended period of time, including throughout the duration of the patient's life in order to ameliorate or otherwise control or limit the symptoms of the patient's disease or condition. In certain embodiments wherein a patient's status does improve, the dose of therapeutic agent being administered may be temporarily reduced or temporarily suspended for a certain length of time (i.e., a "drug holiday"). In specific embodiments, the length of the drug holiday is between 2 days and 1 year, including by way of example only, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 12 days, 15 days, 20 days, 28 days, or more than 28 days. The dose reduction during a drug holiday is, by way of example only, by 10%-100%, including by way of example only 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, and 100%. In certain embodiments, the dose of drug being administered may be temporarily reduced or temporarily suspended for a certain length of time (i.e., a "drug diversion"). In specific embodiments, the length of the drug diversion is between 2 days and 1 year, including by way of example only, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 12 days, 15 days, 20 days, 28 days, or more than 28 days. The dose reduction during a drug diversion is, by way of example only, by 10%-100%, including by way of example only 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, and 100%. After a suitable length of time, the normal dosing schedule is optionally reinstated.

[00123] In some embodiments, once improvement of the patient's conditions has occurred, a maintenance dose is administered if necessary. Subsequently, in specific embodiments, the dosage or

the frequency of administration, or both, is reduced, as a function of the symptoms, to a level at which the improved disease, disorder or condition is retained. In certain embodiments, however, the patient requires intermittent treatment on a long-term basis upon any recurrence of symptoms.

[00124] Toxicity and therapeutic efficacy of such therapeutic regimens are determined by standard pharmaceutical procedures in cell cultures or experimental animals, including, but not limited to, the determination of the LD50 and the ED50. The dose ratio between the toxic and therapeutic effects is the therapeutic index and it is expressed as the ratio between LD50 and ED50. In certain embodiments, the data obtained from cell culture assays and animal studies are used in formulating the therapeutically effective daily dosage range and/or the therapeutically effective unit dosage amount for use in mammals, including humans. In some embodiments, the daily dosage amount of the therapeutic agent described herein lies within a range of circulating concentrations that include the ED50 with minimal toxicity. In certain embodiments, the daily dosage range and/or the unit dosage amount varies within this range depending upon the dosage form employed and the route of administration utilized.

[00125] *Additional Therapeutic*

[00126] A therapeutic agent may be used alone or in combination with an additional therapeutic agent. In some cases, an “additional therapeutic agent” as used herein is administered alone. The therapeutic agents may be administered together or sequentially. The combination therapies may be administered within the same day, or may be administered one or more days, weeks, months, or years apart. In some cases, a therapeutic agent provided herein is administered if the subject is determined to be non-responsive to a first line of therapy, e.g., such as TNF inhibitor. Such determination may be made by treatment with the first line therapy and monitoring of disease state and/or diagnostic determination that the subject would be non-responsive to the first line therapy.

[00127] In some embodiments, the additional therapeutic agent comprises an anti-TNF therapy, e.g., an anti-TNF α therapy. In some embodiments, the additional therapeutic agent comprises a second-line treatment to an anti-TNF therapy. In some embodiments, the additional therapeutic agent comprises an immunosuppressant, or a class of drugs that suppress, or reduce, the strength of the immune system. In some embodiments, the immunosuppressant is an antibody. Non-limiting examples of immunosuppressant therapeutic agents include STELARA® (ustekinumab) azathioprine (AZA), 6-mercaptopurine (6-MP), methotrexate, cyclosporin A. (CsA).

[00128] In some embodiments, the additional therapeutic agent comprises a selective anti-inflammatory drug, or a class of drugs that specifically target pro-inflammatory molecules in the body. In some embodiments, the anti-inflammatory drug comprises an antibody. In some embodiments, the anti-inflammatory drug comprises a small molecule. Non-limiting examples of anti-inflammatory drugs include ENTYVIO (vedolizumab), corticosteroids, aminosalicylates, mesalamine, balsalazide (Colazal) and olsalazine (Dipentum).

[00129] In some embodiments, the additional therapeutic agent comprises a stem cell therapy. The stem cell therapy may be embryonic or somatic stem cells. The stem cells may be isolated from a donor (allogeneic) or isolated from the subject (autologous). The stem cells may be expanded adipose-derived stem cells (eASCs), hematopoietic stem cells (HSCs), mesenchymal stem (stromal) cells (MSCs), or induced pluripotent stem cells (iPSCs) derived from the cells of the subject. In some embodiments, the therapeutic agent comprises Cx601 / Alofisel® (darvadstrocel).

[00130] In some embodiments, the additional therapeutic agent comprises a small molecule. The small molecule may be used to treat inflammatory diseases or conditions, or fibrostenotic or fibrotic disease. Non-limiting examples of small molecules include Otezla® (apremilast), alicaforsen, or ozanimod (RPC-1063).

[00131] In some embodiments, the additional therapeutic agent comprises an agonist of TL1A, JAK1, GPR35, ADCY7, IFNG, TNFSF8, PFKFB3, SKAP2 GPR65, SPRED2, IL18RAP, GSDMB, and gene expression products from genes implicated in the pathogenesis of inflammatory, fibrotic, or fibrostenotic disease. The therapeutic agent may be an allosteric modulator of TL1A, JAK1, GPR35, ADCY7, IFNG, TNFSF8, PFKFB3, SKAP2 GPR65, SPRED2, IL18RAP, GSDMB, and gene expression products from genes implicated in the pathogenesis of inflammatory, fibrotic, or fibrostenotic disease.

[00132] In some embodiments, the additional therapeutic agent comprises an antagonist. The antagonist may comprise an inhibitor of the activity or expression of TL1A, JAK1, GPR35, ADCY7, IFNG, TNFSF8, PFKFB3, SKAP2 GPR65, SPRED2, IL18R1, GSDMB, and gene expression products from genes implicated in the pathogenesis of inflammatory, fibrotic, or fibrostenotic disease. Non-limiting examples of JAK1 inhibitors include Ruxolitinib (INCB018424), S-Ruxolitinib (INCB018424), Baricitinib (LY3009104, INCB028050), Filgotinib (GLPG0634), Momelotinib (CYT387), Cerdulatinib (PRT062070, PRT2070), LY2784544, NVP-BSK805, 2HCl, Tofacitinib (CP-690550, Tasocitinib), XL019, Pacritinib (SB1518), or ZM 39923 HCl.

[00133] In some embodiments the additional therapeutic agent comprises an inhibitor of TL1A expression or activity. In some cases, the inhibitor of TL1A expression or activity is effective to inhibit TL1A-DR3 binding. In some embodiments, the inhibitor of TL1A expression or activity comprises an allosteric modulator of TL1A. An allosteric modulator of TL1A may indirectly influence the effects TL1A on DR3, or TR6/DcR3 on TL1A or DR3. The inhibitor of TL1A expression or activity may be a direct inhibitor or indirect inhibitor. Non-limiting examples of an inhibitor of TL1A expression include RNA to protein TL1A translation inhibitors, antisense oligonucleotides targeting the TNFSF15 mRNA (such as miRNAs, or siRNA), epigenetic editing (such as targeting the DNA-binding domain of TNFSF15, or post-translational modifications of histone tails and/or DNA molecules). Non-limiting examples of an inhibitor of TL1A activity include antagonists to the TL1A receptors, (DR3 and TR6/DcR3), antagonists to TL1A antigen, and antagonists to gene expression products involved in TL1A mediated disease. Antagonists as disclosed

herein, may include, but are not limited to, an anti-TL1A antibody, an anti-TL1A-binding antibody fragment, or a small molecule. The small molecule may be a small molecule that binds to TL1A or DR3. The anti-TL1A antibody may be monoclonal or polyclonal. The anti-TL1A antibody may be humanized or chimeric. The anti-TL1A antibody may be a fusion protein. The anti-TL1A antibody may be a blocking anti-TL1A antibody. A blocking antibody blocks binding between two proteins, e.g., a ligand and its receptor. Therefore, a TL1A blocking antibody includes an antibody that prevents binding of TL1A to DR3 or TR6/DcR3 receptors. In a non-limiting example, the TL1A blocking antibody binds to DR3. In another example, the TL1A blocking antibody binds to DcR3. In some cases, the TL1A antibody is an anti-TL1A antibody that specifically binds to TL1A.

[00134] In some embodiments the additional therapeutic agent comprises an inhibitor of CD30L expression or activity. The inhibitor of CD30L expression or activity may be a direct inhibitor or indirect inhibitor. Non-limiting examples of an inhibitor of CD30L expression include RNA to protein TL1A translation inhibitors, antisense oligonucleotides targeting the mRNA (such as miRNAs, or siRNA), epigenetic editing (such as targeting the DNA-binding domain of CD30L, or post-translational modifications of histone tails and/or DNA molecules). In some embodiments, the CD30L inhibitor is an anti-CD30L antibody. The anti-CD30L antibody may be monoclonal or polyclonal. The anti-CD30L antibody may be humanized or chimeric.

[00135] In some instances, the additional therapeutic agent comprises administering to the subject an active agent that modulates CARD9 activity or expression. In various embodiments, the inhibitor of CARD9 activity or expression comprises a CARD9 antibody, a small molecule, a direct inhibitor of CARD9, an indirect inhibitor of CARD9, an allosteric modulator of CARD9, an anti-CARD9 antibody or antibody fragment, antibody or antibody fragment that specifically binds to Rubicon, an anti-ripartite Motif Containing 62 (TRIM62) antibody or antibody fragment, an antibody or antibody fragment that specifically binds to B Cell CLL/Lymphoma 10 (BCL10), an inhibitor of CARD9-Rubicon interaction, an inhibitor of CARD9-Tripartite Motif Containing 62 (TRIM62) interaction, an inhibitor of CARD9-B Cell CLL/Lymphoma 10 (BCL10) interaction, a small molecule that specifically binds CARD9 a small molecule that specifically binds to Rubicon, a small molecule that specifically binds to Tripartite Motif Containing 62 (TRIM62), a small molecule that specifically binds to B Cell CLL/Lymphoma 10 (BCL10), an inhibitor of CARD9-Rubicon interaction, an inhibitor of CARD9-Tripartite Motif Containing 62 (TRIM62) interaction, an inhibitor of B Cell CLL/Lymphoma 10 (BCL10)-CARD9 interaction, or a combination thereof. In some other embodiments, the inhibitor of CARD9 activity or expression comprises the small molecule inhibitor BRD5529, BRD4203, BRD8991, BRD4098 or a combination thereof. In some embodiments, the CARD9 antibody recognizes the total CARD9 protein. In other embodiments, the CARD9 antibody recognizes 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, or 10% of the total CARD9 protein. In some embodiments, the modulator of CARD9 comprises a stem cell therapy. The stem cell therapy may be embryonic or somatic stem cells. The stem cells may be isolated from a donor (allogeneic) or isolated

from the subject (autologous). The stem cells may be expanded adipose-derived stem cells (eASCs), hematopoietic stem cells (HSCs), mesenchymal stem (stromal) cells (MSCs), or induced pluripotent stem cells (iPSCs) derived from the cells of the subject.

[00136] In some embodiments, the additional therapeutic agent comprises administering to the subject an antibody or antibody fragment, a small molecule, an allosteric modulator, an agonist, an antagonist, a direct modulator of Dectin-1A, an indirect modulator of Dectin-1A, or a combination thereof. In other embodiments, the treatment is an inhibitor of C-type lectin-like receptors. In various embodiments, the agonist is soluble β -glucan antagonist laminarin. In various other embodiments, the antagonist is soluble β -glucan antagonist laminarin. In some embodiments, the antibody binds to the C-type lectin-like receptors. In some embodiments, the Dectin-1 antibody recognizes the total Dectin-1 protein. In other embodiments, the Dectin-1 antibody recognizes 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, or 10% of the total Dectin-1A protein. In some embodiments, the modulator of Dectin-1A comprises a stem cell therapy. The stem cell therapy may be embryonic or somatic stem cells. The stem cells may be isolated from a donor (allogeneic) or isolated from the subject (autologous). The stem cells may be expanded adipose-derived stem cells (eASCs), hematopoietic stem cells (HSCs), mesenchymal stem (stromal) cells (MSCs), or induced pluripotent stem cells (iPSCs) derived from the cells of the subject.

[00137] In some instances, the additional therapeutic agent comprises administering to the subject an antimycotic agent. In some instances, the antimycotic agent comprises an active agent that inhibits growth of a fungus. In some instances, the antimycotic agent comprises an active agent that kills a fungus. In some embodiments, the antimycotic agent comprises polyene, an azole, an echinocandin, an flucytosine, an allylamine, a tolnaftate, or griseofulvin, or a combination thereof. In other embodiments, the azole comprises triazole, imidazole, clotrimazole, ketoconazole, itraconazole, terconazole, oxiconazole, miconazole, econazole, tioconazole, voriconazole, fluconazole, isavuconazole, itraconazole, pramiconazole, ravuconazole, or posaconazole. In some other embodiments, the polyene comprises amphotericin B, nystatin, or natamycin. In yet other embodiments, the echinocandin comprises caspofungin, anidulafungin, or micafungin. In various other embodiments, the allylamine comprises naftifine or terbinafine.

[00138] Pharmaceutical Composition

[00139] A pharmaceutical composition, as used herein, refers to a mixture of a therapeutic agent, with other chemical components (i.e. pharmaceutically acceptable inactive ingredients), such as carriers, excipients, binders, filling agents, suspending agents, flavoring agents, sweetening agents, disintegrating agents, dispersing agents, surfactants, lubricants, colorants, diluents, solubilizers, moistening agents, plasticizers, stabilizers, penetration enhancers, wetting agents, anti-foaming agents, antioxidants, preservatives, or one or more combination thereof. Optionally, the compositions include two or more therapeutic agent (e.g., one or more therapeutic agents and one or more additional agents) as discussed herein. In practicing the methods of treatment or use provided herein,

therapeutically effective amounts of therapeutic agents described herein are administered in a pharmaceutical composition to a mammal having a disease, disorder, or condition to be treated, e.g., an inflammatory disease, fibrostenotic disease, and/or fibrotic disease. In some embodiments, the mammal is a human. A therapeutically effective amount can vary widely depending on the severity of the disease, the age and relative health of the subject, the potency of the therapeutic agent used and other factors. The therapeutic agents can be used singly or in combination with one or more therapeutic agents as components of mixtures.

[00140] The pharmaceutical formulations described herein are administered to a subject by appropriate administration routes, including but not limited to, intravenous, intraarterial, oral, parenteral, buccal, topical, transdermal, rectal, intramuscular, subcutaneous, intraosseous, transmucosal, inhalation, or intraperitoneal administration routes. The pharmaceutical formulations described herein include, but are not limited to, aqueous liquid dispersions, self-emulsifying dispersions, solid solutions, liposomal dispersions, aerosols, solid dosage forms, powders, immediate release formulations, controlled release formulations, fast melt formulations, tablets, capsules, pills, delayed release formulations, extended release formulations, pulsatile release formulations, multiparticulate formulations, and mixed immediate and controlled release formulations.

[00141] Pharmaceutical compositions including a therapeutic agent are manufactured in a conventional manner, such as, by way of example only, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or compression processes.

[00142] The pharmaceutical compositions may include at least a therapeutic agent as an active ingredient in free-acid or free-base form, or in a pharmaceutically acceptable salt form. In addition, the methods and pharmaceutical compositions described herein include the use of *N*-oxides (if appropriate), crystalline forms, amorphous phases, as well as active metabolites of these compounds having the same type of activity. In some embodiments, therapeutic agents exist in unsolvated form or in solvated forms with pharmaceutically acceptable solvents such as water, ethanol, and the like. The solvated forms of the therapeutic agents are also considered to be disclosed herein.

[00143] In some embodiments, a therapeutic agent exists as a tautomer. All tautomers are included within the scope of the agents presented herein. As such, it is to be understood that a therapeutic agent or a salt thereof may exhibit the phenomenon of tautomerism whereby two chemical compounds that are capable of facile interconversion by exchanging a hydrogen atom between two atoms, to either of which it forms a covalent bond. Since the tautomeric compounds exist in mobile equilibrium with each other they may be regarded as different isomeric forms of the same compound.

[00144] In some embodiments, a therapeutic agent exists as an enantiomer, diastereomer, or other stereoisomeric form. The agents disclosed herein include all enantiomeric, diastereomeric, and epimeric forms as well as mixtures thereof.

[00145] In some embodiments, therapeutic agents described herein may be prepared as prodrugs. A "prodrug" refers to an agent that is converted into the parent drug in vivo. Prodrugs are often useful because, in some situations, they may be easier to administer than the parent drug. They may, for instance, be bioavailable by oral administration whereas the parent is not. The prodrug may also have improved solubility in pharmaceutical compositions over the parent drug. An example, without limitation, of a prodrug would be a therapeutic agent described herein, which is administered as an ester (the "prodrug") to facilitate transmittal across a cell membrane where water solubility is detrimental to mobility but which then is metabolically hydrolyzed to the carboxylic acid, the active entity, once inside the cell where water-solubility is beneficial. A further example of a prodrug might be a short peptide (polyaminoacid) bonded to an acid group where the peptide is metabolized to reveal the active moiety. In certain embodiments, upon in vivo administration, a prodrug is chemically converted to the biologically, pharmaceutically or therapeutically active form of the therapeutic agent. In certain embodiments, a prodrug is enzymatically metabolized by one or more steps or processes to the biologically, pharmaceutically or therapeutically active form of the therapeutic agent.

[00146] Prodrug forms of the therapeutic agents, wherein the prodrug is metabolized in vivo to produce an agent as set forth herein are included within the scope of the claims. Prodrug forms of the herein described therapeutic agents, wherein the prodrug is metabolized in vivo to produce an agent as set forth herein are included within the scope of the claims. In some cases, some of the therapeutic agents described herein may be a prodrug for another derivative or active compound. In some embodiments described herein, hydrazones are metabolized in vivo to produce a therapeutic agent.

[00147] In certain embodiments, compositions provided herein include one or more preservatives to inhibit microbial activity. Suitable preservatives include mercury-containing substances such as merfen and thiomersal; stabilized chlorine dioxide; and quaternary ammonium compounds such as benzalkonium chloride, cetyltrimethylammonium bromide and cetylpyridinium chloride.

[00148] In some embodiments, formulations described herein benefit from antioxidants, metal chelating agents, thiol containing compounds and other general stabilizing agents. Examples of such stabilizing agents, include, but are not limited to: (a) about 0.5% to about 2% w/v glycerol, (b) about 0.1% to about 1% w/v methionine, (c) about 0.1% to about 2% w/v monothioglycerol, (d) about 1 mM to about 10 mM EDTA, (e) about 0.01% to about 2% w/v ascorbic acid, (f) 0.003% to about 0.02% w/v polysorbate 80, (g) 0.001% to about 0.05% w/v. polysorbate 20, (h) arginine, (i) heparin, (j) dextran sulfate, (k) cyclodextrins, (l) pentosan polysulfate and other heparinoids, (m) divalent cations such as magnesium and zinc; or (n) combinations thereof.

[00149] The pharmaceutical compositions described herein are formulated into any suitable dosage form, including but not limited to, aqueous oral dispersions, liquids, gels, syrups, elixirs, slurries, suspensions, solid oral dosage forms, aerosols, controlled release formulations, fast melt formulations, effervescent formulations, lyophilized formulations, tablets, powders, pills, dragees, capsules, delayed release formulations, extended release formulations, pulsatile release formulations, multiparticulate

formulations, and mixed immediate release and controlled release formulations. In one aspect, a therapeutic agent as discussed herein, e.g., therapeutic agent is formulated into a pharmaceutical composition suitable for intramuscular, subcutaneous, or intravenous injection. In one aspect, formulations suitable for intramuscular, subcutaneous, or intravenous injection include physiologically acceptable sterile aqueous or non-aqueous solutions, dispersions, suspensions or emulsions, and sterile powders for reconstitution into sterile injectable solutions or dispersions. Examples of suitable aqueous and non-aqueous carriers, diluents, solvents, or vehicles include water, ethanol, polyols (propyleneglycol, polyethylene-glycol, glycerol, cremophor and the like), suitable mixtures thereof, vegetable oils (such as olive oil) and injectable organic esters such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants. In some embodiments, formulations suitable for subcutaneous injection also contain additives such as preserving, wetting, emulsifying, and dispensing agents. Prevention of the growth of microorganisms can be ensured by various antibacterial and antifungal agents, such as parabens, chlorobutanol, phenol, sorbic acid, and the like. In some cases it is desirable to include isotonic agents, such as sugars, sodium chloride, and the like. Prolonged absorption of the injectable pharmaceutical form can be brought about by the use of agents delaying absorption, such as aluminum monostearate and gelatin.

[00150] For intravenous injections or drips or infusions, a therapeutic agent described herein is formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hank's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art. For other parenteral injections, appropriate formulations include aqueous or nonaqueous solutions, preferably with physiologically compatible buffers or excipients. Such excipients are known.

[00151] Parenteral injections may involve bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The pharmaceutical composition described herein may be in a form suitable for parenteral injection as a sterile suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. In one aspect, the active ingredient is in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

[00152] For administration by inhalation, a therapeutic agent is formulated for use as an aerosol, a mist or a powder. Pharmaceutical compositions described herein are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol, the dosage unit may be determined

by providing a valve to deliver a metered amount. Capsules and cartridges of, such as, by way of example only, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the therapeutic agent described herein and a suitable powder base such as lactose or starch.

[00153] Representative intranasal formulations are described in, for example, U.S. Pat. Nos. 4,476,116, 5,116,817 and 6,391,452. Formulations that include a therapeutic agent are prepared as solutions in saline, employing benzyl alcohol or other suitable preservatives, fluorocarbons, and/or other solubilizing or dispersing agents known in the art. See, for example, Ansel, H. C. *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery Systems*, Sixth Ed. (1995). Preferably these compositions and formulations are prepared with suitable nontoxic pharmaceutically acceptable ingredients. These ingredients are known to those skilled in the preparation of nasal dosage forms and some of these can be found in REMINGTON: THE SCIENCE AND PRACTICE OF PHARMACY, 21st edition, 2005. The choice of suitable carriers is dependent upon the exact nature of the nasal dosage form desired, e.g., solutions, suspensions, ointments, or gels. Nasal dosage forms generally contain large amounts of water in addition to the active ingredient. Minor amounts of other ingredients such as pH adjusters, emulsifiers or dispersing agents, preservatives, surfactants, gelling agents, or buffering and other stabilizing and solubilizing agents are optionally present. Preferably, the nasal dosage form should be isotonic with nasal secretions.

[00154] Pharmaceutical preparations for oral use are obtained by mixing one or more solid excipient with one or more of the therapeutic agents described herein, optionally grinding the resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients include, for example, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methylcellulose, microcrystalline cellulose, hydroxypropylmethylcellulose, sodium carboxymethylcellulose; or others such as: polyvinylpyrrolidone (PVP or povidone) or calcium phosphate. If desired, disintegrating agents are added, such as the cross-linked croscarmellose sodium, polyvinylpyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. In some embodiments, dyestuffs or pigments are added to the tablets or dragee coatings for identification or to characterize different combinations of active therapeutic agent doses.

[00155] In some embodiments, pharmaceutical formulations of a therapeutic agent are in the form of capsules, including push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active therapeutic agent is dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In some embodiments, stabilizers are added. A capsule may be prepared, for example, by placing the bulk blend of the formulation of the therapeutic agent inside of a capsule. In some

embodiments, the formulations (non-aqueous suspensions and solutions) are placed in a soft gelatin capsule. In other embodiments, the formulations are placed in standard gelatin capsules or non-gelatin capsules such as capsules comprising HPMC. In other embodiments, the formulation is placed in a sprinkle capsule, wherein the capsule is swallowed whole or the capsule is opened and the contents sprinkled on food prior to eating.

[00156] All formulations for oral administration are in dosages suitable for such administration. In one aspect, solid oral dosage forms are prepared by mixing a therapeutic agent with one or more of the following: antioxidants, flavoring agents, and carrier materials such as binders, suspending agents, disintegration agents, filling agents, surfactants, solubilizers, stabilizers, lubricants, wetting agents, and diluents. In some embodiments, the solid dosage forms disclosed herein are in the form of a tablet, (including a suspension tablet, a fast-melt tablet, a bite-disintegration tablet, a rapid-disintegration tablet, an effervescent tablet, or a caplet), a pill, a powder, a capsule, solid dispersion, solid solution, bioerodible dosage form, controlled release formulations, pulsatile release dosage forms, multiparticulate dosage forms, beads, pellets, granules. In other embodiments, the pharmaceutical formulation is in the form of a powder. Compressed tablets are solid dosage forms prepared by compacting the bulk blend of the formulations described above. In various embodiments, tablets will include one or more flavoring agents. In other embodiments, the tablets will include a film surrounding the final compressed tablet. In some embodiments, the film coating can provide a delayed release of a therapeutic agent from the formulation. In other embodiments, the film coating aids in patient compliance (e.g., Opadry® coatings or sugar coating). Film coatings including Opadry® typically range from about 1% to about 3% of the tablet weight. In some embodiments, solid dosage forms, e.g., tablets, effervescent tablets, and capsules, are prepared by mixing particles of a therapeutic agent with one or more pharmaceutical excipients to form a bulk blend composition. The bulk blend is readily subdivided into equally effective unit dosage forms, such as tablets, pills, and capsules. In some embodiments, the individual unit dosages include film coatings. These formulations are manufactured by conventional formulation techniques.

[00157] In another aspect, dosage forms include microencapsulated formulations. In some embodiments, one or more other compatible materials are present in the microencapsulation material. Exemplary materials include, but are not limited to, pH modifiers, erosion facilitators, anti-foaming agents, antioxidants, flavoring agents, and carrier materials such as binders, suspending agents, disintegration agents, filling agents, surfactants, solubilizers, stabilizers, lubricants, wetting agents, and diluents. Exemplary useful microencapsulation materials include, but are not limited to, hydroxypropyl cellulose ethers (HPC) such as Klucel® or Nisso HPC, low-substituted hydroxypropyl cellulose ethers (L-HPC), hydroxypropyl methyl cellulose ethers (HPMC) such as Seppifilm-LC, Pharmacoat®, Metolose SR, Methocel®-E, Opadry YS, PrimaFlo, Benecel MP824, and Benecel MP843, methylcellulose polymers such as Methocel®-A, hydroxypropylmethylcellulose acetate stearate Aqoat (HF-LS, HF-LG, HF-MS) and Metolose®, Ethylcelluloses (EC) and mixtures thereof

such as E461, Ethocel®, Aqualon®-EC, Surelease®, Polyvinyl alcohol (PVA) such as Opadry AMB, hydroxyethylcelluloses such as Natrosol®, carboxymethylcelluloses and salts of carboxymethylcelluloses (CMC) such as Aqualon®-CMC, polyvinyl alcohol and polyethylene glycol co-polymers such as Kollicoat IR®, monoglycerides (Myverol), triglycerides (KLX), polyethylene glycols, modified food starch, acrylic polymers and mixtures of acrylic polymers with cellulose ethers such as Eudragit® EPO, Eudragit® L30D-55, Eudragit® FS 30D Eudragit® L100-55, Eudragit® L100, Eudragit® S100, Eudragit® RD100, Eudragit® E100, Eudragit® L12.5, Eudragit® S12.5, Eudragit® NE30D, and Eudragit® NE 40D, cellulose acetate phthalate, sepiifilms such as mixtures of HPMC and stearic acid, cyclodextrins, and mixtures of these materials.

[00158] Liquid formulation dosage forms for oral administration are optionally aqueous suspensions selected from the group including, but not limited to, pharmaceutically acceptable aqueous oral dispersions, emulsions, solutions, elixirs, gels, and syrups. See, e.g., Singh et al., Encyclopedia of Pharmaceutical Technology, 2nd Ed., pp. 754-757 (2002). In addition to therapeutic agent the liquid dosage forms optionally include additives, such as: (a) disintegrating agents; (b) dispersing agents; (c) wetting agents; (d) at least one preservative, (e) viscosity enhancing agents, (f) at least one sweetening agent, and (g) at least one flavoring agent. In some embodiments, the aqueous dispersions further includes a crystal-forming inhibitor.

[00159] In some embodiments, the pharmaceutical formulations described herein are self-emulsifying drug delivery systems (SEDDS). Emulsions are dispersions of one immiscible phase in another, usually in the form of droplets. Generally, emulsions are created by vigorous mechanical dispersion. SEDDS, as opposed to emulsions or microemulsions, spontaneously form emulsions when added to an excess of water without any external mechanical dispersion or agitation. An advantage of SEDDS is that only gentle mixing is required to distribute the droplets throughout the solution. Additionally, water or the aqueous phase is optionally added just prior to administration, which ensures stability of an unstable or hydrophobic active ingredient. Thus, the SEDDS provides an effective delivery system for oral and parenteral delivery of hydrophobic active ingredients. In some embodiments, SEDDS provides improvements in the bioavailability of hydrophobic active ingredients. Methods of producing self-emulsifying dosage forms include, but are not limited to, for example, U.S. Pat. Nos. 5,858,401, 6,667,048, and 6,960,563.

[00160] Buccal formulations that include a therapeutic agent are administered using a variety of formulations known in the art. For example, such formulations include, but are not limited to, U.S. Pat. Nos. 4,229,447, 4,596,795, 4,755,386, and 5,739,136. In addition, the buccal dosage forms described herein can further include a bioerodible (hydrolysable) polymeric carrier that also serves to adhere the dosage form to the buccal mucosa. For buccal or sublingual administration, the compositions may take the form of tablets, lozenges, or gels formulated in a conventional manner.

[00161] For intravenous injections, a therapeutic agent is optionally formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hank's solution, Ringer's solution, or

physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. For other parenteral injections, appropriate formulations include aqueous or nonaqueous solutions, preferably with physiologically compatible buffers or excipients.

[00162] Parenteral injections optionally involve bolus injection or continuous infusion. Formulations for injection are optionally presented in unit dosage form, e.g., in ampoules or in multi dose containers, with an added preservative. In some embodiments, a pharmaceutical composition described herein is in a form suitable for parenteral injection as a sterile suspensions, solutions or emulsions in oily or aqueous vehicles, and contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Pharmaceutical formulations for parenteral administration include aqueous solutions of an agent that modulates the activity of a carotid body in water soluble form. Additionally, suspensions of an agent that modulates the activity of a carotid body are optionally prepared as appropriate, e.g., oily injection suspensions.

[00163] Conventional formulation techniques include, e.g., one or a combination of methods: (1) dry mixing, (2) direct compression, (3) milling, (4) dry or non-aqueous granulation, (5) wet granulation, or (6) fusion. Other methods include, e.g., spray drying, pan coating, melt granulation, granulation, fluidized bed spray drying or coating (e.g., wurster coating), tangential coating, top spraying, tableting, extruding and the like.

[00164] Suitable carriers for use in the solid dosage forms described herein include, but are not limited to, acacia, gelatin, colloidal silicon dioxide, calcium glycerophosphate, calcium lactate, maltodextrin, glycerine, magnesium silicate, sodium caseinate, soy lecithin, sodium chloride, tricalcium phosphate, dipotassium phosphate, sodium stearyl lactylate, carrageenan, monoglyceride, diglyceride, pregelatinized starch, hydroxypropylmethylcellulose, hydroxypropylmethylcellulose acetate stearate, sucrose, microcrystalline cellulose, lactose, mannitol and the like.

[00165] Suitable filling agents for use in the solid dosage forms described herein include, but are not limited to, lactose, calcium carbonate, calcium phosphate, dibasic calcium phosphate, calcium sulfate, microcrystalline cellulose, cellulose powder, dextrose, dextrans, dextran, starches, pregelatinized starch, hydroxypropylmethylcellulose (HPMC), hydroxypropylmethylcellulose phthalate, hydroxypropylmethylcellulose acetate stearate (HPMCAS), sucrose, xylitol, lactitol, mannitol, sorbitol, sodium chloride, polyethylene glycol, and the like.

[00166] Suitable disintegrants for use in the solid dosage forms described herein include, but are not limited to, natural starch such as corn starch or potato starch, a pregelatinized starch, or sodium starch glycolate, a cellulose such as methylcrystalline cellulose, methylcellulose, microcrystalline cellulose, croscarmellose, or a cross-linked cellulose, such as cross-linked sodium carboxymethylcellulose, cross-linked carboxymethylcellulose, or cross-linked croscarmellose, a cross-linked starch such as sodium starch glycolate, a cross-linked polymer such as crospovidone, a cross-linked polyvinylpyrrolidone, alginate such as alginic acid or a salt of alginic acid such as sodium alginate, a

gum such as agar, guar, locust bean, Karaya, pectin, or tragacanth, sodium starch glycolate, bentonite, sodium lauryl sulfate, sodium lauryl sulfate in combination starch, and the like.

[00167] Binders impart cohesiveness to solid oral dosage form formulations: for powder filled capsule formulation, they aid in plug formation that can be filled into soft or hard shell capsules and for tablet formulation, they ensure the tablet remaining intact after compression and help assure blend uniformity prior to a compression or fill step. Materials suitable for use as binders in the solid dosage forms described herein include, but are not limited to, carboxymethylcellulose, methylcellulose, hydroxypropylmethylcellulose, hydroxypropylmethylcellulose acetate stearate, hydroxyethylcellulose, hydroxypropylcellulose, ethylcellulose, and microcrystalline cellulose, microcrystalline dextrose, amylose, magnesium aluminum silicate, polysaccharide acids, bentonites, gelatin, polyvinylpyrrolidone/vinyl acetate copolymer, crospovidone, povidone, starch, pregelatinized starch, tragacanth, dextrin, a sugar, such as sucrose, glucose, dextrose, molasses, mannitol, sorbitol, xylitol, lactose, a natural or synthetic gum such as acacia, tragacanth, ghatti gum, mucilage of isapol husks, starch, polyvinylpyrrolidone, larch arabogalactan, polyethylene glycol, waxes, sodium alginate, and the like.

[00168] In general, binder levels of 20-70% are used in powder-filled gelatin capsule formulations. Binder usage level in tablet formulations varies whether direct compression, wet granulation, roller compaction, or usage of other excipients such as fillers which itself can act as moderate binder. Binder levels of up to 70% in tablet formulations is common.

[00169] Suitable lubricants or glidants for use in the solid dosage forms described herein include, but are not limited to, stearic acid, calcium hydroxide, talc, corn starch, sodium stearyl fumarate, alkali-metal and alkaline earth metal salts, such as aluminum, calcium, magnesium, zinc, stearic acid, sodium stearates, magnesium stearate, zinc stearate, waxes, Stearowet[®], boric acid, sodium benzoate, sodium acetate, sodium chloride, leucine, a polyethylene glycol or a methoxypolyethylene glycol such as Carbowax[™], PEG 4000, PEG 5000, PEG 6000, propylene glycol, sodium oleate, glyceryl behenate, glyceryl palmitostearate, glyceryl benzoate, magnesium or sodium lauryl sulfate, and the like.

[00170] Suitable diluents for use in the solid dosage forms described herein include, but are not limited to, sugars (including lactose, sucrose, and dextrose), polysaccharides (including dextrans and maltodextrin), polyols (including mannitol, xylitol, and sorbitol), cyclodextrins and the like.

[00171] Suitable wetting agents for use in the solid dosage forms described herein include, for example, oleic acid, glyceryl monostearate, sorbitan monooleate, sorbitan monolaurate, triethanolamine oleate, polyoxyethylene sorbitan monooleate, polyoxyethylene sorbitan monolaurate, quaternary ammonium compounds (e.g., Polyquat 10[®]), sodium oleate, sodium lauryl sulfate, magnesium stearate, sodium docusate, triacetin, vitamin E TPGS and the like.

[00172] Suitable surfactants for use in the solid dosage forms described herein include, for example, sodium lauryl sulfate, sorbitan monooleate, polyoxyethylene sorbitan monooleate, polysorbates,

polaxomers, bile salts, glyceryl monostearate, copolymers of ethylene oxide and propylene oxide, e.g., Pluronic® (BASF), and the like.

[00173] Suitable suspending agents for use in the solid dosage forms described here include, but are not limited to, polyvinylpyrrolidone, e.g., polyvinylpyrrolidone K12, polyvinylpyrrolidone K17, polyvinylpyrrolidone K25, or polyvinylpyrrolidone K30, polyethylene glycol, e.g., the polyethylene glycol can have a molecular weight of about 300 to about 6000, or about 3350 to about 4000, or about 7000 to about 5400, vinyl pyrrolidone/vinyl acetate copolymer (S630), sodium carboxymethylcellulose, methylcellulose, hydroxy-propylmethylcellulose, polysorbate-80, hydroxyethylcellulose, sodium alginate, gums, such as, e.g., gum tragacanth and gum acacia, guar gum, xanthans, including xanthan gum, sugars, cellulosics, such as, e.g., sodium carboxymethylcellulose, methylcellulose, sodium carboxymethylcellulose, hydroxypropylmethylcellulose, hydroxyethylcellulose, polysorbate-80, sodium alginate, polyethoxylated sorbitan monolaurate, polyethoxylated sorbitan monolaurate, povidone and the like.

[00174] Suitable antioxidants for use in the solid dosage forms described herein include, for example, e.g., butylated hydroxytoluene (BHT), sodium ascorbate, and tocopherol.

[00175] It should be appreciated that there is considerable overlap between additives used in the solid dosage forms described herein. Thus, the above-listed additives should be taken as merely exemplary, and not limiting, of the types of additives that can be included in solid dosage forms of the pharmaceutical compositions described herein. The amounts of such additives can be readily determined by one skilled in the art, according to the particular properties desired.

[00176] In various embodiments, the particles of a therapeutic agents and one or more excipients are dry blended and compressed into a mass, such as a tablet, having a hardness sufficient to provide a pharmaceutical composition that substantially disintegrates within less than about 30 minutes, less than about 35 minutes, less than about 40 minutes, less than about 45 minutes, less than about 50 minutes, less than about 55 minutes, or less than about 60 minutes, after oral administration, thereby releasing the formulation into the gastrointestinal fluid.

[00177] In other embodiments, a powder including a therapeutic agent is formulated to include one or more pharmaceutical excipients and flavors. Such a powder is prepared, for example, by mixing the therapeutic agent and optional pharmaceutical excipients to form a bulk blend composition. Additional embodiments also include a suspending agent and/or a wetting agent. This bulk blend is uniformly subdivided into unit dosage packaging or multi-dosage packaging units.

[00178] In still other embodiments, effervescent powders are also prepared. Effervescent salts have been used to disperse medicines in water for oral administration.

[00179] In some embodiments, the pharmaceutical dosage forms are formulated to provide a controlled release of a therapeutic agent. Controlled release refers to the release of the therapeutic agent from a dosage form in which it is incorporated according to a desired profile over an extended period of time. Controlled release profiles include, for example, sustained release, prolonged release,

pulsatile release, and delayed release profiles. In contrast to immediate release compositions, controlled release compositions allow delivery of an agent to a subject over an extended period of time according to a predetermined profile. Such release rates can provide therapeutically effective levels of agent for an extended period of time and thereby provide a longer period of pharmacologic response while minimizing side effects as compared to conventional rapid release dosage forms. Such longer periods of response provide for many inherent benefits that are not achieved with the corresponding short acting, immediate release preparations.

[00180] In some embodiments, the solid dosage forms described herein are formulated as enteric coated delayed release oral dosage forms, i.e., as an oral dosage form of a pharmaceutical composition as described herein which utilizes an enteric coating to affect release in the small intestine or large intestine. In one aspect, the enteric coated dosage form is a compressed or molded or extruded tablet/mold (coated or uncoated) containing granules, powder, pellets, beads or particles of the active ingredient and/or other composition components, which are themselves coated or uncoated. In one aspect, the enteric coated oral dosage form is in the form of a capsule containing pellets, beads or granules, which include a therapeutic agent that are coated or uncoated.

[00181] Any coatings should be applied to a sufficient thickness such that the entire coating does not dissolve in the gastrointestinal fluids at pH below about 5, but does dissolve at pH about 5 and above. Coatings are typically selected from any of the following: Shellac - this coating dissolves in media of pH >7; Acrylic polymers - examples of suitable acrylic polymers include methacrylic acid copolymers and ammonium methacrylate copolymers. The Eudragit series E, L, S, RL, RS and NE (Rohm Pharma) are available as solubilized in organic solvent, aqueous dispersion, or dry powders. The Eudragit series RL, NE, and RS are insoluble in the gastrointestinal tract but are permeable and are used primarily for colonic targeting. The Eudragit series E dissolve in the stomach. The Eudragit series L, L-30D and S are insoluble in stomach and dissolve in the intestine; Poly Vinyl Acetate Phthalate (PVAP) - PVAP dissolves in pH >5, and it is much less permeable to water vapor and gastric fluids. Conventional coating techniques such as spray or pan coating are employed to apply coatings. The coating thickness must be sufficient to ensure that the oral dosage form remains intact until the desired site of topical delivery in the intestinal tract is reached.

[00182] In other embodiments, the formulations described herein are delivered using a pulsatile dosage form. A pulsatile dosage form is capable of providing one or more immediate release pulses at predetermined time points after a controlled lag time or at specific sites. Exemplary pulsatile dosage forms and methods of their manufacture are disclosed in U.S. Pat. Nos. 5,011,692, 5,017,381, 5,229,135, 5,840,329 and 5,837,284. In one embodiment, the pulsatile dosage form includes at least two groups of particles, (i.e. multiparticulate) each containing the formulation described herein. The first group of particles provides a substantially immediate dose of a therapeutic agent upon ingestion by a mammal. The first group of particles can be either uncoated or include a coating and/or sealant. In one aspect, the second group of particles comprises coated particles. The coating on the second

group of particles provides a delay of from about 2 hours to about 7 hours following ingestion before release of the second dose. Suitable coatings for pharmaceutical compositions are described herein or known in the art.

[00183] In some embodiments, pharmaceutical formulations are provided that include particles of a therapeutic agent and at least one dispersing agent or suspending agent for oral administration to a subject. The formulations may be a powder and/or granules for suspension, and upon admixture with water, a substantially uniform suspension is obtained.

[00184] In some embodiments, particles formulated for controlled release are incorporated in a gel or a patch or a wound dressing.

[00185] In one aspect, liquid formulation dosage forms for oral administration and/or for topical administration as a wash are in the form of aqueous suspensions selected from the group including, but not limited to, pharmaceutically acceptable aqueous oral dispersions, emulsions, solutions, elixirs, gels, and syrups. See, e.g., Singh *et al.*, Encyclopedia of Pharmaceutical Technology, 2nd Ed., pp. 754-757 (2002). In addition to the particles of a therapeutic agent, the liquid dosage forms include additives, such as: (a) disintegrating agents; (b) dispersing agents; (c) wetting agents; (d) at least one preservative, (e) viscosity enhancing agents, (f) at least one sweetening agent, and (g) at least one flavoring agent. In some embodiments, the aqueous dispersions can further include a crystalline inhibitor.

[00186] In some embodiments, the liquid formulations also include inert diluents commonly used in the art, such as water or other solvents, solubilizing agents, and emulsifiers. Exemplary emulsifiers are ethyl alcohol, isopropyl alcohol, ethyl carbonate, ethyl acetate, benzyl alcohol, benzyl benzoate, propyleneglycol, 1,3-butyleneglycol, dimethylformamide, sodium lauryl sulfate, sodium docusate, cholesterol, cholesterol esters, taurocholic acid, phosphatidylcholine, oils, such as cottonseed oil, groundnut oil, corn germ oil, olive oil, castor oil, and sesame oil, glycerol, tetrahydrofurfuryl alcohol, polyethylene glycols, fatty acid esters of sorbitan, or mixtures of these substances, and the like.

[00187] Furthermore, pharmaceutical compositions optionally include one or more pH adjusting agents or buffering agents, including acids such as acetic, boric, citric, lactic, phosphoric and hydrochloric acids; bases such as sodium hydroxide, sodium phosphate, sodium borate, sodium citrate, sodium acetate, sodium lactate and tris-hydroxymethylaminomethane; and buffers such as citrate/dextrose, sodium bicarbonate and ammonium chloride. Such acids, bases and buffers are included in an amount required to maintain pH of the composition in an acceptable range.

[00188] Additionally, pharmaceutical compositions optionally include one or more salts in an amount required to bring osmolality of the composition into an acceptable range. Such salts include those having sodium, potassium or ammonium cations and chloride, citrate, ascorbate, borate, phosphate, bicarbonate, sulfate, thiosulfate or bisulfite anions; suitable salts include sodium chloride, potassium chloride, sodium thiosulfate, sodium bisulfite and ammonium sulfate.

[00189] Other pharmaceutical compositions optionally include one or more preservatives to inhibit microbial activity. Suitable preservatives include mercury-containing substances such as merfen and thiomersal; stabilized chlorine dioxide; and quaternary ammonium compounds such as benzalkonium chloride, cetyltrimethylammonium bromide and cetylpyridinium chloride.

[00190] In one embodiment, the aqueous suspensions and dispersions described herein remain in a homogenous state, as defined in The USP Pharmacists' Pharmacopeia (2005 edition, chapter 905), for at least 4 hours. In one embodiment, an aqueous suspension is re-suspended into a homogenous suspension by physical agitation lasting less than 1 minute. In still another embodiment, no agitation is necessary to maintain a homogeneous aqueous dispersion.

[00191] Examples of disintegrating agents for use in the aqueous suspensions and dispersions include, but are not limited to, a starch, e.g., a natural starch such as corn starch or potato starch, a pregelatinized starch, or sodium starch glycolate; a cellulose such as methylcrystalline cellulose, methylcellulose, croscarmellose, or a cross-linked cellulose, such as cross-linked sodium carboxymethylcellulose, cross-linked carboxymethylcellulose, or cross-linked croscarmellose; a cross-linked starch such as sodium starch glycolate; a cross-linked polymer such as crospovidone; a cross-linked polyvinylpyrrolidone; alginate such as alginic acid or a salt of alginic acid such as sodium alginate; a gum such as agar, guar, locust bean, Karaya, pectin, or tragacanth; sodium starch glycolate; bentonite; a natural sponge; a surfactant; a resin such as a cation-exchange resin; citrus pulp; sodium lauryl sulfate; sodium lauryl sulfate in combination starch; and the like.

[00192] In some embodiments, the dispersing agents suitable for the aqueous suspensions and dispersions described herein include, for example, hydrophilic polymers, electrolytes, Tween[®] 60 or 80, PEG, polyvinylpyrrolidone, and the carbohydrate-based dispersing agents such as, for example, hydroxypropylcellulose and hydroxypropyl cellulose ethers, hydroxypropyl methylcellulose and hydroxypropyl methylcellulose ethers, carboxymethylcellulose sodium, methylcellulose, hydroxyethylcellulose, hydroxypropylmethyl-cellulose phthalate, hydroxypropylmethyl-cellulose acetate stearate, noncrystalline cellulose, magnesium aluminum silicate, triethanolamine, polyvinyl alcohol (PVA), polyvinylpyrrolidone/vinyl acetate copolymer, 4-(1,1,3,3-tetramethylbutyl)-phenol polymer with ethylene oxide and formaldehyde (also known as tyloxapol), poloxamers; and poloxamines. In other embodiments, the dispersing agent is selected from a group not comprising one of the following agents: hydrophilic polymers; electrolytes; Tween[®] 60 or 80; PEG; polyvinylpyrrolidone (PVP); hydroxypropylcellulose and hydroxypropyl cellulose ethers; hydroxypropyl methylcellulose and hydroxypropyl methylcellulose ethers; carboxymethylcellulose sodium; methylcellulose; hydroxyethylcellulose; hydroxypropylmethyl-cellulose phthalate; hydroxypropylmethyl-cellulose acetate stearate; non-crystalline cellulose; magnesium aluminum silicate; triethanolamine; polyvinyl alcohol (PVA); 4-(1,1,3,3-tetramethylbutyl)-phenol polymer with ethylene oxide and formaldehyde; poloxamers; or poloxamines.

[00193] Wetting agents suitable for the aqueous suspensions and dispersions described herein include, but are not limited to, cetyl alcohol, glycerol monostearate, polyoxyethylene sorbitan fatty acid esters (e.g., the commercially available Tweens[®] such as e.g., Tween 20[®] and Tween 80[®], and polyethylene glycols, oleic acid, glyceryl monostearate, sorbitan monooleate, sorbitan monolaurate, triethanolamine oleate, polyoxyethylene sorbitan monooleate, polyoxyethylene sorbitan monolaurate, sodium oleate, sodium lauryl sulfate, sodium docusate, triacetin, vitamin E TPGS, sodium taurocholate, simethicone, phosphatidylcholine and the like.

[00194] Suitable preservatives for the aqueous suspensions or dispersions described herein include, for example, potassium sorbate, parabens (e.g., methylparaben and propylparaben), benzoic acid and its salts, other esters of parahydroxybenzoic acid such as butylparaben, alcohols such as ethyl alcohol or benzyl alcohol, phenolic compounds such as phenol, or quaternary compounds such as benzalkonium chloride. Preservatives, as used herein, are incorporated into the dosage form at a concentration sufficient to inhibit microbial growth.

[00195] Suitable viscosity enhancing agents for the aqueous suspensions or dispersions described herein include, but are not limited to, methyl cellulose, xanthan gum, carboxymethyl cellulose, hydroxypropyl cellulose, hydroxypropylmethyl cellulose, Plasdon[®] S-630, carbomer, polyvinyl alcohol, alginates, acacia, chitosans and combinations thereof. The concentration of the viscosity enhancing agent will depend upon the agent selected and the viscosity desired.

[00196] Examples of sweetening agents suitable for the aqueous suspensions or dispersions described herein include, for example, acacia syrup, acesulfame K, alitame, aspartame, chocolate, cinnamon, citrus, cocoa, cyclamate, dextrose, fructose, ginger, glycyrrhetinate, glycyrrhiza (licorice) syrup, monoammonium glycyrrhizinate (MagnaSweet[®]), malitol, mannitol, menthol, neohesperidine DC, neotame, Prosweet[®] Powder, saccharin, sorbitol, stevia, sucralose, sucrose, sodium saccharin, saccharin, aspartame, acesulfame potassium, mannitol, sucralose, tagatose, thaumatin, vanilla, xylitol, or any combination thereof.

[00197] In some embodiments, a therapeutic agent is prepared as transdermal dosage form. In some embodiments, the transdermal formulations described herein include at least three components: (1) a therapeutic agent; (2) a penetration enhancer; and (3) an optional aqueous adjuvant. In some embodiments the transdermal formulations include additional components such as, but not limited to, gelling agents, creams and ointment bases, and the like. In some embodiments, the transdermal formulation is presented as a patch or a wound dressing. In some embodiments, the transdermal formulation further include a woven or non-woven backing material to enhance absorption and prevent the removal of the transdermal formulation from the skin. In other embodiments, the transdermal formulations described herein can maintain a saturated or supersaturated state to promote diffusion into the skin.

[00198] In one aspect, formulations suitable for transdermal administration of a therapeutic agent described herein employ transdermal delivery devices and transdermal delivery patches and can be

lipophilic emulsions or buffered, aqueous solutions, dissolved and/or dispersed in a polymer or an adhesive. In one aspect, such patches are constructed for continuous, pulsatile, or on demand delivery of pharmaceutical agents. Still further, transdermal delivery of the therapeutic agents described herein can be accomplished by means of iontophoretic patches and the like. In one aspect, transdermal patches provide controlled delivery of a therapeutic agent. In one aspect, transdermal devices are in the form of a bandage comprising a backing member, a reservoir containing the therapeutic agent optionally with carriers, optionally a rate controlling barrier to deliver the therapeutic agent to the skin of the host at a controlled and predetermined rate over a prolonged period of time, and means to secure the device to the skin.

[00199] In further embodiments, topical formulations include gel formulations (e.g., gel patches which adhere to the skin). In some of such embodiments, a gel composition includes any polymer that forms a gel upon contact with the body (e.g., gel formulations comprising hyaluronic acid, pluronic polymers, poly(lactic-co-glycolic acid (PLGA)-based polymers or the like). In some forms of the compositions, the formulation comprises a low-melting wax such as, but not limited to, a mixture of fatty acid glycerides, optionally in combination with cocoa butter which is first melted. Optionally, the formulations further comprise a moisturizing agent.

[00200] In certain embodiments, delivery systems for pharmaceutical therapeutic agents may be employed, such as, for example, liposomes and emulsions. In certain embodiments, compositions provided herein can also include an mucoadhesive polymer, selected from among, for example, carboxymethylcellulose, carbomer (acrylic acid polymer), poly(methylmethacrylate), polyacrylamide, polycarboxiphil, acrylic acid/butyl acrylate copolymer, sodium alginate and dextran.

[00201] In some embodiments, a therapeutic agent described herein may be administered topically and can be formulated into a variety of topically administrable compositions, such as solutions, suspensions, lotions, gels, pastes, medicated sticks, balms, creams or ointments. Such pharmaceutical therapeutic agents can contain solubilizers, stabilizers, tonicity enhancing agents, buffers and preservatives.

KITS AND COMPOSITIONS

[00202] Compositions

[00203] Disclosed herein, in some embodiments, are compositions useful for the detection of a genotype or biomarker in a sample obtained from a subject according to the methods described herein. Aspects disclosed herein provide compositions comprising a polynucleotide sequence comprising at least 10 but less than 50 contiguous nucleotides encoding one or more IL18R1 risk genotypes comprising rs13001325, rs1420101, rs12479210, rs950880, rs13020553, rs13019081, rs12712141, rs2287037, rs1420102, rs12466380, rs1997467, rs1558619, rs1420088, rs12999364, rs4142132, rs12987977, rs11690443, rs1362350, rs12996505, rs873022, rs974389, rs3771177, rs3732129, rs17026974, rs6706844, rs13020793, rs11685480, rs1558622, rs10183388, rs12712135, rs10189711, rs11685424, rs10189202, rs10191914, rs11123918, rs1968171, rs6733174, rs59247511, rs1558620,

rs1921622, rs12998521, rs13017455, rs1362349, rs11123923, rs10190555, rs1035127, rs17027087, rs2080289, rs4851570, rs17027060, rs12712145, rs1420098, rs3732123, rs2287034, rs3860444, rs3821203, rs56258475, rs2270298, rs4851006, rs6710885, rs1568681, rs2241117, rs17027037, rs2270297, rs6753717, rs3755274, rs17027071, rs6750020, rs17027006, rs11683700, rs2058622, rs4851007, rs3732126, rs1807782, rs12469506, rs4851575, rs3771172, rs11465633, rs1135354, rs1558627, rs55927292, rs3771171, rs13015714, rs2160202, rs55883125, rs2041740, rs1035130, rs1420103, rs67723747, rs6543116, rs55664618, rs4851005, rs17027056, rs1420089, rs62152661, rs1420095, rs56030066, rs62152714, rs17696376, rs12105808, rs78248680, rs56151044, rs62152662, rs17651485, rs3771170, rs11123926, rs76721133, rs4988955, rs9807962, rs9808453, rs13424006, rs11695627, rs3771166, rs10173193, rs11465575, rs4851566, rs9308857, rs1974675, rs6751967, rs3771162, rs56386507, rs1997466, rs12712140, and/or rs1362348, or reverse complements thereof, wherein the contiguous polynucleotide sequence comprises a detectable molecule. In various embodiments, the detectable molecule comprises a fluorophore. In other embodiments, the polynucleotide sequences further comprise a quencher.

[00204] Also disclosed herein are compositions comprising an antibody or antigen-binding fragment that specifically binds to IL18R1, wherein the antibody or antigen-binding fragment comprises a detectable molecule. In various embodiments, the antibody comprises a monoclonal antibody, a chimeric antibody, a CDR-grafted antibody, a Fab, a Fab', a F(ab')₂, a Fv, a disulfide linked Fv, a scFv, a single domain antibody, a diabody, a multispecific antibody, a dual specific antibody, an anti-idiotypic antibody, or a bispecific antibody. In some embodiments, the antibody or antigen-binding fragment comprises an IgG antibody, an IgM antibody, and/or an IgE antibody. In some embodiments, the detectable molecule comprises a fluorophore. In some embodiments, the antibody or antigen-binding fragment is conjugated to a paramagnetic particle (e.g., bead).

[00205] Kits

[00206] Disclosed herein, in some embodiments, are kits useful for to detect the genotypes and/or biomarkers disclosed herein. In some embodiments, the kits disclosed herein may be used to diagnose and/or treat a disease or condition in a subject; or select a patient for treatment and/or monitor a treatment disclosed herein. In some embodiments, the kit comprises the compositions described herein, which can be used to perform the methods described herein. Kits comprise an assemblage of materials or components, including at least one of the compositions. Thus, in some embodiments the kit contains a composition including of the pharmaceutical composition, for the treatment of IBD. In other embodiments, the kits contains all of the components necessary and/or sufficient to perform an assay for detecting and measuring IBD markers, including all controls, directions for performing assays, and any necessary software for analysis and presentation of results.

[00207] In some instances, the kits described herein comprise components comprising the compositions described herein for detecting the presence, absence, and/or quantity of a target nucleic acid (e.g., IL18R1, IL18R1 SNPs) and/or protein (e.g., IL18R1) described herein. In some

embodiments, the kit further comprises components for detecting the presence, absence, and/or quantity of a serological marker described herein. In some embodiments, the kit comprises the compositions (e.g., primers, probes, antibodies) described herein. The disclosure provides kits suitable for assays such as enzyme-linked immunosorbent assay (ELISA), single-molecular array (Simoa), PCR, and qPCR. The exact nature of the components configured in the kit depends on its intended purpose. For example, some embodiments are configured for the purpose of treating a disease or condition disclosed herein (e.g., IBD, CD, UC) in a subject. In some embodiments, the kit is configured particularly for the purpose of treating mammalian subjects. In some embodiments, the kit is configured particularly for the purpose of treating human subjects. In further embodiments, the kit is configured for veterinary applications, treating subjects such as, but not limited to, farm animals, domestic animals, and laboratory animals. In some embodiments, the kit is configured to select a subject for a therapeutic agent, such as those disclosed herein. In some embodiments, the kit is configured to select a subject for treatment with Crohn's disease, inflammatory bowel disease, or ulcerative colitis.

[00208] In some embodiments, the kit is used to detect a IL18R1 risk genotype in a sample obtained from a subject in need thereof. In some instances, the IL18R1 risk genotype comprises one or more SNPs and/or indels selected at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP in linkage disequilibrium therewith. In some instances, the SNP comprises a risk allele which may be a minor allele, a major allele, or an insertion/deletion of a nucleobase. In some instances, the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some instances, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some instances, the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP. In some instances, the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some instances, the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some instances, the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some instances, the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP. In some instances, the IL18R1 risk genotype 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 SNPs and/or indels. In some instances, if one or more of the above SNPs and/or indels is detected, the subject is "positive" for the IL18R1 risk genotype. In some instances, the kit comprises a pharmaceutical composition comprising a modulator of IL18R1 described herein (e.g., antagonist of IL18R1). In some instances, the subject is administered the antagonist of IL18R1 provided the subject tests "positive" for the IL18R1 risk genotype. In some instances, if one or more of the above SNPs and/or indels is detected, the subject is diagnosed with, or predicted to develop, moderate to severe form of inflammatory bowel disease (IBD, UC, CD), or a subtype of IBD, UC, or CD (e.g., mrUC, stricturing and/or penetrating disease, anti-TNF non-response or loss of response, and the like).

[00209] In some instances, the kit is used to determine a level of a gene expression product expressed from a cis gene described herein (e.g. Mitogen-Activated Protein Kinase Kinase Kinase Kinase 4 (*MAP4K4*), Interleukin 1 Receptor Like 1 (*IL1RL1*), Transmembrane Protein 182 (*TMEM182*), and Interleukin 18 Receptor Accessory Protein (*IL18RAP*), and the like) in a sample obtained from a subject in need thereof. In some instances, the level of the gene expression product detected using the kit described herein is high relative to a normal individual. In some instances, the level of the gene expression product detected using the kit described herein is low relative to a normal individual. In some instances, the subject is administered the agonist of IL18R1 provided the subject has a high or a low expression of the gene expression product. In some instances, if one or more gene expression products is detected, the subject is diagnosed with, or predicted to develop, moderate to severe form of inflammatory bowel disease (IBD, UC, CD), or a subtype of IBD, UC, or CD (e.g., mrUC, stricturing and/or penetrating disease, anti-TNF non-response or loss of response, and the like).

[00210] In some instances, the kit is used to detect both the one or more SNPs or indels described above and one or more gene expression product expressed from a cis gene described herein. In some instances, the subject is administered the agonist of IL18R1 provided the subject has a high or a low expression of the gene expression product, and tests “positive” for the IL18R1 risk genotype. In some instances, if the high or low level of the one or more gene expression products is detected and if the subject tests “positive” for the IL18R1 risk genotype, the subject is diagnosed with, or predicted to develop moderate to severe form of inflammatory bowel disease (IBD, UC, CD), or a subtype of IBD, UC, or CD (e.g., mrUC, stricturing and/or penetrating disease, anti-TNF non-response or loss of response, and the like).

[00211] Instructions for use may be included in the kit. Optionally, the kit also contains other useful components, such as, diluents, buffers, pharmaceutically acceptable carriers, syringes, catheters, applicators, pipetting or measuring tools, bandaging materials or other useful paraphernalia. The materials or components assembled in the kit can be provided to the practitioner stored in any convenient and suitable ways that preserve their operability and utility. For example the components can be in dissolved, dehydrated, or lyophilized form; they can be provided at room, refrigerated or frozen temperatures. The components are typically contained in suitable packaging material(s). As employed herein, the phrase “packaging material” refers to one or more physical structures used to house the contents of the kit, such as compositions and the like. The packaging material is constructed by well-known methods, preferably to provide a sterile, contaminant-free environment. The packaging materials employed in the kit are those customarily utilized in gene expression assays and in the administration of treatments. As used herein, the term “package” refers to a suitable solid matrix or material such as glass, plastic, paper, foil, and the like, capable of holding the individual kit components. Thus, for example, a package can be a glass vial or prefilled syringes used to contain suitable quantities of the pharmaceutical composition. The packaging material has an external label which indicates the contents and/or purpose of the kit and its components.

SYSTEMS

[00212] Disclosed herein, in some embodiments, is a system for detecting a particular SNP in IL18R1 in a subject. The system is configured to implement the methods described in this disclosure, including, but not limited to, detecting the presence of a particular CD subtype to determine whether the subject is suitable for treatment with a particular therapy.

[00213] In some embodiments, disclosed herein is a system for detecting one or more SNPs in IL18R1 in a subject, comprising: (a) a computer processing device, optionally connected to a computer network; and (b) a software module executed by the computer processing device to analyze a target nucleic acid sequence of one or more IL18R1 risk genotypes in a sample from a subject. In some instances, the one or more IL18R1 risk genotypes comprises rs13001325, rs1420101, rs12479210, rs950880, rs13020553, rs13019081, rs12712141, rs2287037, rs1420102, rs12466380, rs1997467, rs1558619, rs1420088, rs12999364, rs4142132, rs12987977, rs11690443, rs1362350, rs12996505, rs873022, rs974389, rs3771177, rs3732129, rs17026974, rs6706844, rs13020793, rs11685480, rs1558622, rs10183388, rs12712135, rs10189711, rs11685424, rs10189202, rs10191914, rs11123918, rs1968171, rs6733174, rs59247511, rs1558620, rs1921622, rs12998521, rs13017455, rs1362349, rs11123923, rs10190555, rs1035127, rs17027087, rs2080289, rs4851570, rs17027060, rs12712145, rs1420098, rs3732123, rs2287034, rs3860444, rs3821203, rs56258475, rs2270298, rs4851006, rs6710885, rs1568681, rs2241117, rs17027037, rs2270297, rs6753717, rs3755274, rs17027071, rs6750020, rs17027006, rs11683700, rs2058622, rs4851007, rs3732126, rs1807782, rs12469506, rs4851575, rs3771172, rs11465633, rs1135354, rs1558627, rs55927292, rs3771171, rs13015714, rs2160202, rs55883125, rs2041740, rs1035130, rs1420103, rs67723747, rs6543116, rs55664618, rs4851005, rs17027056, rs1420089, rs62152661, rs1420095, rs56030066, rs62152714, rs17696376, rs12105808, rs78248680, rs56151044, rs62152662, rs17651485, rs3771170, rs11123926, rs76721133, rs4988955, rs9807962, rs9808453, rs13424006, rs11695627, rs3771166, rs10173193, rs11465575, rs4851566, rs9308857, rs1974675, rs6751967, rs3771162, rs56386507, rs1997466, rs12712140, and/or rs1362348, or SNP in linkage disequilibrium therewith.

In some instances, the system comprises a central processing unit (CPU), memory (e.g., random access memory, flash memory), electronic storage unit, computer program, communication interface to communicate with one or more other systems, and any combination thereof. In some instances, the system is coupled to a computer network, for example, the Internet, intranet, and/or extranet that is in communication with the Internet, a telecommunication, or data network. In some embodiments, the system comprises a storage unit to store data and information regarding any aspect of the methods described in this disclosure. Various aspects of the system are a product or article or manufacture.

[00214] One feature of a computer program includes a sequence of instructions, executable in the digital processing device's CPU, written to perform a specified task. In some embodiments, computer readable instructions are implemented as program modules, such as functions, features, Application Programming Interfaces (APIs), data structures, and the like, that perform particular tasks

or implement particular abstract data types. In light of the disclosure provided herein, those of skill in the art will recognize that a computer program may be written in various versions of various languages.

[00215] The functionality of the computer readable instructions are combined or distributed as desired in various environments. In some instances, a computer program comprises one sequence of instructions or a plurality of sequences of instructions. A computer program may be provided from one location. A computer program may be provided from a plurality of locations. In some embodiment, a computer program includes one or more software modules. In some embodiments, a computer program includes, in part or in whole, one or more web applications, one or more mobile applications, one or more standalone applications, one or more web browser plug-ins, extensions, add-ins, or add-ons, or combinations thereof.

[00216] *Web application*

[00217] In some embodiments, a computer program includes a web application. In light of the disclosure provided herein, those of skill in the art will recognize that a web application may utilize one or more software frameworks and one or more database systems. A web application, for example, is created upon a software framework such as Microsoft® .NET or Ruby on Rails (RoR). A web application, in some instances, utilizes one or more database systems including, by way of non-limiting examples, relational, non-relational, feature oriented, associative, and XML database systems. Suitable relational database systems include, by way of non-limiting examples, Microsoft® SQL Server, mySQL™, and Oracle®. Those of skill in the art will also recognize that a web application may be written in one or more versions of one or more languages. In some embodiments, a web application is written in one or more markup languages, presentation definition languages, client-side scripting languages, server-side coding languages, database query languages, or combinations thereof. In some embodiments, a web application is written to some extent in a markup language such as Hypertext Markup Language (HTML), Extensible Hypertext Markup Language (XHTML), or eXtensible Markup Language (XML). In some embodiments, a web application is written to some extent in a presentation definition language such as Cascading Style Sheets (CSS). In some embodiments, a web application is written to some extent in a client-side scripting language such as Asynchronous Javascript and XML (AJAX), Flash® Actionscript, Javascript, or Silverlight®. In some embodiments, a web application is written to some extent in a server-side coding language such as Active Server Pages (ASP), ColdFusion®, Perl, Java™, JavaServer Pages (JSP), Hypertext Preprocessor (PHP), Python™, Ruby, Tcl, Smalltalk, WebDNA®, or Groovy. In some embodiments, a web application is written to some extent in a database query language such as Structured Query Language (SQL). A web application may integrate enterprise server products such as IBM® Lotus Domino®. A web application may include a media player element. A media player element may utilize one or more of many suitable multimedia technologies including, by way of non-limiting

examples, Adobe® Flash®, HTML 5, Apple® QuickTime®, Microsoft® Silverlight®, Java™, and Unity®.

[00218] Mobile application

[00219] In some instances, a computer program includes a mobile application provided to a mobile digital processing device. The mobile application may be provided to a mobile digital processing device at the time it is manufactured. The mobile application may be provided to a mobile digital processing device via the computer network described herein.

[00220] A mobile application is created by techniques known to those of skill in the art using hardware, languages, and development environments known to the art. Those of skill in the art will recognize that mobile applications may be written in several languages. Suitable programming languages include, by way of non-limiting examples, C, C++, C#, Featureive-C, Java™, Javascript, Pascal, Feature Pascal, Python™, Ruby, VB.NET, WML, and XHTML/HTML with or without CSS, or combinations thereof.

[00221] Suitable mobile application development environments are available from several sources. Commercially available development environments include, by way of non-limiting examples, AirplaySDK, alcheMo, Appcelerator®, Celsius, Bedrock, Flash Lite, .NET Compact Framework, Rhomobile, and WorkLight Mobile Platform. Other development environments may be available without cost including, by way of non-limiting examples, Lazarus, MobiFlex, MoSync, and Phonegap. Also, mobile device manufacturers distribute software developer kits including, by way of non-limiting examples, iPhone and iPad (iOS) SDK, Android™ SDK, BlackBerry® SDK, BREW SDK, Palm® OS SDK, Symbian SDK, webOS SDK, and Windows® Mobile SDK.

[00222] Those of skill in the art will recognize that several commercial forums are available for distribution of mobile applications including, by way of non-limiting examples, Apple® App Store, Android™ Market, BlackBerry® App World, App Store for Palm devices, App Catalog for webOS, Windows® Marketplace for Mobile, Ovi Store for Nokia® devices, Samsung® Apps, and Nintendo® DSi Shop.

[00223] Standalone application

[00224] In some embodiments, a computer program includes a standalone application, which is a program that may be run as an independent computer process, not an add-on to an existing process, e.g., not a plug-in. Those of skill in the art will recognize that standalone applications are sometimes compiled. In some instances, a compiler is a computer program(s) that transforms source code written in a programming language into binary feature code such as assembly language or machine code. Suitable compiled programming languages include, by way of non-limiting examples, C, C++, Featureive-C, COBOL, Delphi, Eiffel, Java™, Lisp, Python™, Visual Basic, and VB .NET, or combinations thereof. Compilation may be often performed, at least in part, to create an executable program. In some instances, a computer program includes one or more executable compiled applications.

[00225] Web browser plug-in

[00226] A computer program, in some aspects, includes a web browser plug-in. In computing, a plug-in, in some instances, is one or more software components that add specific functionality to a larger software application. Makers of software applications may support plug-ins to enable third-party developers to create abilities which extend an application, to support easily adding new features, and to reduce the size of an application. When supported, plug-ins enable customizing the functionality of a software application. For example, plug-ins are commonly used in web browsers to play video, generate interactivity, scan for viruses, and display particular file types. Those of skill in the art will be familiar with several web browser plug-ins including, Adobe® Flash® Player, Microsoft® Silverlight®, and Apple® QuickTime®. The toolbar may comprise one or more web browser extensions, add-ins, or add-ons. The toolbar may comprise one or more explorer bars, tool bands, or desk bands.

[00227] In view of the disclosure provided herein, those of skill in the art will recognize that several plug-in frameworks are available that enable development of plug-ins in various programming languages, including, by way of non-limiting examples, C++, Delphi, Java™, PHP, Python™, and VB .NET, or combinations thereof.

[00228] In some embodiments, Web browsers (also called Internet browsers) are software applications, designed for use with network-connected digital processing devices, for retrieving, presenting, and traversing information resources on the World Wide Web. Suitable web browsers include, by way of non-limiting examples, Microsoft® Internet Explorer®, Mozilla® Firefox®, Google® Chrome, Apple® Safari®, Opera Software® Opera®, and KDE Konqueror. The web browser, in some instances, is a mobile web browser. Mobile web browsers (also called microbrowsers, mini-browsers, and wireless browsers) may be designed for use on mobile digital processing devices including, by way of non-limiting examples, handheld computers, tablet computers, netbook computers, subnotebook computers, smartphones, music players, personal digital assistants (PDAs), and handheld video game systems. Suitable mobile web browsers include, by way of non-limiting examples, Google® Android® browser, RIM BlackBerry® Browser, Apple® Safari®, Palm® Blazer, Palm® WebOS® Browser, Mozilla® Firefox® for mobile, Microsoft® Internet Explorer® Mobile, Amazon® Kindle® Basic Web, Nokia® Browser, Opera Software® Opera® Mobile, and Sony® PSP™ browser.

[00229] Software modules

[00230] The medium, method, and system disclosed herein comprise one or more softwares, servers, and database modules, or use of the same. In view of the disclosure provided herein, software modules may be created by techniques known to those of skill in the art using machines, software, and languages known to the art. The software modules disclosed herein may be implemented in a multitude of ways. In some embodiments, a software module comprises a file, a section of code, a programming feature, a programming structure, or combinations thereof. A software module may

comprise a plurality of files, a plurality of sections of code, a plurality of programming features, a plurality of programming structures, or combinations thereof. By way of non-limiting examples, the one or more software modules comprise a web application, a mobile application, and/or a standalone application. Software modules may be in one computer program or application. Software modules may be in more than one computer program or application. Software modules may be hosted on one machine. Software modules may be hosted on more than one machine. Software modules may be hosted on cloud computing platforms. Software modules may be hosted on one or more machines in one location. Software modules may be hosted on one or more machines in more than one location.

[00231] Databases

[00232] The medium, method, and system disclosed herein comprise one or more databases, or use of the same. In view of the disclosure provided herein, those of skill in the art will recognize that many databases are suitable for storage and retrieval of geologic profile, operator activities, division of interest, and/or contact information of royalty owners. Suitable databases include, by way of non-limiting examples, relational databases, non-relational databases, feature oriented databases, feature databases, entity-relationship model databases, associative databases, and XML databases. In some embodiments, a database is internet-based. In some embodiments, a database is web-based. In some embodiments, a database is cloud computing-based. A database may be based on one or more local computer storage devices.

[00233] Data transmission

[00234] The subject matter described herein, including methods for detecting a particular CD subtype, are configured to be performed in one or more facilities at one or more locations. Facility locations are not limited by country and include any country or territory. In some instances, one or more steps are performed in a different country than another step of the method. In some instances, one or more steps for obtaining a sample are performed in a different country than one or more steps for detecting the presence or absence of a particular CD subtype from a sample. In some embodiments, one or more method steps involving a computer system are performed in a different country than another step of the methods provided herein. In some embodiments, data processing and analyses are performed in a different country or location than one or more steps of the methods described herein. In some embodiments, one or more articles, products, or data are transferred from one or more of the facilities to one or more different facilities for analysis or further analysis. An article includes, but is not limited to, one or more components obtained from a subject, e.g., processed cellular material. Processed cellular material includes, but is not limited to, cDNA reverse transcribed from RNA, amplified RNA, amplified cDNA, sequenced DNA, isolated and/or purified RNA, isolated and/or purified DNA, and isolated and/or purified polypeptide. Data includes, but is not limited to, information regarding the stratification of a subject, and any data produced by the methods disclosed herein. In some embodiments of the methods and systems described herein, the analysis is performed and a subsequent data transmission step will convey or transmit the results of the analysis.

[00235] In some embodiments, any step of any method described herein is performed by a software program or module on a computer. In additional or further embodiments, data from any step of any method described herein is transferred to and from facilities located within the same or different countries, including analysis performed in one facility in a particular location and the data shipped to another location or directly to an individual in the same or a different country. In additional or further embodiments, data from any step of any method described herein is transferred to and/or received from a facility located within the same or different countries, including analysis of a data input, such as genetic or processed cellular material, performed in one facility in a particular location and corresponding data transmitted to another location, or directly to an individual, such as data related to the diagnosis, prognosis, responsiveness to therapy, or the like, in the same or different location or country.

[00236] *Business Methods Utilizing a Computer*

[00237] The methods described herein may utilize one or more computers. The computer may be used for managing customer and sample information such as sample or customer tracking, database management, analyzing molecular profiling data, analyzing cytological data, storing data, billing, marketing, reporting results, storing results, or a combination thereof. The computer may include a monitor or other graphical interface for displaying data, results, billing information, marketing information (e.g. demographics), customer information, or sample information. The computer may also include means for data or information input. The computer may include a processing unit and fixed or removable media or a combination thereof. The computer may be accessed by a user in physical proximity to the computer, for example via a keyboard and/or mouse, or by a user that does not necessarily have access to the physical computer through a communication medium such as a modem, an internet connection, a telephone connection, or a wired or wireless communication signal carrier wave. In some cases, the computer may be connected to a server or other communication device for relaying information from a user to the computer or from the computer to a user. In some cases, the user may store data or information obtained from the computer through a communication medium on media, such as removable media. It is envisioned that data relating to the methods can be transmitted over such networks or connections for reception and/or review by a party. The receiving party can be but is not limited to an individual, a health care provider or a health care manager. In one embodiment, a computer-readable medium includes a medium suitable for transmission of a result of an analysis of a biological sample, such as exosome bio-signatures. The medium can include a result regarding an exosome bio-signature of a subject, wherein such a result is derived using the methods described herein.

[00238] The entity obtaining a diagnosis, prognosis, or selecting a patient for a treatment with an antagonist of IL18R1 may enter sample information into a database for the purpose of one or more of the following: inventory tracking, assay result tracking, order tracking, customer management, customer service, billing, and sales. Sample information may include, but is not limited to: customer

name, unique customer identification, customer associated medical professional, indicated assay or assays, assay results, adequacy status, indicated adequacy tests, medical history of the individual, preliminary diagnosis, suspected diagnosis, sample history, insurance provider, medical provider, third party testing center or any information suitable for storage in a database. Sample history may include but is not limited to: age of the sample, type of sample, method of acquisition, method of storage, or method of transport.

[00239] The database may be accessible by a customer, medical professional, insurance provider, or other third party. Database access may take the form of electronic communication such as a computer or telephone. The database may be accessed through an intermediary such as a customer service representative, business representative, consultant, independent testing center, or medical professional. The availability or degree of database access or sample information, such as assay results, may change upon payment of a fee for products and services rendered or to be rendered. The degree of database access or sample information may be restricted to comply with generally accepted or legal requirements for patient or customer confidentiality.

EMBODIMENTS

1. A method of treating or preventing a disease or condition in a subject, the method comprising administering a modulator of interleukin 18 receptor 1 (IL18R1) activity or expression to the subject, provided the subject has a genotype characterized by the presence of one or more SNPs provided in Tables 1-5.
2. A method of reducing activity or expression of interleukin 18 receptor 1 (IL18R1) in a subject having a genotype characterized by the presence of one or more SNPs provided in Tables 1-5, the method comprising administering to the subject a modulator of IL18R1.
3. The method of embodiment 1 or embodiment 2, further comprising determining the genotype of the subject.
4. The method of embodiment 3, provided that determining the genotype of the subject comprises determining the presence or absence of the one or more SNPs provided Tables 1-5.
5. The method of any previous embodiment, wherein the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof.
6. The method of any previous embodiment, provided that the subject does not comprise the minor allele shown in Tables 1-5.
7. The method of any previous embodiment, provided that the disease or condition is inflammatory bowel disease (IBD).
8. The method of embodiment 7, provided that the IBD comprises Crohn's disease and/or ulcerative colitis.

9. The method of any previous embodiment, provided that the one or more SNPs comprises rs13001325, rs1420101, rs12479210, rs950880, rs13020553, rs13019081, rs12712141, rs2287037, rs1420102, rs12466380, rs1997467, rs1558619, rs1420088, rs12999364, rs4142132, rs12987977, rs11690443, rs1362350, rs12996505, rs873022, rs974389, rs3771177, rs3732129, rs17026974, rs6706844, rs13020793, rs11685480, rs1558622, rs10183388, rs12712135, rs10189711, rs11685424, rs10189202, rs10191914, rs11123918, rs1968171, rs6733174, rs59247511, rs1558620, rs1921622, rs12998521, rs13017455, rs1362349, rs11123923, rs10190555, rs1035127, rs17027087, rs2080289, rs4851570, rs17027060, rs12712145, rs1420098, rs3732123, rs2287034, rs3860444, rs3821203, rs56258475, rs2270298, rs4851006, rs6710885, rs1568681, rs2241117, rs17027037, rs2270297, rs6753717, rs3755274, rs17027071, rs6750020, rs17027006, rs11683700, rs2058622, rs4851007, rs3732126, rs1807782, rs12469506, rs4851575, rs3771172, rs11465633, rs1135354, rs1558627, rs55927292, rs3771171, rs13015714, rs2160202, rs55883125, rs2041740, rs1035130, rs1420103, rs67723747, rs6543116, rs55664618, rs4851005, rs17027056, rs1420089, rs62152661, rs1420095, rs56030066, rs62152714, rs17696376, rs12105808, rs78248680, rs56151044, rs62152662, rs17651485, rs3771170, rs11123926, rs76721133, rs4988955, rs9807962, rs9808453, rs13424006, rs11695627, rs3771166, rs10173193, rs11465575, rs4851566, rs9308857, rs1974675, rs6751967, rs3771162, rs56386507, rs1997466, rs12712140, and rs1362348, or a SNP in linkage disequilibrium therewith, or a combination thereof.
10. The method of any previous embodiment, provided that the one or more SNPs comprises rs13001325.
11. The method of any previous embodiment, provided that the one or more SNPs comprises rs1420101.
12. The method of any previous embodiment, provided that the one or more SNPs comprises rs12479210.
13. The method of any previous embodiment, provided that the one or more SNPs comprises rs950880.
14. The method of any previous embodiment, provided that the one or more SNPs comprises rs13020553.
15. The method of any previous embodiment, provided that the one or more SNPs comprises rs13019081.
16. The method of any previous embodiment, provided that the one or more SNPs comprises rs12712141.
17. The method of any previous embodiment, provided that the one or more SNPs comprises rs2287037.

18. The method of any previous embodiment, provided that the one or more SNPs comprises rs1420102.
19. The method of any previous embodiment, provided that the one or more SNPs comprises rs12466380.
20. The method of any previous embodiment, provided that the one or more SNPs comprises rs1997467.
21. The method of any previous embodiment, provided that the one or more SNPs comprises rs1558619.
22. The method of any previous embodiment, provided that the one or more SNPs comprises rs1420088.
23. The method of any previous embodiment, provided that the one or more SNPs comprises rs12999364.
24. The method of any previous embodiment, provided that the one or more SNPs comprises rs4142132.
25. The method of any previous embodiment, provided that the one or more SNPs comprises rs12987977.
26. The method of any previous embodiment, provided that the one or more SNPs comprises rs11690443.
27. The method of any previous embodiment, provided that the one or more SNPs comprises rs1362350.
28. The method of any previous embodiment, provided that the one or more SNPs comprises rs12996505.
29. The method of any previous embodiment, provided that the one or more SNPs comprises rs873022.
30. The method of any previous embodiment, provided that the one or more SNPs comprises rs974389.
31. The method of any previous embodiment, provided that the one or more SNPs comprises rs3771177.
32. The method of any previous embodiment, provided that the one or more SNPs comprises rs3732129.
33. The method of any previous embodiment, provided that the one or more SNPs comprises rs17026974.
34. The method of any previous embodiment, provided that the one or more SNPs comprises rs6706844.
35. The method of any previous embodiment, provided that the one or more SNPs comprises rs13020793.

36. The method of any previous embodiment, provided that the one or more SNPs comprises rs11685480.
37. The method of any previous embodiment, provided that the one or more SNPs comprises rs1558622.
38. The method of any previous embodiment, provided that the one or more SNPs comprises rs10183388.
39. The method of any previous embodiment, provided that the one or more SNPs comprises rs12712135.
40. The method of any previous embodiment, provided that the one or more SNPs comprises rs10189711.
41. The method of any previous embodiment, provided that the one or more SNPs comprises rs11685424.
42. The method of any previous embodiment, provided that the one or more SNPs comprises rs10189202.
43. The method of any previous embodiment, provided that the one or more SNPs comprises rs10191914.
44. The method of any previous embodiment, provided that the one or more SNPs comprises rs11123918.
45. The method of any previous embodiment, provided that the one or more SNPs comprises rs1968171.
46. The method of any previous embodiment, provided that the one or more SNPs comprises rs6733174.
47. The method of any previous embodiment, provided that the one or more SNPs comprises rs59247511.
48. The method of any previous embodiment, provided that the one or more SNPs comprises rs1558620.
49. The method of any previous embodiment, provided that the one or more SNPs comprises rs1921622.
50. The method of any previous embodiment, provided that the one or more SNPs comprises rs12998521.
51. The method of any previous embodiment, provided that the one or more SNPs comprises rs13017455.
52. The method of any previous embodiment, provided that the one or more SNPs comprises rs1362349.
53. The method of any previous embodiment, provided that the one or more SNPs comprises rs11123923.

54. The method of any previous embodiment, provided that the one or more SNPs comprises rs10190555.
55. The method of any previous embodiment, provided that the one or more SNPs comprises rs1035127.
56. The method of any previous embodiment, provided that the one or more SNPs comprises rs17027087.
57. The method of any previous embodiment, provided that the one or more SNPs comprises rs2080289.
58. The method of any previous embodiment, provided that the one or more SNPs comprises rs4851570.
59. The method of any previous embodiment, provided that the one or more SNPs comprises rs17027060.
60. The method of any previous embodiment, provided that the one or more SNPs comprises rs12712145.
61. The method of any previous embodiment, provided that the one or more SNPs comprises rs1420098.
62. The method of any previous embodiment, provided that the one or more SNPs comprises rs3732123.
63. The method of any previous embodiment, provided that the one or more SNPs comprises rs2287034.
64. The method of any previous embodiment, provided that the one or more SNPs comprises rs3860444.
65. The method of any previous embodiment, provided that the one or more SNPs comprises rs3821203.
66. The method of any previous embodiment, provided that the one or more SNPs comprises rs56258475.
67. The method of any previous embodiment, provided that the one or more SNPs comprises rs2270298.
68. The method of any previous embodiment, provided that the one or more SNPs comprises rs4851006.
69. The method of any previous embodiment, provided that the one or more SNPs comprises rs6710885.
70. The method of any previous embodiment, provided that the one or more SNPs comprises rs1568681.
71. The method of any previous embodiment, provided that the one or more SNPs comprises rs2241117.

72. The method of any previous embodiment, provided that the one or more SNPs comprises rs17027037.
73. The method of any previous embodiment, provided that the one or more SNPs comprises rs2270297.
74. The method of any previous embodiment, provided that the one or more SNPs comprises rs6753717.
75. The method of any previous embodiment, provided that the one or more SNPs comprises rs3755274.
76. The method of any previous embodiment, provided that the one or more SNPs comprises rs17027071.
77. The method of any previous embodiment, provided that the one or more SNPs comprises rs6750020.
78. The method of any previous embodiment, provided that the one or more SNPs comprises rs17027006.
79. The method of any previous embodiment, provided that the one or more SNPs comprises rs11683700.
80. The method of any previous embodiment, provided that the one or more SNPs comprises rs2058622.
81. The method of any previous embodiment, provided that the one or more SNPs comprises rs4851007.
82. The method of any previous embodiment, provided that the one or more SNPs comprises rs3732126.
83. The method of any previous embodiment, provided that the one or more SNPs comprises rs1807782.
84. The method of any previous embodiment, provided that the one or more SNPs comprises rs12469506.
85. The method of any previous embodiment, provided that the one or more SNPs comprises rs4851575.
86. The method of any previous embodiment, provided that the one or more SNPs comprises rs3771172.
87. The method of any previous embodiment, provided that the one or more SNPs comprises rs11465633.
88. The method of any previous embodiment, provided that the one or more SNPs comprises rs1135354.
89. The method of any previous embodiment, provided that the one or more SNPs comprises rs1558627.

90. The method of any previous embodiment, provided that the one or more SNPs comprises rs55927292.
91. The method of any previous embodiment, provided that the one or more SNPs comprises rs3771171.
92. The method of any previous embodiment, provided that the one or more SNPs comprises rs13015714.
93. The method of any previous embodiment, provided that the one or more SNPs comprises rs2160202.
94. The method of any previous embodiment, provided that the one or more SNPs comprises rs55883125.
95. The method of any previous embodiment, provided that the one or more SNPs comprises rs2041740.
96. The method of any previous embodiment, provided that the one or more SNPs comprises rs1035130.
97. The method of any previous embodiment, provided that the one or more SNPs comprises rs1420103.
98. The method of any previous embodiment, provided that the one or more SNPs comprises rs67723747.
99. The method of any previous embodiment, provided that the one or more SNPs comprises rs6543116.
100. The method of any previous embodiment, provided that the one or more SNPs comprises rs55664618.
101. The method of any previous embodiment, provided that the one or more SNPs comprises rs4851005.
102. The method of any previous embodiment, provided that the one or more SNPs comprises rs17027056.
103. The method of any previous embodiment, provided that the one or more SNPs comprises rs1420089.
104. The method of any previous embodiment, provided that the one or more SNPs comprises rs62152661.
105. The method of any previous embodiment, provided that the one or more SNPs comprises rs1420095.
106. The method of any previous embodiment, provided that the one or more SNPs comprises rs56030066.
107. The method of any previous embodiment, provided that the one or more SNPs comprises rs62152714.

108. The method of any previous embodiment, provided that the one or more SNPs comprises rs17696376.
109. The method of any previous embodiment, provided that the one or more SNPs comprises rs12105808.
110. The method of any previous embodiment, provided that the one or more SNPs comprises rs78248680.
111. The method of any previous embodiment, provided that the one or more SNPs comprises rs56151044.
112. The method of any previous embodiment, provided that the one or more SNPs comprises rs62152662.
113. The method of any previous embodiment, provided that the one or more SNPs comprises rs17651485.
114. The method of any previous embodiment, provided that the one or more SNPs comprises rs3771170.
115. The method of any previous embodiment, provided that the one or more SNPs comprises rs11123926.
116. The method of any previous embodiment, provided that the one or more SNPs comprises rs76721133.
117. The method of any previous embodiment, provided that the one or more SNPs comprises rs4988955.
118. The method of any previous embodiment, provided that the one or more SNPs comprises rs9807962.
119. The method of any previous embodiment, provided that the one or more SNPs comprises rs9808453.
120. The method of any previous embodiment, provided that the one or more SNPs comprises rs13424006.
121. The method of any previous embodiment, provided that the one or more SNPs comprises rs11695627.
122. The method of any previous embodiment, provided that the one or more SNPs comprises rs3771166.
123. The method of any previous embodiment, provided that the one or more SNPs comprises rs10173193.
124. The method of any previous embodiment, provided that the one or more SNPs comprises rs11465575.
125. The method of any previous embodiment, provided that the one or more SNPs comprises rs4851566.

126. The method of any previous embodiment, provided that the one or more SNPs comprises rs9308857.
127. The method of any previous embodiment, provided that the one or more SNPs comprises rs1974675.
128. The method of any previous embodiment, provided that the one or more SNPs comprises rs6751967.
129. The method of any previous embodiment, provided that the one or more SNPs comprises rs3771162.
130. The method of any previous embodiment, provided that the one or more SNPs comprises rs56386507.
131. The method of any previous embodiment, provided that the one or more SNPs comprises rs1997466.
132. The method of any previous embodiment, provided that the one or more SNPs comprises rs12712140.
133. The method of any previous embodiment, provided that the one or more SNPs comprises rs1362348.
134. The method of any previous embodiment, provided that the subject has CD.
135. The method of embodiment 134, provided that the one or more SNPs comprises a SNP listed in Table 1.
136. The method of embodiment 134, wherein the single nucleotide polymorphism is associated with structuring.
137. The method of embodiment 136, wherein the stricturing is isolated to an ileocolonic region of an intestine.
138. The method of embodiment 136 or 137, provided that the one or more SNPs comprises a SNP listed in Table 2.
139. The method of embodiment 134, wherein the single nucleotide polymorphism is associated with a risk of a subject developing morphological defects in ileal Paneth cells.
140. The method of embodiment 139, provided that the one or more SNPs comprises a SNP listed in Table 3.
141. The method of any previous embodiment, provided that the subject has IBD.
142. The method of embodiment 141, provided that the one or more SNPs comprises a SNP listed in Table 4.
143. The method of any previous embodiment, provided that the subject has UC.
144. The method of embodiment 143, provided that the one or more SNPs comprises a SNP listed in Table 5.
145. The method of any previous embodiments, provided that the one or more SNPs comprises a SNP listed in FIG. 1A to FIG. 1Q.

FURTHER EMBODIMENTS

1. A computer system for evaluating a biological sample from a subject, the system comprising:
 - a) a central computing environment;
 - b) an input device operatively connected to said central computing environment, wherein said input device is configured to receive a presence or absence of a genotype that correlates with a disease state in the biological sample;
 - c) a trained algorithm executed by said central computing environment, wherein the trained algorithm is configured to use the presence or absence of the genotype to classify said biological sample as a disease or normal sample at an accuracy of at least 85%; and
 - d) an output device operatively connected to said central computing environment, wherein said output device is configured to provide information on the classification to a user.
2. The computer system of embodiment 1, wherein the disease state comprises an inflammatory, fibrostenotic, and/or fibrotic disease or condition.
3. The computer system of embodiment 1 or embodiment 2, wherein the disease state comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis.
4. The computer system of any previous embodiment, wherein the biological sample comprises whole blood, plasma, serum, or tissue.
5. The computer system of any previous embodiment, wherein the genotype comprises one or more single nucleotide polymorphisms (SNPs) at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof.
6. The computer system of any previous embodiment, wherein the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
7. The computer system of any previous embodiment, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some cases, the SNP is rs10213846 and comprises a "G" or a "T" allele.
8. The computer system of any previous embodiment, wherein the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP.
9. The computer system of any previous embodiment, wherein the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
10. The computer system of any previous embodiment, wherein the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
11. The computer system of any previous embodiment, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
12. The computer system of any previous embodiment, wherein the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.

13. The computer system of any previous embodiment, wherein the Indel at rs1921622 is within SEQ ID NO: 1.
14. The computer system of any previous embodiment, wherein the SNP at rs2287037 is within SEQ ID NO: 2.
15. The computer system of any previous embodiment, wherein the SNP at rs1974675 is within SEQ ID NO: 3.
16. The computer system of any previous embodiment, wherein the SNP at rs2041739 is within s SEQ ID NO: 4.
17. The computer system of any previous embodiment, wherein the SNP at rs76362690 is within SEQ ID NO: 5.
18. The computer system of any previous embodiment, wherein the SNP at rs2287037 is within SEQ ID NO: 6.
19. The computer system of any previous embodiment, wherein the SNP at rs80256362 is within SEQ ID NO: 7.
20. The computer system of embodiment 5, where LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0.
21. The computer system of any previous embodiment, wherein the genotype comprises one or more single nucleotide polymorphisms (SNPs) located at a gene comprising IL18R1.
22. The computer system of any previous embodiment, wherein the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
23. The computer system of any previous embodiment, wherein said output device provides a report summarizing said information on said classification.
24. The computer system of any previous embodiment, wherein said report comprises a recommendation for treatment of said disease state.
25. The computer system of embodiment 24, wherein the treatment comprises administration of a modulator of IL18R1 activity or expression.
26. The computer system of embodiment 25, wherein the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1.
27. The computer system of embodiment 25, wherein the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1.
28. The computer system of embodiment 26, wherein the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule.

29. The computer system of embodiments 26-27, wherein the modulator of IL18R1 activity or expression comprises an inverse agonist.
30. The computer system of embodiment 25, wherein the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM).
31. The computer system of embodiment 25, wherein the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM).
32. The computer system of embodiments 25-31, wherein the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both.
33. The computer system of embodiments 25-31, wherein the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both.
34. The computer system of embodiments 25-31, wherein the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide.
35. The computer system of embodiment 25, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9.
36. The computer system of embodiment 25, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide.
37. The computer system of embodiments 25-36, wherein the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both
38. The computer system of embodiments 25-38, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling.
39. The computer system of embodiments 25-38, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding.
40. The computer system of any preceding embodiment, wherein said genotype is determined with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof.
41. Use of a composition comprising one or more binding agents for generating a report that classifies a biological sample from as subject as disease or non-disease, wherein the one or more binding agents specifically bind to one or more polymorphisms of one or more genes selected from MAP4K4, IL1RL1, TMEM182, and IL18RAP, or their complement.
42. The use of embodiment 41, wherein generating the report further comprises:
 - (a) providing the biological sample from the subject;

- (b) assaying the biological sample from the subject for detecting the presence of the one or more polymorphisms of the one or more genes;
 - (c) generating the report based on the result of step (b); and
 - (d) determining whether said subject has or is likely to have the disease based on the results of step (b).
- 43. The use of embodiment 41 or 42, wherein the disease state comprises an inflammatory, fibrostenotic, and/or fibrotic disease or condition.
 - 44. The use of embodiment 41 or embodiment 42, wherein the disease state comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis.
 - 45. The use of any of embodiments 41-44, wherein the biological sample comprises whole blood, plasma, serum, or tissue.
 - 46. The use of embodiment 42, wherein the assaying step (b) comprises: (a) contacting the biological sample with the one or more binding agents that specifically bind to the one or more polymorphisms; and (b) determining whether the biological sample specifically binds to said one or more binding agents, wherein binding of the biological sample to the one or more binding agents indicates the presence of the polymorphism in the subject.
 - 47. The use of embodiment 46, wherein the detecting assaying step (b) comprises sequencing of the biological sample.
 - 48. The use of embodiment 46, wherein the detecting assaying step (b) comprises quantifying the amount of DNA comprising the one or more polymorphs.
 - 49. The use of embodiment 48, wherein the quantifying comprises PCR.
 - 50. The use of embodiment 49, wherein the PCR comprises real-time PCR.
 - 51. The use of embodiment 48, wherein the quantifying comprises hybridization.
 - 52. A composition comprising one or more binding agents that specifically bind to the one or more polymorphisms of one or more genes selected from MAP4K4, IL1RL1, TMEM182, and IL18RAP, or their complement, wherein the one or more binding agents are selected to classify a biological sample as disease or non-disease.
 - 53. The composition of embodiment 52, wherein the one or more binding agents comprise oligonucleotides.
 - 54. The composition of embodiment 53, wherein the oligonucleotides comprise RNA or DNA.
 - 55. The composition of embodiment 52, wherein the one or more binding agents comprise aptamers, antibodies, peptide nucleic acids, or pyranosyl RNA.
 - 56. The composition of embodiment 52, wherein the one or more polymorphisms comprise deletions or duplications.
 - 57. A kit for diagnosing detecting a disease or condition in a subject, the kit comprising: (a) at least one binding agent that specifically binds to the one or more polymorphisms of one or

- more genes selected from the group consisting of MAP4K4, IL1RL1, TMEM182, and IL18RAP, or their complement, wherein the at least one binding agent is selected to detect a disease or non-disease state; and (b) reagents for detecting binding of said at least one binding agent to a DNA sample from a subject.
58. The kit of embodiment 57, wherein the composition comprises binding agents for at most 10,000 genes.
 59. The kit of embodiment 57, wherein the at least one binding agent comprises at least one oligonucleotide.
 60. The kit of embodiment 57, wherein the at least one binding agent comprises at least one aptamer, antibody, peptide nucleic acid, or pyranosyl RNA.
 61. The kit of embodiment 57, wherein the at least one binding agent is labelled with a detectable label.
 62. The kit of embodiment 57, wherein the at least one binding agent is immobilized to a surface.
 63. A system for generating a report that classifies a biological sample a disease or non-disease, comprising: (a) a computer system that (i) generates a molecular profile of a DNA sample based upon the presence of one or more polymorphisms of one or more genes selected from MAP4K4, IL1RL1, TMEM182, and IL18RAP, or their complement, and (ii) generates a report that classifies the biological sample based on said molecular profile; and (b) a computer screen that displays said report.
 64. The system of embodiment 63, wherein the presence of one or more polymorphisms is based on the result of an assay of said DNA sample, which result is entered into a database.
 65. The system of embodiment 64, further comprising an input for said result.

EXAMPLES

[00240] Example 1. IL18R1 SNPs Associated with Crohn's Disease

[00241] Subjects were recruited and diagnosed as having or not having inflammatory bowel disease (IBD). Some IBD patients were further characterized as having Crohn's disease (CD) or ulcerative colitis (UC). Diagnosis was based on standard endoscopic, histologic, and/or radiographic features. Select subjects were further characterized based on genetic and/or phenotypic traits.

[00242] Blood samples were collected from the subjects at the time of enrollment. Genotyping was performed on the samples using Illumina ImmunoChip (Illumina, San Diego, CA) per manufacturer's protocol. Markers were excluded from analysis based on: Hardy-Weinberg Equilibrium $p \leq 1.0E-5$; genotyping rate $< 95\%$; minor allele frequency $< 1\%$. Related individuals (Pi-hat scores > 0.25) were identified using identity-by-descent and excluded from analysis (PLINK). Admixture was used to generate ethnicity proportion estimations for all individuals. Only subjects identified by admixture as Caucasian (proportion < 0.75) were included in the analysis.

[00243] Multiple large-scale case-control association studies involving CD, UC, and IBD, and subclinical phenotypes of CD, UC, and IBD, in populations using gene-based single nucleotide polymorphism (SNP) markers were performed. The studies included subjects recruited at the Cedars-Sinai Inflammatory Bowel Disease Centers. The studies also included GWAS data derived from the International Inflammatory Bowel Diseases Genetic Consortium (IIBDGC) and cohorts from DeLange et al., “Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease,” *Nature Genetics*. Vol. 49, No. 2 (February 2017). Results showed that SNPs at the IL18R1 locus provided in **Table 1** are significantly associated with Crohn’s Disease.

[00244] Genotyping data was produced from tissue samples from patients diagnosed with IBD and healthy patients without IBD. eQTL mapping was performed on these samples. Transcriptomic data was generated on the tissue. Briefly, uninflamed tissue from formalin-fixed paraffin-embedded (FFPE) resection margins of subjects requiring surgery at Cedars-Sinai Medical Center for Crohn’s disease was identified. Whole-thickness ileal tissue was scraped from the FFPE tissue sections followed by RNA extraction using the RNeasy FFPE kit (Qiagen) according to the manufacturer's instructions. The Transplex Whole Transcriptome Amplification kit (WTA2; Sigma) was used for cDNA synthesis and amplification. Subsequent purification of the cDNA product was performed with the PCR Purification kit (Qiagen). Sample quality was confirmed using the Agilent Bioanalyzer. For samples passing quality control, Cy5 labeling with the ULST Fluorescent Labeling kit (Kreatech) and hybridization (performed in duplicate for each sample) to Whole Human Genome 4x44k Microarrays (Agilent) was performed.

[00245] Single channel microarray expression data extracted using Agilent feature extraction software was received from Genome Technology Access Center at Washington University in St. Louis. Raw expression data available in technical duplicates was normalized using LIMMA package implemented in R version 3.2.2. The expression data preprocessing included background correction of the expression data, followed by log2-transformation and quantile-normalization. Unsupervised hierarchical clustering of expression data was used to remove outlier subjects. eQTL mapping was implemented in Matrix eQTL R package using the available expression and genotype data from patients. Associations between genotype and probe expression level were performed using a linear regression model with additive genotype effects. All associations were adjusted for gender, age and population sub-structure using the first two principal components. Gene bounds were defined using a 1 Mb window around the transcription start position of given gene as obtained from UCSC Genome Browser. For cis-eQTL mapping, a 1Mb cis distance from gene bounds was used. Cis-eQTLs were defined as association signals from SNPs located within 1 Mb from each of the gene bounds. False discovery rates (FDR) were estimated to correct for multiple testing using Matrix eQTL according to the Benjamini and Hochberg method. Note that FDR calculation in matrix eQTL does not take into account “linkage disequilibrium” between the SNPs and may be overly stringent. A negative beta

value indicates a decrease in IL18R1 gene expression. A positive beta value indicates an increase in IL18R1 gene expression.

[00246] Tables 1-5 provide meta-analysis of SNPs and/or indels considered predictive of disease (IBD, CD, UC), phenotype, and/or suitability to treatment with a modulator of IL18R1 (p value cutoff of 1.0 E-3). FIG. 1A to FIG. 1Q provides the entire meta-analysis, without p value cutoff.

These results show strong associations between the SNPs listed in the tables, and the associated diseases (IBD, CD, UC) and phenotypes. The results also show that particular SNPs are associated with decreased or increased expression of IL18R1, MAP4K4, IL1RL1, TMEM182, and IL18RAP in patients diagnosed with IBD, CD, or UC having the provided phenotypes. Table 6 and Table 7 provide a description of the headers of Tables 1-5, and FIG. 1A to FIG. 1Q.

[00247] To determine Paneth genotype, genotyping data was collected from patients with Crohn's Disease (CD) with morphological defects of ileal Paneth cells, as determined using the classification set forth in VanDussen et al., "Genetic Variants Synthesize the Produce Paneth Cell Phenotypes That Define Subtypes of Crohn's Disease," Gastroenterology 2014; 146:200-209.

Table 1. IL18R1 SNPs Significantly Correlated with Crohn's disease (CD)

PHENO TYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_CH2	cis_eGE NE	eqtl_bet a	eqtl_p	priority
CD vs. Ctrl	imm_2_1 0230546 8	rs130013 25	<1.0E-3	A	94040	-0.1236	1029390 36	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0232414 8	rs142010 1	<1.0E-3	A	94080	-0.1230	1029577 16	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231559 3	rs124792 10	<1.0E-3	A	94088	-0.1226	1029491 61	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229899 4	rs950880	<1.0E-3	A	94092	-0.1212	1029325 62	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229825 8	rs130205 53	<1.0E-3	G	94088	-0.1213	1029318 26	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231725 4	rs130190 81	<1.0E-3	C	91372	-0.1206	1029508 22	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231949 9	rs127121 41	<1.0E-3	A	94101	0.1112	1029530 67	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0234546 0	rs228703 7	<1.0E-3	A	90448	-0.1179	1029790 28	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231525 1	rs142010 2	<1.0E-3	G	94059	0.1104	1029488 19	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231537 1	rs124663 80	<1.0E-3	A	94097	0.1100	1029489 39	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231750 5	rs199746 7	<1.0E-3	A	94088	0.1100	1029510 73	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229798 2	rs155861 9	<1.0E-3	C	94094	0.1099	1029315 50	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0230586 6	rs142008 8	<1.0E-3	A	94092	0.1099	1029394 34	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0234056 1	rs129993 64	<1.0E-3	A	94085	-0.1139	1029741 29	NA	NA	NA	NA

CD vs. Ctrl	imm_2_1 0230391 4	rs414213 2	<1.0E-3	G	94098	0.1096	1029374 82	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0234176 8	rs129879 77	<1.0E-3	C	94101	-0.1136	1029753 36	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0230256 3	rs116904 43	<1.0E-3	T	94088	0.1095	1029361 31	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231823 0	rs136235 0	<1.0E-3	G	93070	0.1104	1029517 98	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229823 4	rs129965 05	<1.0E-3	A	94097	0.1092	1029318 02	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0232211 5	rs873022	<1.0E-3	A	94097	-0.1245	1029556 83	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0230341 3	rs974389	<1.0E-3	G	94098	0.1090	1029369 81	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0232229 2	rs377117 7	<1.0E-3	A	94098	-0.1244	1029558 60	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0232396 4	rs373212 9	<1.0E-3	G	94095	-0.1243	1029575 32	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231879 2	rs170269 74	<1.0E-3	A	94079	-0.1243	1029523 60	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0230684 4	rs670684 4	<1.0E-3	A	94078	0.1086	1029404 12	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229835 8	rs130207 93	<1.0E-3	G	94087	0.1086	1029319 26	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229351 8	rs116854 80	<1.0E-3	G	94076	0.1084	1029270 86	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229657 9	rs155862 2	<1.0E-3	G	94067	0.1083	1029301 47	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229867 9	rs101833 88	<1.0E-3	G	94099	0.1082	1029322 47	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229738 0	rs127121 35	<1.0E-3	A	94095	0.1081	1029309 48	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229731 3	rs101897 11	<1.0E-3	A	94093	0.1080	1029308 81	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229341 3	rs116854 24	<1.0E-3	G	94097	0.1079	1029269 81	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229681 2	rs101892 02	<1.0E-3	A	94101	0.1078	1029303 80	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229708 9	rs101919 14	<1.0E-3	A	94098	0.1078	1029306 57	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0230166 9	rs111239 18	<1.0E-3	A	93761	0.1081	1029352 37	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229998 4	rs196817 1	<1.0E-3	NA	NA	0.1121	1029335 52	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229544 4	rs673317 4	<1.0E-3	A	94099	0.1077	1029290 12	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0232062 2	rs592475 11	<1.0E-3	G	88756	-0.1102	1029541 90	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0229782	rs155862 0	<1.0E-3	A	89819	0.1088	1029313 95	NA	NA	NA	NA

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CD vs. Ctrl	imm_2_1 0233249 9	rs192162 2	<1.0E-3	G	94090	0.1070	1029660 67	MAP4K 4	0.0496	0.0167	0
CD vs. Ctrl	rs129985 21	rs129985 21	<1.0E-3	A	92721	-0.1116	1029744 17	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0233117 4	rs130174 55	<1.0E-3	A	91754	-0.1103	1029647 42	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231840 4	rs136234 9	<1.0E-3	C	87425	-0.1071	1029519 72	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0233427 6	rs111239 23	<1.0E-3	A	94070	-0.1068	1029678 44	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0236048 8	rs101905 55	<1.0E-3	A	93178	0.1198	1029940 56	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0238635 1	rs103512 7	<1.0E-3	A	94060	0.1189	1030199 19	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0238235 0	rs170270 87	<1.0E-3	A	94100	-0.1165	1030159 18	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0236145 2	rs208028 9	<1.0E-3	A	94058	-0.1164	1029950 20	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0237281 9	rs485157 0	<1.0E-3	G	94084	-0.1161	1030063 87	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0237399 9	rs170270 60	<1.0E-3	G	94097	-0.1158	1030075 67	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0237514 2	rs127121 45	<1.0E-3	A	94090	0.1178	1030087 10	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0235071 1	rs142009 8	<1.0E-3	G	86682	-0.1084	1029842 79	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0238450 9	rs373212 3	<1.0E-3	G	94095	-0.1159	1030180 77	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0237702 0	rs228703 4	<1.0E-3	A	94095	-0.1156	1030105 88	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0237405 5	rs386044 4	<1.0E-3	A	94084	0.1172	1030076 23	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0236330 4	rs382120 3	<1.0E-3	A	94040	-0.1155	1029968 72	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0236574 4	rs562584 75	<1.0E-3	G	94064	-0.1154	1029993 12	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0235851 1	rs227029 8	<1.0E-3	G	94101	-0.1153	1029920 79	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0239117 0	rs485100 6	<1.0E-3	A	93111	-0.1164	1030247 38	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0234396 9	rs671088 5	<1.0E-3	G	87495	-0.1078	1029775 37	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0238112 8	rs156868 1	<1.0E-3	G	94078	0.1169	1030146 96	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0236947 5	rs224111 7	<1.0E-3	A	94101	0.1168	1030030 43	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0236131 6	rs170270 37	<1.0E-3	G	94084	-0.1150	1029948 84	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0235910	rs227029 7	<1.0E-3	A	94087	0.1167	1029926 75	NA	NA	NA	NA

	7										
CD vs. Ctrl	imm_2_1 0235959 3	rs675371 7	<1.0E-3	A	94088	0.1167	1029931 61	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0236882 7	rs375527 4	<1.0E-3	A	94096	0.1165	1030023 95	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0237910 6	rs170270 71	<1.0E-3	A	94100	-0.1148	1030126 74	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0236114 6	rs675002 0	<1.0E-3	G	94092	0.1165	1029947 14	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0233176 4	rs170270 06	<1.0E-3	C	94096	-0.1150	1029653 32	IL1RL1	-0.0663	0.0409	IL1RL1
CD vs. Ctrl	imm_2_1 0236323 7	rs116837 00	<1.0E-3	A	94100	-0.1146	1029968 05	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0235185 6	rs205862 2	<1.0E-3	A	94099	0.1166	1029854 24	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0239124 5	rs485100 7	<1.0E-3	A	94090	0.1162	1030248 13	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0238039 4	rs373212 6	<1.0E-3	C	89806	-0.1162	1030139 62	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0239957 9	rs180778 2	<1.0E-3	G	94057	0.1159	1030331 47	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0233230 3	rs124695 06	<1.0E-3	A	94099	-0.1139	1029658 71	IL1RL1	-0.0659	0.0477	IL1RL1
CD vs. Ctrl	imm_2_1 0239163 5	rs485157 5	<1.0E-3	G	93053	0.1164	1030252 03	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0235224 4	rs377117 2	<1.0E-3	A	94093	-0.1129	1029858 12	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0236416 5	rs114656 33	<1.0E-3	A	93025	-0.1139	1029977 33	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0238073 4	rs113535 4	<1.0E-3	C	94075	-0.1127	1030143 02	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0235111 6	rs155862 7	<1.0E-3	G	92154	0.1166	1029846 84	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0233129 3	rs559272 92	<1.0E-3	A	94066	-0.1129	1029648 61	IL1RL1	-0.0700	0.0305	IL1RL1
CD vs. Ctrl	imm_2_1 0235238 2	rs377117 1	<1.0E-3	G	93096	-0.1132	1029859 50	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0233829 7	rs130157 14	<1.0E-3	C	94091	0.1140	1029718 65	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0235258 6	rs216020 2	<1.0E-3	A	93116	-0.1130	1029861 54	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0239076 3	rs558831 25	<1.0E-3	A	89792	-0.1132	1030243 31	IL1RL1	-0.0673	0.0437	0
CD vs. Ctrl	imm_2_1 0235616 6	rs204174 0	<1.0E-3	A	89771	0.1128	1029897 34	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0236783 4	rs103513 0	<1.0E-3	A	87767	-0.1101	1030014 02	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 0231506 4	rs142010 3	<1.0E-3	A	94095	0.1050	1029486 32	NA	NA	NA	NA
CD vs.	imm_2_1	rs677237	<1.0E-3	NA	NA	-0.1089	1029698	NA	NA	NA	NA

Ctrl	02336239	47					07				
CD vs. Ctrl	imm_2_1 02294158	rs6543116	<1.0E-3	A	94078	0.1020	102927726	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 02382648	rs55664618	<1.0E-3	A	94101	-0.0865	103016216	IL1RL1	-0.0559	0.0418	0
CD vs. Ctrl	imm_2_1 02377984	rs4851005	<1.0E-3	A	94039	-0.0752	103011552	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 02373483	rs17027056	<1.0E-3	A	94095	-0.1052	103007051	NA	NA	NA	NA
CD vs. Ctrl	imm_2_1 02304821	rs1420089	<1.0E-3	G	94092	0.0653	102938389	IL1R2, IL1RL2	0.231497338126034, 0.122966178554851	0.0403730838316627, 0.0456541874537971	0, 0
CD vs. Ctrl	imm_2_1 02326078	rs62152661	<1.0E-3	G	94094	0.0636	102959646	IL1R2, IL1RL2	0.231497338126034, 0.122966178554851	0.0403730838316627, 0.0456541874537971	0, 0
CD vs. Ctrl	imm_2_1 02379334	rs1420095	<1.0E-3	G	94076	0.0691	103012902	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.0838534335200365, 0.11811725329138, - 0.231864788573836, 0.170724364161569, - 0.263402645000446	0.00372427407991006, 0.0200804208351232, 0.0239002404371004, 0.0257519329018087, 0.0334284392287019	0, 0, 0, 0, 0
CD vs. Ctrl	imm_2_1 02369466	rs56030066	<1.0E-3	C	94101	0.0688	103003034	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.0838534335200365, 0.11811725329138, - 0.231864788573836, 0.170724364161569, - 0.263402645000446	0.00372427407991006, 0.0200804208351232, 0.0239002404371004, 0.0257519329018087, 0.0334284392287019	0, 0, 0, 0, 0
CD vs. Ctrl	imm_2_1 02399158	rs62152714	<1.0E-3	G	94099	0.0668	103032726	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.0838534335200365, 0.11811725329138, - 0.231864788573836, 0.170724364161569, - 0.263402645000446	0.00372427407991006, 0.0200804208351232, 0.0239002404371004, 0.0257519329018087, 0.0334284392287019	0, IL18RAP, 0, 0, 0
CD vs. Ctrl	imm_2_1 02331585	rs17696376	<1.0E-3	A	94096	0.0625	102965153	IL1R1, IL1R2, IL1RL2	0.0496830463208274, 0.237344	0.0406804596047685, 0.043046	0, 0, 0

									3783960 56, 0.126970 2544269 39	3438168 161, 0.046936 0657670 677	
CD vs. Ctrl	imm_2_1 0234065 4	rs121058 08	<1.0E-3	T	94095	0.0604	1029742 22	IL1R1, IL1R2, IL1RL2	0.049683 0463208 274, 0.237344 3783960 56, 0.126970 2544269 39	0.040680 4596047 685, 0.043046 3438168 161, 0.046936 0657670 677	0, 0, 0
CD vs. Ctrl	imm_2_1 0233510 2	rs782486 80	<1.0E-3	G	94094	0.0599	1029686 70	IL1R1, IL1R2, IL1RL2	0.049683 0463208 274, 0.237344 3783960 56, 0.126970 2544269 39	0.040680 4596047 685, 0.043046 3438168 161, 0.046936 0657670 677	0, 0, 0
CD vs. Ctrl	imm_2_1 0237776 1	rs561510 44	<1.0E-3	A	94074	-0.0625	1030113 29	TMEM1 82	-0.2142	0.0381	0
CD vs. Ctrl	imm_2_1 0232877 3	rs621526 62	<1.0E-3	A	93166	0.0592	1029623 41	IL1R1, IL1R2, IL1RL2	0.049683 0463208 274, 0.237344 3783960 56, 0.126970 2544269 39	0.040680 4596047 685, 0.043046 3438168 161, 0.046936 0657670 677	0, 0, 0
CD vs. Ctrl	imm_2_1 0236808 2	rs176514 85	<1.0E-3	A	94085	-0.0607	1030016 50	TMEM1 82	-0.2142	0.0381	0
Crohn's Disease vs. non- IBD Controls	imm_2_1 0233249 9	rs192162 2	<1.0E-3	G	7967	1.2020	1029660 67	MAP4K 4	0.0496	0.0167	0
Crohn's Disease vs. non- IBD Controls	imm_2_1 0234056 1	rs129993 64	<1.0E-3	A	7967	0.8526	1029741 29	NA	NA	NA	NA
Crohn's Disease vs. non- IBD Controls	imm_2_1 0234176 8	rs129879 77	<1.0E-3	C	7967	0.8526	1029753 36	NA	NA	NA	NA
Crohn's Disease vs. non- IBD Controls	imm_2_1 0234546 0	rs228703 7	<1.0E-3	A	7965	0.8533	1029790 28	NA	NA	NA	NA
Crohn's Disease vs. non- IBD Controls	imm_2_1 0232414 8	rs142010 1	<1.0E-3	A	7966	0.8529	1029577 16	NA	NA	NA	NA
Crohn's Disease vs. non- IBD Controls	rs129985 21	rs129985 21	<1.0E-3	A	7965	0.8541	1029744 17	NA	NA	NA	NA
Crohn's Disease vs. non- IBD Controls	imm_2_1 0233427 6	rs111239 23	<1.0E-3	A	7967	0.8550	1029678 44	NA	NA	NA	NA
Crohn's Disease	imm_2_1 0230546	rs130013 25	<1.0E-3	A	7967	0.8551	1029390 36	NA	NA	NA	NA

vs. non-IBD Controls	8										
Crohn's Disease vs. non-IBD Controls	imm_2_1 0231559 3	rs124792 10	<1.0E-3	A	7967	0.8553	1029491 61	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0229825 8	rs130205 53	<1.0E-3	G	7966	0.8556	1029318 26	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0229899 4	rs950880	<1.0E-3	A	7967	0.8559	1029325 62	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0235111 6	rs155862 7	<1.0E-3	G	7956	1.1840	1029846 84	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0235241 2	rs377117 0	<1.0E-3	A	7966	1.1830	1029859 80	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0235185 6	rs205862 2	<1.0E-3	A	7967	1.1830	1029854 24	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0233829 7	rs130157 14	<1.0E-3	C	7964	1.1790	1029718 65	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0235910 7	rs227029 7	<1.0E-3	A	7967	1.1740	1029926 75	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0235959 3	rs675371 7	<1.0E-3	A	7967	1.1740	1029931 61	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0236048 8	rs101905 55	<1.0E-3	A	7967	1.1740	1029940 56	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0236114 6	rs675002 0	<1.0E-3	G	7967	1.1740	1029947 14	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0236882 7	rs375527 4	<1.0E-3	A	7967	1.1740	1030023 95	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0236947 5	rs224111 7	<1.0E-3	A	7967	1.1740	1030030 43	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_1 0237514 2	rs127121 45	<1.0E-3	A	7965	1.1720	1030087 10	NA	NA	NA	NA
Crohn's	imm_2_1	rs386044	<1.0E-3	A	7967	1.1720	1030076	NA	NA	NA	NA

Disease vs. non-IBD Controls	02374055	4					23				
Crohn's Disease vs. non-IBD Controls	imm_2_102381128	rs1568681	<1.0E-3	G	7967	1.1710	103014696	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102382476	rs11123926	<1.0E-3	C	7967	1.1700	103016044	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102391245	rs4851007	<1.0E-3	A	7965	1.1680	103024813	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102315064	rs1420103	<1.0E-3	A	7967	1.1660	102948632	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102294158	rs6543116	<1.0E-3	A	7967	1.1660	102927726	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102399579	rs1807782	<1.0E-3	G	7967	1.1670	103033147	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102386351	rs1035127	<1.0E-3	A	7962	1.1650	103019919	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102318792	rs17026974	<1.0E-3	A	7967	0.8639	102952360	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102322115	rs873022	>1.0E-3	A	7967	0.8662	102955683	NA	NA	NA	NA
Crohn's Disease vs. non-IBD Controls	imm_2_102323964	rs3732129	>1.0E-3	G	7967	0.8662	102957532	NA	NA	NA	NA

[00248] Example 2. IL18R1 SNPs Associated with CD and Stricturing Phenotype Isolated to the Ileocolonic Region of the Intestine

[00249] Genotyping data was collected from a cohort of patients diagnosed with Crohn's disease (CD) with stricturing and CD localized at the ileocolonic region of the intestine. Genotyping was performed at Cedars-Sinai Medical Center using the Illumina Immuno-BeadChip array. Markers were excluded from analysis based on: Hardy-Weinberg Equilibrium $p \leq 10^{-4}$; missingness in SNPs of >2%; minor allele frequency < 1%. Related individuals (Pi-hat scores >0.25) were identified using identity-by-descent and excluded from analysis (PLINK). Admixture was used to generate ethnicity proportion estimations for all individuals. Only subjects identified by admixture as Caucasian (proportion <0.75)

were included in the analysis. **Table 2** provides SNPs associated with stricturing with evidence of penetrating and CD localized at the ileocolonic region of the intestine.

Table 2. IL18R1 SNPs Associated with CD and Stricturing with Evidence of Penetrating Phenotype Isolated to the Ileocolonic Region of the Intestine (L3 B2a+B2b v. B1)

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_mis	OR_Z_B	base_pair_CH2	cis_eGENE	eql_beta	eql_p	priority
CD	L3 B2a+B2b vs B1	imm_2_102351116	rs1558627	<1.0E-3	G	6053	1.4020	102984684	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102352412	rs3771170	<1.0E-3	A	6063	1.3960	102985980	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102351856	rs2058622	<1.0E-3	A	6064	1.3950	102985424	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102338297	rs13015714	<1.0E-3	C	6062	1.3800	102971865	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102359107	rs2270297	<1.0E-3	A	6064	1.3710	102992675	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102359593	rs6753717	<1.0E-3	A	6064	1.3710	102993161	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102360488	rs10190555	<1.0E-3	A	6064	1.3710	102994056	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102361146	rs6750020	<1.0E-3	G	6064	1.3710	102994714	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102368827	rs3755274	<1.0E-3	A	6064	1.3710	103002395	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102369475	rs2241117	<1.0E-3	A	6064	1.3710	103003043	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102381128	rs1568681	<1.0E-3	G	6064	1.3690	103014696	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102375142	rs12712145	<1.0E-3	A	6062	1.3690	103008710	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102374055	rs3860444	<1.0E-3	A	6064	1.3680	103007623	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102382476	rs11123926	<1.0E-3	C	6064	1.3680	103016044	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102399579	rs1807782	<1.0E-3	G	6064	1.3650	103033147	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102391245	rs4851007	<1.0E-3	A	6063	1.3650	103024813	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102386351	rs1035127	<1.0E-3	A	6061	1.3600	103019919	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102294158	rs6543116	<1.0E-3	A	6064	1.3540	102927726	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102315064	rs1420103	<1.0E-3	A	6064	1.3540	102948632	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102332499	rs1921622	<1.0E-3	A	6064	0.7923	102966067	MAP4K4	0.0496	0.0167	0

[00250] Example 3. IL18R1 SNPs Significantly Correlated with Morphological Defects of Ileal Paneth Cells

[00251] Genotyping data was collected from patients with Crohn's Disease (CD) with morphological defects of ileal Paneth cells, as determined using the classification set forth in VanDussen et al., "Genetic Variants Synthesize the Produce Paneth Cell Phenotypes That Define Subtypes of Crohn's Disease," *Gastroenterology* 2014; 146:200-209. Genotyping was performed at Cedars-Sinai Medical Center using the Illumina Immuno-BeadChip array. Markers were excluded from analysis based on: Hardy-Weinberg Equilibrium $p \leq 10^{-4}$; missingness in SNPs of $>2\%$; minor allele frequency $< 1\%$. Related individuals (Pi-hat scores >0.25) were identified using identity-by-descent and excluded from analysis (PLINK). Admixture was used to generate ethnicity proportion estimations for all individuals. Only subjects identified by admixture as Caucasian (proportion <0.75) were included in the analysis. Results showed that SNPs at the IL18R1 locus provided in **Table 3** are associated with morphological defects of ileal Paneth cells in CD subjects.

Table 3. IL18R1 SNPs Significantly Correlated with Defects of Ileal Paneth Cells

Populati on	PHENOTY PE	Marker	dbSNP	p_val ue	A 1	n_mi ss	OR_Z_ B	base_pair_C H2	cis_eGE NE	eqtl_be ta	eqtl_ p	priori ty
CD	Paneth-D5 phenotype	imm_2_1023413 43	rs767211 33	$<1.0E-3$	C	155	3.1900	102974911	NA	NA	NA	NA

[00252] Example 4. IL18R1 SNPs Associated with Inflammatory Bowel Disease

[00253] Multiple large-scale case-control association studies involving inflammatory bowel disease (IBD) in populations using gene-based single nucleotide polymorphism (SNP) markers were performed. The studies included subjects recruited at the Cedars-Sinai Inflammatory Bowel Disease Centers. The studies also included GWAS data derived from the International Inflammatory Bowel Diseases Genetic Consortium (IIBDGC) and cohorts from DeLange et al., "Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease," *Nature Genetics*. Vol. 49, No. 2 (February 2017). Results showed that SNPs at the IL18R1 locus provided in **Table 4** are significantly associated with IBD.

Table 4. IL18R1 SNPs Significantly Correlated with IBD

PHENO TYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_CH2	cis_eGE NE	eqtl_beta	eqtl_p	priority
IBD vs. Ctrl	imm_2_1 02305468	rs130013 25	$<1.0E-3$	A	128356	-0.0989	10293903 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02324148	rs142010 1	$<1.0E-3$	A	128415	-0.0988	10295771 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02315593	rs124792 10	$<1.0E-3$	A	128424	-0.0983	10294916 1	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02341768	rs129879 77	$<1.0E-3$	C	128443	-0.0963	10297533 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02298258	rs130205 53	$<1.0E-3$	G	128429	-0.0972	10293182 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02298994	rs950880	$<1.0E-3$	A	128433	-0.0972	10293256 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02340561	rs129993 64	$<1.0E-3$	A	128422	-0.0961	10297412 9	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02345460	rs228703 7	$<1.0E-3$	A	123133	-0.0985	10297902 8	NA	NA	NA	NA
IBD vs. Ctrl	rs129985 21	rs129985 21	$<1.0E-3$	A	126705	-0.0946	10297441 7	NA	NA	NA	NA

IBD vs. Ctrl	imm_2_1 02317254	rs130190 81	<1.0E-3	C	124874	-0.0962	10295082 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02323964	rs373212 9	<1.0E-3	G	128430	-0.1016	10295753 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02322292	rs377117 7	<1.0E-3	A	128438	-0.1016	10295586 0	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02322115	rs873022	<1.0E-3	A	128438	-0.1016	10295568 3	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02318792	rs170269 74	<1.0E-3	A	128409	-0.1007	10295236 0	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02315251	rs142010 2	<1.0E-3	G	128385	0.0883	10294881 9	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02331174	rs130174 55	<1.0E-3	A	125514	-0.0929	10296474 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02319499	rs127121 41	<1.0E-3	A	128443	0.0881	10295306 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02305866	rs142008 8	<1.0E-3	A	128434	0.0878	10293943 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02297982	rs155861 9	<1.0E-3	C	128433	0.0877	10293155 0	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02315371	rs124663 80	<1.0E-3	A	128438	0.0876	10294893 9	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02317505	rs199746 7	<1.0E-3	A	128423	0.0876	10295107 3	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02302563	rs116904 43	<1.0E-3	T	128429	0.0872	10293613 1	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02303914	rs414213 2	<1.0E-3	G	128437	0.0870	10293748 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02334276	rs111239 23	<1.0E-3	A	128409	-0.0900	10296784 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02297380	rs127121 35	<1.0E-3	A	128436	0.0869	10293094 8	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02318230	rs136235 0	<1.0E-3	G	127309	0.0876	10295179 8	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02303413	rs974389	<1.0E-3	G	128439	0.0867	10293698 1	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02298234	rs129965 05	<1.0E-3	A	128438	0.0868	10293180 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02293518	rs116854 80	<1.0E-3	G	128411	0.0864	10292708 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02293413	rs116854 24	<1.0E-3	G	128439	0.0863	10292698 1	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02306844	rs670684 4	<1.0E-3	A	128412	0.0864	10294041 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02298679	rs101833 88	<1.0E-3	G	128439	0.0863	10293224 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02298358	rs130207 93	<1.0E-3	G	128421	0.0863	10293192 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02297313	rs101897 11	<1.0E-3	A	128434	0.0862	10293088 1	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02296579	rs115862 2	<1.0E-3	G	128397	0.0859	10293014 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02295444	rs673317 4	<1.0E-3	A	128441	0.0862	10292901 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02296812	rs101892 02	<1.0E-3	A	128443	0.0856	10293038 0	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02297089	rs101919 14	<1.0E-3	A	128440	0.0856	10293065 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02320622	rs592475 11	<1.0E-3	A	122976	0.0876	10295419 0	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02301669	rs111239 18	<1.0E-3	A	127911	0.0857	10293523 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02350711	rs142009 8	<1.0E-3	G	120004	-0.0906	10298427 9	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02331764	rs170270 06	<1.0E-3	C	128437	-0.0967	10296533 2	IL1RL1	-0.0663	0.0409	IL1RL1
IBD vs. Ctrl	imm_2_1 02343969	rs671088 5	<1.0E-3	G	121235	-0.0902	10297753 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02332499	rs192162 2	<1.0E-3	G	128426	0.0853	10296606 7	MAP4K4	0.0496	0.0167	0
IBD vs. Ctrl	imm_2_1 02332303	rs124695 06	<1.0E-3	A	128441	-0.0959	10296587 1	IL1RL1	-0.0659	0.0477	IL1RL1
IBD vs.	imm_2_1	rs208028	<1.0E-3	A	128393	-0.0956	10299502	IL1RL1	-0.0673	0.0437	0

Ctrl	02361452	9				0					
IBD vs. Ctrl	imm_2_1 02372819	rs485157 0	<1.0E-3	G	128424	-0.0955	10300638 7	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02352382	rs377117 1	<1.0E-3	G	127351	-0.0960	10298595 0	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02352244	rs377117 2	<1.0E-3	A	128434	-0.0954	10298581 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02382350	rs170270 87	<1.0E-3	A	128442	-0.0952	10301591 8	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02352586	rs216020 2	<1.0E-3	A	127368	-0.0957	10298615 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02391170	rs485100 6	<1.0E-3	A	127366	-0.0957	10302473 8	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02331293	rs559272 92	<1.0E-3	A	128397	-0.0950	10296486 1	IL1RL1	-0.0700	0.0305	IL1RL1
IBD vs. Ctrl	imm_2_1 02297827	rs155862 0	<1.0E-3	A	124132	0.0848	10293139 5	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02377020	rs228703 4	<1.0E-3	A	128430	-0.0950	10301058 8	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02363304	rs382120 3	<1.0E-3	A	128369	-0.0950	10299687 2	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02373999	rs170270 60	<1.0E-3	G	128438	-0.0950	10300756 7	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02365744	rs562584 75	<1.0E-3	G	128385	-0.0949	10299931 2	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02361316	rs170270 37	<1.0E-3	G	128418	-0.0949	10299488 4	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02358511	rs227029 8	<1.0E-3	G	128440	-0.0947	10299207 9	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02384509	rs373212 3	<1.0E-3	G	128437	-0.0947	10301807 7	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02379106	rs170270 71	<1.0E-3	A	128442	-0.0943	10301267 4	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02363237	rs116837 00	<1.0E-3	A	128441	-0.0943	10299680 5	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02364165	rs114656 33	<1.0E-3	A	127248	-0.0940	10299773 3	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02318404	rs136234 9	<1.0E-3	G	121312	0.0842	10295197 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02299984	rs196817 1	<1.0E-3	NA	NA	0.0844	10293355 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02380394	rs373212 6	<1.0E-3	C	124130	-0.0937	10301396 2	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02380734	rs113535 4	<1.0E-3	C	128411	-0.0920	10301430 2	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02390763	rs558831 25	<1.0E-3	A	124115	-0.0909	10302433 1	IL1RL1	-0.0673	0.0437	0
IBD vs. Ctrl	imm_2_1 02336239	rs677237 47	<1.0E-3	NA	NA	-0.0921	10296980 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02360488	rs101905 55	<1.0E-3	A	127048	0.0904	10299405 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02367834	rs103513 0	<1.0E-3	A	121324	-0.0884	10300140 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02386351	rs103512 7	<1.0E-3	A	128385	0.0885	10301991 9	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02375142	rs127121 45	<1.0E-3	A	128424	0.0874	10300871 0	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02369475	rs224111 7	<1.0E-3	A	128442	0.0866	10300304 3	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02368827	rs375527 4	<1.0E-3	A	128437	0.0864	10300239 5	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02381128	rs156868 1	<1.0E-3	G	128410	0.0864	10301469 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02359107	rs227029 7	<1.0E-3	A	128426	0.0864	10299267 5	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02374055	rs386044 4	<1.0E-3	A	128415	0.0863	10300762 3	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02351856	rs205862 2	<1.0E-3	A	128439	0.0863	10298542 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02361146	rs675002 0	<1.0E-3	G	128434	0.0861	10299471 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02391245	rs485100 7	<1.0E-3	A	128428	0.0861	10302481 3	NA	NA	NA	NA

IBD vs. Ctrl	imm_2_1 02359593	rs675371 7	<1.0E-3	A	128424	0.0859	10299316 1	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02399579	rs180778 2	<1.0E-3	G	128384	0.0856	10303314 7	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02391635	rs485157 5	<1.0E-3	G	127285	0.0857	10302520 3	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02351116	rs155862 7	<1.0E-3	G	126175	0.0856	10298468 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02382648	rs556646 18	<1.0E-3	A	128443	-0.0730	10301621 6	IL1RL1	-0.0559	0.0418	0
IBD vs. Ctrl	imm_2_1 02338297	rs130157 14	<1.0E-3	C	128429	0.0844	10297186 5	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02356166	rs204174 0	<1.0E-3	A	124067	0.0818	10298973 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02315064	rs142010 3	<1.0E-3	A	128436	0.0754	10294863 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02294158	rs654311 6	<1.0E-3	A	128409	0.0739	10292772 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02377984	rs485100 5	<1.0E-3	A	128361	-0.0600	10301155 2	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02326078	rs621526 61	<1.0E-3	G	128435	0.0593	10295964 6	IL1R2, IL1RL2	0.231497 33812603 4, 0.122966 17855485 1	0.040373 08383166 27, 0.045654 18745379 71	0, 0
IBD vs. Ctrl	imm_2_1 02304821	rs142008 9	<1.0E-3	G	128433	0.0592	10293838 9	IL1R2, IL1RL2	0.231497 33812603 4, 0.122966 17855485 1	0.040373 08383166 27, 0.045654 18745379 71	0, 0
IBD vs. Ctrl	imm_2_1 02331585	rs176963 76	<1.0E-3	A	128437	0.0588	10296515 3	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
IBD vs. Ctrl	imm_2_1 02340654	rs121058 08	<1.0E-3	T	128437	0.0588	10297422 2	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
IBD vs. Ctrl	imm_2_1 02379334	rs142009 5	<1.0E-3	G	128411	0.0625	10301290 2	IL1R1, IL18RAP , RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	0, 0, 0, 0, 0
IBD vs. Ctrl	imm_2_1 02369466	rs560300 66	<1.0E-3	C	128443	0.0623	10300303 4	IL1R1, IL18RAP , RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	0, 0, 0, 0, 0

									0.170724 36416156 9, - 0.263402 64500044 6	0.025751 93290180 87, 0.033428 43922870 19	
IBD vs. Ctrl	imm_2_1 02335102	rs782486 80	<1.0E-3	G	128435	0.0559	10296867 0	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
IBD vs. Ctrl	imm_2_1 02328773	rs621526 62	<1.0E-3	A	127038	0.0551	10296234 1	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
IBD vs. Ctrl	imm_2_1 023399158	rs621527 14	<1.0E-3	G	128441	0.0575	10303272 6	IL1R1, IL18RAP , RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	0, IL18RAP , 0, 0, 0
IBD vs. Ctrl	imm_2_1 02373483	rs170270 56	<1.0E-3	A	128436	-0.0678	10300705 1	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02334360	rs498895 5	<1.0E-3	G	128413	0.0302	10296792 8	IL1RL1	0.0533	0.0425	IL1RL1
IBD vs. Ctrl	imm_2_1 02338096	rs980796 2	<1.0E-3	G	127307	0.0304	10297166 4	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02337738	rs980845 3	<1.0E-3	A	128328	0.0301	10297130 6	IL1RL1	0.0533	0.0425	IL1RL1
IBD vs. Ctrl	imm_2_1 02333668	rs134240 06	<1.0E-3	G	128431	0.0301	10296723 6	IL1RL1	0.0533	0.0425	IL1RL1
IBD vs. Ctrl	imm_2_1 02336537	rs116956 27	<1.0E-3	G	127909	0.0298	10297010 5	IL1RL1	0.0533	0.0425	IL1RL1
IBD vs. Ctrl	imm_2_1 02352654	rs377116 6	<1.0E-3	A	128393	0.0295	10298622 2	IL1RL1	0.0533	0.0425	0
IBD vs. Ctrl	imm_2_1 02341482	rs101731 93	<1.0E-3	A	128395	0.0293	10297505 0	IL1RL1	0.0533	0.0425	0
IBD vs. Ctrl	imm_2_1 02347408	rs114655 75	<1.0E-3	G	127363	0.0948	10298097 6	NA	NA	NA	NA
IBD vs. Ctrl	imm_2_1 02339231	rs485156 6	<1.0E-3	C	126710	0.0293	10297279 9	IL1RL1	0.0533	0.0425	0
IBD vs. Ctrl	imm_2_1 02346056	rs930885 7	<1.0E-3	A	128434	0.0290	10297962 4	IL1RL1	0.0533	0.0425	0
IBD vs. Ctrl	imm_2_1 02352807	rs197467 5	<1.0E-3	A	128436	0.0287	10298637 5	IL1RL1	0.0533	0.0425	0
IBD vs. Ctrl	imm_2_1 02333845	rs675196 7	<1.0E-3	G	128440	0.0284	10296741 3	IL1RL1	0.0533	0.0425	IL1RL1
IBD vs. non-IBD Controls	imm_2_1 02332499	rs192162 2	<1.0E-3	G	9366	1.2030	10296606 7	MAP4K4	0.0496	0.0167	0
IBD vs. non-IBD Controls	imm_2_1 02324148	rs142010 1	<1.0E-3	A	9365	0.8460	10295771 6	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02340561	rs129993 64	<1.0E-3	A	9366	0.8480	10297412 9	NA	NA	NA	NA

IBD vs. non-IBD Controls	imm_2_1 02341768	rs129879 77	<1.0E-3	C	9366	0.8481	10297533 6	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02305468	rs130013 25	<1.0E-3	A	9366	0.8475	10293903 6	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02315593	rs124792 10	<1.0E-3	A	9366	0.8477	10294916 1	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02345460	rs228703 7	<1.0E-3	A	9364	0.8490	10297902 8	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02334276	rs111239 23	<1.0E-3	A	9366	0.8491	10296784 4	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02298258	rs130205 53	<1.0E-3	G	9365	0.8486	10293182 6	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02298994	rs950880	<1.0E-3	A	9366	0.8487	10293256 2	NA	NA	NA	NA
IBD vs. non-IBD Controls	rs129985 21	rs129985 21	<1.0E-3	A	9364	0.8494	10297441 7	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02351116	rs155862 7	<1.0E-3	G	9355	1.1690	10298468 4	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02352412	rs377117 0	<1.0E-3	A	9365	1.1680	10298598 0	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02351856	rs205862 2	<1.0E-3	A	9366	1.1680	10298542 4	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02338297	rs130157 14	<1.0E-3	C	9363	1.1650	10297186 5	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02382476	rs111239 26	<1.0E-3	C	9366	1.1610	10301604 4	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02359107	rs227029 7	<1.0E-3	A	9366	1.1600	10299267 5	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02359593	rs675371 7	<1.0E-3	A	9366	1.1600	10299316 1	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02360488	rs101905 55	<1.0E-3	A	9366	1.1600	10299405 6	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02361146	rs675002 0	<1.0E-3	G	9366	1.1600	10299471 4	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02368827	rs375527 4	<1.0E-3	A	9366	1.1600	10300239 5	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02369475	rs224111 7	<1.0E-3	A	9366	1.1600	10300304 3	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02318792	rs170269 74	<1.0E-3	A	9366	0.8605	10295236 0	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02375142	rs127121 45	<1.0E-3	A	9364	1.1600	10300871 0	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02374055	rs386044 4	<1.0E-3	A	9366	1.1600	10300762 3	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02381128	rs156868 1	<1.0E-3	G	9366	1.1600	10301469 6	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02391245	rs485100 7	<1.0E-3	A	9364	1.1580	10302481 3	NA	NA	NA	NA
IBD vs. non-IBD	imm_2_1 02399579	rs180778 2	<1.0E-3	G	9366	1.1580	10303314 7	NA	NA	NA	NA

Controls											
IBD vs. non-IBD Controls	imm_2_1 02322292	rs377117 7	<1.0E-3	A	9364	0.8621	10295586 0	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02322115	rs873022	<1.0E-3	A	9366	0.8622	10295568 3	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02323964	rs373212 9	<1.0E-3	G	9366	0.8622	10295753 2	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02386351	rs103512 7	<1.0E-3	A	9361	1.1580	10301991 9	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02294158	rs654311 6	<1.0E-3	A	9366	1.1450	10292772 6	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02315064	rs142010 3	<1.0E-3	A	9366	1.1450	10294863 2	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02363606	rs377116 2	<1.0E-3	A	9364	0.8713	10299717 4	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02382350	rs170270 87	<1.0E-3	A	9366	0.8711	10301591 8	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02337597	rs563865 07	<1.0E-3	A	9366	0.8721	10297116 5	IL1RL1	-0.0675	0.0376	IL1RL1
IBD vs. non-IBD Controls	imm_2_1 02361452	rs208028 9	<1.0E-3	A	9364	0.8722	10299502 0	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02352244	rs377117 2	<1.0E-3	A	9366	0.8724	10298581 2	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02358511	rs227029 8	<1.0E-3	G	9366	0.8727	10299207 9	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02363304	rs382120 3	<1.0E-3	A	9366	0.8727	10299687 2	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02365744	rs562584 75	<1.0E-3	G	9366	0.8727	10299931 2	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02372819	rs485157 0	<1.0E-3	G	9366	0.8727	10300638 7	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02373999	rs170270 60	<1.0E-3	G	9366	0.8727	10300756 7	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02384509	rs373212 3	<1.0E-3	G	9366	0.8727	10301807 7	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02331764	rs170270 06	<1.0E-3	C	9366	0.8729	10296533 2	IL1RL1	-0.0663	0.0409	IL1RL1
IBD vs. non-IBD Controls	imm_2_1 02319499	rs127121 41	<1.0E-3	A	9366	1.1240	10295306 7	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02377020	rs228703 4	<1.0E-3	A	9365	0.8732	10301058 8	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02361316	rs170270 37	<1.0E-3	G	9366	0.8735	10299488 4	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02380734	rs113535 4	<1.0E-3	C	9362	0.8737	10301430 2	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02332303	rs124695 06	<1.0E-3	A	9366	0.8737	10296587 1	IL1RL1	-0.0659	0.0477	IL1RL1
IBD vs. non-IBD Controls	imm_2_1 02363237	rs116837 00	<1.0E-3	A	9366	0.8743	10299680 5	IL1RL1	-0.0673	0.0437	0
IBD vs.	imm_2_1	rs559272	<1.0E-3	A	9365	0.8776	10296486	IL1RL1	-0.0700	0.0305	IL1RL1

non-IBD Controls	02331293	92					1				
IBD vs. non-IBD Controls	imm_2_1 02379106	rs17027071	<1.0E-3	A	9366	0.8777	103012674	IL1RL1	-0.0673	0.0437	0
IBD vs. non-IBD Controls	imm_2_1 02317505	rs1997467	<1.0E-3	A	9361	1.1150	102951073	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02317899	rs1997466	<1.0E-3	G	9365	1.1140	102951467	NA	NA	NA	NA
IBD vs. non-IBD Controls	imm_2_1 02317494	rs12712140	<1.0E-3	C	9366	1.1130	102951062	NA	NA	NA	NA

[00254] Example 5. IL18R1 SNPs Associated with Ulcerative Colitis

[00255] Multiple large-scale case-control association studies involving ulcerative colitis (UC) in populations using gene-based single nucleotide polymorphism (SNP) markers were performed. The studies included subjects recruited at the Cedars-Sinai Inflammatory Bowel Disease Centers. The studies also included GWAS data derived from the International Inflammatory Bowel Diseases Genetic Consortium (IIBDGC) and cohorts from DeLange et al., “Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease,” Nature Genetics. Vol. 49, No. 2 (February 2017). Results showed that SNPs at the IL18R1 locus provided in **Table 5** are significantly associated with UC.

Table 5. IL18R1 SNPs Associated with UC

PHENOTYPE	Marker	dbSNP	p_value	A1	n_mis	OR_Z_B	base_pair_CH2	cis_eGENE	eqtl_beta	eqtl_p	priority
UC vs. Ctrl	imm_2_102341768	rs12987977	<1.0E-3	C	95393	-0.0773	102975336	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102340561	rs12999364	<1.0E-3	A	95381	-0.0768	102974129	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102345460	rs2287037	<1.0E-3	A	92068	-0.0786	102979028	NA	NA	NA	NA
UC vs. Ctrl	rs12998521	rs12998521	<1.0E-3	A	94754	-0.0764	102974417	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102334276	rs11123923	<1.0E-3	A	95379	-0.0719	102967844	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102350711	rs1420098	<1.0E-3	G	88812	-0.0730	102984279	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102331174	rs13017455	<1.0E-3	A	93635	-0.0724	102964742	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102343969	rs6710885	<1.0E-3	G	89377	-0.0726	102977537	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102305468	rs13001325	<1.0E-3	A	95338	-0.0713	102939036	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102315593	rs12479210	<1.0E-3	A	95383	-0.0710	102949161	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102324148	rs1420101	<1.0E-3	A	95374	-0.0706	102957716	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102298258	rs13020553	<1.0E-3	G	95381	-0.0703	102931826	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102298994	rs950880	<1.0E-3	A	95388	-0.0703	102932562	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102323964	rs3732129	<1.0E-3	G	95381	-0.0753	102957532	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102322292	rs3771177	<1.0E-3	A	95389	-0.0752	102955860	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102322115	rs873022	<1.0E-3	A	95390	-0.0751	102955683	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102317254	rs13019081	<1.0E-3	C	93843	-0.0692	102950822	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102352382	rs3771171	<1.0E-3	G	94548	-0.0748	102985950	NA	NA	NA	NA

UC vs. Ctrl	imm_2_102318792	rs17026974	<1.0E-3	A	95369	-0.0738	102952360	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102331764	rs17027006	<1.0E-3	C	95391	-0.0740	102965332	IL1RL1	-0.0663	0.0409	IL1RL1
UC vs. Ctrl	imm_2_102352586	rs2160202	<1.0E-3	A	94558	-0.0742	102986154	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102352244	rs3771172	<1.0E-3	A	95387	-0.0739	102985812	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102332303	rs12469506	<1.0E-3	A	95392	-0.0737	102965871	IL1RL1	-0.0659	0.0477	IL1RL1
UC vs. Ctrl	imm_2_102315251	rs1420102	<1.0E-3	G	95356	0.0643	102948819	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102331293	rs55927292	<1.0E-3	A	95358	-0.0727	102964861	IL1RL1	-0.0700	0.0305	IL1RL1
UC vs. Ctrl	imm_2_102297380	rs12712135	<1.0E-3	A	95390	0.0638	102930948	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102305866	rs1420088	<1.0E-3	A	95388	0.0637	102939434	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102298234	rs12996505	<1.0E-3	A	95390	0.0635	102931802	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102297982	rs1558619	<1.0E-3	C	95387	0.0635	102931550	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102317505	rs1997467	<1.0E-3	A	95378	0.0634	102951073	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102303914	rs4142132	<1.0E-3	G	95388	0.0632	102937482	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102315371	rs12466380	<1.0E-3	A	95390	0.0631	102948939	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102361452	rs2080289	<1.0E-3	A	95372	-0.0716	102995020	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102298679	rs1018338	<1.0E-3	G	95390	0.0630	102932247	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102302563	rs11690443	<1.0E-3	T	95389	0.0629	102936131	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102361316	rs17027037	<1.0E-3	G	95375	-0.0714	102994884	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102372819	rs4851570	<1.0E-3	G	95382	-0.0713	103006387	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102306844	rs6706844	<1.0E-3	A	95369	0.0628	102940412	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102293518	rs11685480	<1.0E-3	G	95373	0.0628	102927086	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102336239	rs67723747	<1.0E-3	NA	NA	-0.0730	102969807	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102303413	rs974389	<1.0E-3	G	95390	0.0627	102936981	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102319499	rs12712141	<1.0E-3	A	95393	0.0627	102953067	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102301669	rs11123918	<1.0E-3	A	95145	0.0628	102935237	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102365744	rs56258475	<1.0E-3	G	95358	-0.0710	102999312	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102320622	rs59247511	<1.0E-3	A	90228	0.0634	102954190	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102363304	rs3821203	<1.0E-3	A	95344	-0.0710	102996872	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102391170	rs4851006	<1.0E-3	A	94559	-0.0712	103024738	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102379106	rs17027071	<1.0E-3	A	95393	-0.0708	103012674	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102295444	rs6733174	<1.0E-3	A	95392	0.0624	102929012	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102377020	rs2287034	<1.0E-3	A	95383	-0.0708	103010588	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102358511	rs2270298	<1.0E-3	G	95390	-0.0708	102992079	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102382350	rs17027087	<1.0E-3	A	95392	-0.0707	103015918	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102298358	rs13020793	<1.0E-3	G	95378	0.0622	102931926	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102380394	rs3732126	<1.0E-3	C	91115	-0.0712	103013962	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_10231823	rs1362350	<1.0E-3	G	94516	0.0624	102951798	NA	NA	NA	NA

	0		3								
UC vs. Ctrl	imm_2_102296812	rs10189202	<1.0E-3	A	95393	0.0621	102930380	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102373999	rs17027060	<1.0E-3	G	95390	-0.0704	103007567	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102363237	rs11683700	<1.0E-3	A	95391	-0.0704	102996805	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102297089	rs10191914	<1.0E-3	A	95392	0.0620	102930657	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102293413	rs11685424	<1.0E-3	G	95391	0.0621	102926981	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102297313	rs10189711	<1.0E-3	A	95387	0.0619	102930881	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102296579	rs1558622	<1.0E-3	G	95364	0.0619	102930147	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102384509	rs3732123	<1.0E-3	G	95389	-0.0700	103018077	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102364165	rs11465633	<1.0E-3	A	94483	-0.0702	102997733	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102380734	rs1135354	<1.0E-3	C	95377	-0.0682	103014302	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102297827	rs1558620	<1.0E-3	A	91113	0.0600	102931395	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102332499	rs1921622	<1.0E-3	G	95383	0.0599	102966067	MAP4K4	0.0496	0.0167	0
UC vs. Ctrl	imm_2_102318404	rs1362349	<1.0E-3	G	89644	0.0604	102951972	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102390763	rs55883125	<1.0E-3	A	91103	-0.0671	103024331	IL1RL1	-0.0673	0.0437	0
UC vs. Ctrl	imm_2_102367834	rs1035130	<1.0E-3	A	90081	-0.0662	103001402	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102382648	rs55664618	<1.0E-3	A	95393	-0.0578	103016216	IL1RL1	-0.0559	0.0418	0
UC vs. Ctrl	imm_2_102299984	rs1968171	<1.0E-3	NA	NA	0.0557	102933552	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102360488	rs10190555	<1.0E-3	A	94433	0.0590	102994056	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102386351	rs1035127	<1.0E-3	A	95362	0.0542	103019919	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102375142	rs12712145	<1.0E-3	A	95381	0.0540	103008710	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102381128	rs1568681	<1.0E-3	G	95371	0.0531	103014696	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102351856	rs2058622	<1.0E-3	A	95389	0.0531	102985424	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102368827	rs3755274	<1.0E-3	A	95390	0.0529	103002395	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102361146	rs6750020	<1.0E-3	G	95385	0.0528	102994714	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102369475	rs2241117	<1.0E-3	A	95392	0.0528	103003043	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102359593	rs6753717	<1.0E-3	A	95379	0.0528	102993161	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102359107	rs2270297	<1.0E-3	A	95381	0.0527	102992675	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102374055	rs3860444	<1.0E-3	A	95375	0.0527	103007623	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102351116	rs1558627	<1.0E-3	G	94316	0.0527	102984684	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102399579	rs1807782	<1.0E-3	G	95356	0.0523	103033147	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102391245	rs4851007	<1.0E-3	A	95381	0.0516	103024813	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102338297	rs13015714	<1.0E-3	C	95382	0.0512	102971865	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102391635	rs4851575	<1.0E-3	G	94510	0.0503	103025203	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102356166	rs2041740	<1.0E-3	A	91089	0.0496	102989734	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102377984	rs4851005	<1.0E-3	A	95340	-0.0409	103011552	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102338096	rs9807962	<1.0E-3	G	94529	0.0380	102971664	NA	NA	NA	NA

UC vs. Ctrl	imm_2_102341482	rs10173193	<1.0E-3	A	95368	0.0372	102975050	IL1RL1	0.0533	0.0425	0
UC vs. Ctrl	imm_2_102334360	rs4988955	<1.0E-3	G	95373	0.0371	102967928	IL1RL1	0.0533	0.0425	IL1RL1
UC vs. Ctrl	imm_2_102346056	rs9308857	<1.0E-3	A	95388	0.0371	102979624	IL1RL1	0.0533	0.0425	0
UC vs. Ctrl	imm_2_102337738	rs9808453	<1.0E-3	A	95325	0.0370	102971306	IL1RL1	0.0533	0.0425	IL1RL1
UC vs. Ctrl	imm_2_102339231	rs4851566	<1.0E-3	C	94760	0.0372	102972799	IL1RL1	0.0533	0.0425	0
UC vs. Ctrl	imm_2_102333668	rs13424006	<1.0E-3	G	95385	0.0369	102967236	IL1RL1	0.0533	0.0425	IL1RL1
UC vs. Ctrl	imm_2_102352654	rs3771166	<1.0E-3	A	95357	0.0369	102986222	IL1RL1	0.0533	0.0425	0
UC vs. Ctrl	imm_2_102294158	rs6543116	<1.0E-3	A	95366	0.0411	102927726	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102351056	rs1362348	<1.0E-3	G	90305	0.0369	102984624	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102315064	rs1420103	<1.0E-3	A	95390	0.0411	102948632	NA	NA	NA	NA
UC vs. Ctrl	imm_2_102333845	rs6751967	<1.0E-3	G	95391	0.0361	102967413	IL1RL1	0.0533	0.0425	IL1RL1
Ulcerative Colitis vs. non-IBD Controls	imm_2_102332499	rs1921622	<1.0E-3	G	6864	1.1940	102966067	MAP4K4	0.0496	0.0167	0
Ulcerative Colitis vs. non-IBD Controls	imm_2_102334276	rs11123923	<1.0E-3	A	6864	0.8381	102967844	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102340561	rs12999364	<1.0E-3	A	6864	0.8396	102974129	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102341768	rs12987977	<1.0E-3	C	6864	0.8399	102975336	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	rs12998521	rs12998521	<1.0E-3	A	6863	0.8403	102974417	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102345460	rs2287037	<1.0E-3	A	6862	0.8408	102979028	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102305468	rs13001325	<1.0E-3	A	6864	0.8415	102939036	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102315593	rs12479210	<1.0E-3	A	6864	0.8417	102949161	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102298258	rs13020553	<1.0E-3	G	6864	0.8433	102931826	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102298994	rs950880	<1.0E-3	A	6864	0.8433	102932562	NA	NA	NA	NA
Ulcerative Colitis vs. non-IBD Controls	imm_2_102324148	rs1420101	<1.0E-3	A	6863	0.8442	102957716	NA	NA	NA	NA

Table 6. Description of Abbreviations Used in Disclosed Tables

Term	Description
dbSNP	dbSNP 147 rsID for SNP associated with phenotype
A1	Minor allele for SNP

Study Size (n miss)	Number of subjects in cohort
Beta (OR_Z_B)	Odds ratio for logistic regression(OR) or Z (Hazard ratio for coxph regression) or Beta for linear regression or meta-analysis (B) If $OR < 1$; ($Z < 1$); ($B < 0$) the minor allele correlates to a reduced risk of a patient exhibiting the listed phenotype If $OR > 1$; ($Z > 1$); ($B > 0$), the minor allele correlates to an increased risk of a patient exhibiting the listed phenotype
P (p_value)	Statistical significance of association between phenotype and SNP presence
BP (base_pair)	Base pair; Genomic location in hg2 coordinates
Chr	Chromosome
snp location	Location of SNP on gene
Gene (cis_eGene)	Local gene on same chromosome as the SNP that is differentially regulated in patients having the related SNP
eql_beta	Negative value indicates decreased expression of cis gene in subjects having the related SNP; positive value indicates increased expression of cis gene in subjects having the related SNP
eql_p	Statistical significance of association between cisgene and SNP presence
priority	Defined as eQTL where the SNP is part of the cis-eGene that it regulates

Table 7. Description of phenotype abbreviations

Phenotype/Disease location	Description
L1	Disease location – ileal
L2	Disease location – colonic
L2_colonic	Disease location – colonic
L3	Disease location – ileocolonic
B1	Non-stricturing/non-penetrating
B2a	Stricturing
B2b	Stricturing and penetrating
B2a + B2b	Stricturing with evidence of penetrating
B3	Isolated internal penetrating
E Nodosum	Erythema nodosum
Paneth-D0	% normal Paneth cells
Paneth-D1	% abnormal Paneth cells
Paneth-D1234	% abnormal Paneth cells
Paneth-D3	% abnormal Paneth cells
Paneth-D4	% abnormal Paneth cells
Paneth-D5	% abnormal Paneth cells
Paneth high (>20%) vs low (<20%)	High-low % abnormal Paneth cells
anti-TNF time to loss of response	Subjects non-responsive to anti-TNF in months. The loss of response was characterized by a reappearance of symptoms consistent with a flare after initial anti-TNF response, and the time from induction of therapy to loss of response was recorded.
ANCA	Antineutrophil cytoplasmic antibody
Arthralgias	Arthralgias

ASCA	<i>Saccharomyces cerevisiae</i> Antibodies
IGA ASCA	<i>Saccharomyces cerevisiae</i> Antibodies IGA
IGG ASCA	<i>Saccharomyces cerevisiae</i> Antibodies IGG
OMPC	Anti-outer-membrane porin C antibody
Cbir	Antibody against flagellin
i2	Antibody against <i>Pseudomonas fluorescens</i>
PDM	Perianal disease modifier
Oral ulcers	Oral ulcers
PSC	Primary sclerosing cholangitis
Psoriasis	Psoriasis
Time to First Surgery	As defined in Soon Man Yoon et al., "Colonic Phenotypes are Associated with Poorer Response to Anti-TNF Therapies in Patients with IBD," <i>Inflamm. Bowel Dis.</i> , Volume 0, Number 0 (2017)
Smoking Status	Current smoker
Smokinghx	History of smoking
MRUC	Medically Refractory Ulcerative Colitis
PyodermaG	pyoderma gangrenosum
A_Spondylitis	Spondylitis
Arthralgias	Various types of arthralgia

[00256] Example 6. IL18R1 SNPs Associated with Celiac Disease

[00257] A genome-wide association study meta-analysis of 4,533 individuals with celiac disease (cases) and 10,750 controls of European descent were performed on Illumina Infinium HumanHap300 beadchip. A further 231,362 additional non-HLA markers from Illumina Hap550 marker set were tested for association in 3,796 cases and 8,154 controls. Genotype imputation using BEAGLE software and HapMap3 reference samples for samples typed on HumanHap300 chip was performed. After QC SNPs from 113 loci were selected for replication in 4,918 cases and 5,684 controls. All tests for association were conducted using PLINK v1.07 allowing the discovery of 13 novel celiac disease susceptibility loci.

[00258] Single nucleotide polymorphisms (SNPs) at the IL18R1 gene or genetic locus was found to be associated with celiac disease in time to celiac disease analyses ($10^{-4} > P > 5.8 \times 10^{-6}$). The hazard ratios (HR) for the SNPs with the smallest P value was 1.45.

[00259] Example 7. IL18R1 SNPs Associated with Primary Biliary Cihrosis

[00260] Toll-like receptors (TLRs) play a key role in innate immunity. Apart from their function in host defense, dysregulation in TLR signaling can confer risk to autoimmune diseases, septic shock or cancer. SNPs conferring risk to primary biliary cirrhosis (PBC), inflammatory bowel disease (IBD) and celiac disease were found to be immune response eQTLs for IL18R1. Thus, IL18R1 represents a plausible candidate for studying the pathophysiology of these disorders in the context of TLR4 activation.

[00261] Example 8. IL18R1 SNPs Associated with Asthma

[00262] IL18R1 has been implicated in the pathophysiology of asthma and maps to an asthma susceptibility locus on chromosome 2q12. The possibility of association between polymorphisms in

IL18R1 and asthma was examined by genotyping seven SNPs in 294, 342 and 100 families from Denmark, United Kingdom and Norway and conducting family-based association analyses for asthma, atopic asthma and bronchial hyper-reactivity (BHR) phenotypes. Three SNPs in IL18R1 were associated with asthma ($0.01131 < \text{or} = P < \text{or} = 0.01377$), five with atopic asthma ($0.00066 < \text{or} = P < \text{or} = 0.00405$) and two with BHR ($0.01450 < \text{or} = P < \text{or} = 0.03203$) in the Danish population; two SNPs were associated with atopic asthma ($0.00397 < \text{or} = P < \text{or} = 0.01481$) and four with BHR ($0.00435 < \text{or} = P < \text{or} = 0.03544$) in the UK population; four SNPs showed associations with asthma ($0.00015 < \text{or} = P < \text{or} = 0.03062$), two with atopic asthma ($0.01269 < \text{or} = P < \text{or} = 0.04042$) and three with BHR ($0.00259 < \text{or} = P < \text{or} = 0.01401$) in the Norwegian population; five SNPs showed associations with asthma ($0.00005 < \text{or} = P < \text{or} = 0.03744$), five with atopic asthma ($0.00001 < \text{or} = P < \text{or} = 0.04491$) and three with BHR ($0.03568 < \text{or} = P < \text{or} = 0.04778$) in the combined population. Three intronic SNPs (rs1420099, rs1362348 and rs1974675) showed replicated association for at least one asthma-related phenotype. These results demonstrate significant association between polymorphisms in IL18R1 and asthma.

Example 9: Phase 1A Clinical Trial

[00263] A phase 1A clinical trial is performed to evaluate the safety, tolerability, pharmacokinetics, and pharmacodynamics of a compound disclosed herein, e.g., an modulator of IL18R1, in subjects with moderate to severely active Crohn's disease. Eligible subjects are men and women 18 years and older. Optionally, two groups of subjects are selected: (i) subjects having an IL18R1 risk genotype comprising one or more of rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith; and (ii) subjects lacking the genotype.

[00264] Inclusion Criteria: Eligible subjects are men and women 18 years and older. Two groups of subjects are selected: (i) subjects having a genotype comprising one or more of rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith; and (ii) subjects lacking the genotype. Subjects are patients with Crohn's disease of at least 3 months' duration, confirmed at any time in the past by radiography, histology, and/or endoscopy. Female patient of childbearing potential must have a negative highly sensitive serum (beta-human chorionic gonadotropin [b-hCG]) pregnancy test result at screening and a negative urine pregnancy test result at Week 0. Subjects must adhere to the following requirements for concomitant medication for the treatment of Crohn's disease, which are permitted provided that doses meeting these requirements are stable, or have been discontinued, for at least 3 weeks before baseline (Week 0), unless otherwise specified: a) Oral 5-aminosalicylic acid (5-ASA) compounds, b) Oral corticosteroids at a prednisone-equivalent dose at or below 40 milligram per day (mg/day), or 9 mg/day of budesonide, or 5 mg/day beclomethasone dipropionate, c) Antibiotics being used as a primary treatment of Crohn's disease, d) Conventional immunomodulators (that is, azathioprine (AZA), 6-mercaptopurine (6-MP), or Methotrexate (MTX)): participants must have been taking them

for at least 12 weeks and at a stable dose for at least 4 weeks before baseline.. Subjects who has or had extensive colitis for greater than or equal to ($\geq$) 8 years, or disease limited to the left side of the colon for $\geq$ 12 years, must either have had a colonoscopy to assess for the presence of dysplasia within 1 year before the first administration of study agent or a colonoscopy to assess for the presence of malignancy at the screening visit, with no evidence of malignancy. Subjects must have active Crohn's disease, defined as a baseline Crohn's Disease Activity Index (CDAI) score of $\geq$ 220 but $\leq$ 450.

[00265] Experimental (Part I): Placebo. Subjects will receive placebo at Weeks 0, 2, 4, and 6. From Week 8 Placebo-treated subjects who are in clinical response at Week 8 ($\geq$ 100-point reduction from baseline in Crohn's Disease Activity Index (CDAI) or CDAI $<$ 150) will continue to receive placebo every 2 weeks from Week 8 through Week 12. Placebo-treated subjects who are not in clinical response at Week 8 will receive test compound (a compound described herein) 400 mg at Week 8 and then test compound every two weeks from Week 10 through Week 12.

[00266] Experimental (Part I): Placebo. Test Compound. Subjects will receive test compound 400 milligram (mg) at Week 0 then 200 mg every two weeks through Week 22.

[00267] Experimental (Part II): Placebo. Placebo at Weeks 0, 2, 4, and 8. From Week 12, placebo-treated subjects who are in clinical response at Week 8 ($\geq$ 100-point reduction from baseline in CDAI or CDAI $<$ 150) will continue to receive placebo at Weeks 8, 10, and 12. Placebo-treated subjects who are not in clinical response at Week 8 will receive test compound 150 mg at Week 8 and then test compound 75 mg at Weeks 10, and 12.

[00268] Experimental (Part II): Test Compound High Dose. Test compound 400 mg at Week 0 and 200 mg at Weeks 2, 4, 8, and 12.

[00269] Experimental (Part II) Test Compound Middle Dose. Test compound 150 mg at Week 0 and 75 mg at Weeks 2, 4, 8, and 12.

[00270] Experimental (Part II) Test compound Low Dose. Test compound 50 mg at Week 0 and 25 mg at Weeks 2, 4, 8, and 12.

[00271] Primary Outcome Measures: Part I: Change From Baseline in the Crohn's Disease Activity Index (CDAI) Score at Week 8 [Time Frame: Baseline through Week 8] - CDAI will be assessed by collecting information on 8 different Crohn's disease-related variables: extra-intestinal manifestations, abdominal mass, weight, hematocrit, total number of liquid stools, abdominal pain/cramping, use of antidiarrheal drug(s) and/or opiates, and general well-being. The last 4 variables are scored over 7 days by the participant on a diary card. Part II: Change From Baseline in the Crohn's Disease Activity Index (CDAI) Score at Week 8 [Time Frame: Baseline through Week 8] - CDAI are assessed by collecting information on 8 different Crohn's disease-related variables: extra-intestinal manifestations, abdominal mass, weight, hematocrit, total number of liquid stools, abdominal pain/cramping, use of antidiarrheal drug(s) and/or opiates, and general well-being. The last 4 variables are scored over 7 days by the participant on a diary card.

[00272] Secondary Outcome Measures: Part II: Clinical Remission at Week 8 as Measured by Crohn's Disease Activity Index (CDAI <150) [Time Frame: Week 8]. Part II: Clinical Response at Week 8 as Measured by CDAI (≥ 100 -point reduction from baseline in CDAI or CDAI <150) [Time Frame: Week 8]. Part II: Change in Patient-Reported Outcome (PRO)-2 from baseline at Week 8 [Time Frame: Baseline through Week 8] - The PRO-2 score is the sum of the abdominal pain and stool frequency subscores of the CDAI score. Part II: Clinical remission at Week 8 as measured by PRO-2 (PRO-2 <75) [Time Frame: Week 8]. Part II: Clinical response at Week 8 as measured by PRO-2 (≥ 50 -point reduction from baseline in PRO-2 or PRO-2 <75) [Time Frame: Week 8]. Part II: Change in Simple Endoscopic Score for Crohn's Disease (SES-CD) from baseline at Week 12 [Time Frame: Baseline through Week 12] - The SES-CD score is based on the evaluation of 4 endoscopic components (presence/size of ulcers, proportion of mucosal surface covered by ulcers, proportion of mucosal surface affected by any other lesions, and presence/type of narrowing/strictures) across 5 ileocolonic segments. Each endoscopic component is scored from 0 to 3 for each segment, and a total score is derived from the sum of all the component scores (range, 0 to 56).

Example 10: Phase 1B Clinical Trial

[00273] A phase 1B clinical trial is performed to evaluate the efficacy of a compound described herein comprising an modulator of IL18R1, in participants with moderately to severely active Crohn's disease that have a genotype comprising one or more of rs3915617, rs1064448 rs1872691, rs2302712, rs3760012.

[00274] Experimental. 10 patients positive for rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith, are administered the modulator of IL18R1. 5-10 patients negative for rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith, are administered the modulator of IL18R1. Patients are monitored in real-time. Central ready of endoscopy and biopsy is employed, with readers blinded to point of time of treatment and endpoints.

[00275] Inclusion Criteria: Two groups of subjects are selected: (i) subjects having the rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith genotype, and (ii) subjects lacking the rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith genotype.

[00276] Primary Outcome Measures: Simple Endoscopic Score for Crohn's Disease (SESCD), Crohn's Disease Activity Index (CDAI), and Patient Reported Outcome (PRO). If the rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith genotype positive group shows at least 20% reduction from baseline, a Phase 2a clinical trial is performed.

[00277] **Inclusion Criteria:** PRO entry criteria: Abdominal pain score of 2 or more and/or stool frequency score of 4 or more. Primary outcome would be pain core of 0 or 1 and stool frequency score of 3 or less with no worsening from baseline. Endoscopy entry criteria: SESCD ileum only entry at score of 4 and 6 if colon is involved. Primary endoscopic outcome is 40-50% delta of mean SESCD.

Example 11: Phase 2A Clinical Trial

[00278] A phase 2A clinical trial is performed to evaluate efficacy of a compound disclosed herein, *e.g.*, an modulator of IL18R1, in subjects having a genotype comprising rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith, with moderately to severely active Crohn's disease.

[00279] **Experimental.** 40 patients (drug and placebo groups) positive for rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith are administered the modulator of IL18R1 or placebo for 12 weeks. An interim analysis is performed after 20 patients from each group are treated at the highest dose to look for 40-50% delta between placebo and treated group in primary outcome (at least 20% reduction from baseline in SESCD, CDAI, and PRO).

[00280] **Primary Outcome Measures:** Simple Endoscopic Score for Crohn's Disease (SESCD), Crohn's Disease Activity Index (CDAI), and Patient Reported Outcome (PRO).

[00281] **Inclusion Criteria:** PRO entry criteria: Abdominal pain score of 2 or more and/or stool frequency score of 4 or more. Primary outcome would be pain core of 0 or 1 and stool frequency score of 3 or less with no worsening from baseline. Endoscopy entry criteria: SESCD ileum only entry at score of 4 and 6 if colon is involved. Primary endoscopic outcome is 40-50% delta of mean SESCD.

Example 12. Treating Inflammatory Disease

[00282] An inflammatory disease is treated in a subject, by first, determining the IL18R1 risk genotype of the subject. Optionally, the subject is, or is susceptible to be, non-responsive to certain therapies such as anti-TNF, steroids, or immunomodulators, such as those disclosed herein. A sample of whole blood is obtained from the subject. An assay is performed on the sample obtained from the subject to detect a presence or absence of rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith, by Illumina ImmunoArray or polymerase chain reaction (PCR) under standard hybridization conditions. In addition, or alternatively, a sample of intestinal tissue is obtained from the subject. In addition, or alternatively, a sample of intestinal tissue is obtained from the subject. An assay is performed on the sample obtained from the subject to detect a presence of IL18R1, by single molecule detection (*e.g.*, Simoa) accordingly to manufacture instructions.

[00283] The subject is determined to have, or be at risk for developing, moderate to severe Crohn's disease if the IL18R1 risk genotype comprising rs1921622, rs2287037, rs1974675, rs2041739,

rs76362690, rs2287037, or rs80256362, or a SNP or indel in linkage disequilibrium (LD) therewith is detected in the sample obtained from the subject. A therapeutically effective amount of a modulator of IL18R1 is administered to the subject, provided the subject is determined to have the IL18R1 risk genotype.

[00284] Example 13: in vitro and in vivo studies

[00285] Reagent validation in vitro: Patient samples are analyzed to determine IL18R1 expression and to perform a preliminary functional analysis comprising testing IL-18 induction of IL-1, IL-6 and MAPK p38 phosphorylation, controlling for IL-1beta activity.

[00286] In vivo validation: IL18R1-deficient mice from Jackson laboratories are utilized to evaluate disease phenotype and gene expression.

[00287] Example 14. IL18R1 Sequences

[00288] mRNA and protein sequences for IL18R1 are listed in **Tables 8-9**.

Table 8. IL18R1 mRNA Sequences

SE Q ID NO.	NCB I Ref. No.	Variant	Sequence
10	NM_003855.3	1	TCAGGAGGCGGAGATCGCTGCTTCTCACCTACTTTCTGAACTTG GCCTCCGCAGTCGCGACCTGGCGTGAAGGAGGAGCTGCCGCCC CCGCCCCAGCCTCGGGGACGCCTCTCTGAAGAGAAGCCATTG AAGCAGAATCCAAACCATGAATTGTAGAGAATTACCCTTGACC CTTTGGGTGCTTATATCTGTAAGCACTGCAGAATCTTGTACTTC ACGTCCCCACATTACTGTGGTTGAAGGGGAACCTTTCTATCTG AAACATTGCTCGTGTTCCTTGCACATGAGATTGAAACAACCA CCAAAAGCTGGTACAAAAGCAGTGGATCACAGGAACATGTGG AGCTGAACCCAAGGAGTTCCTCGAGAATTGCTTTGCATGATTG TGTTTTGGAGTTTTGGCCAGTTGAGTTGAATGACACAGGATCTT ACTTTTTCCAAATGAAAAATTATACTCAGAAATGGAAATTAAA TGTCATCAGAAGAAATAAACACAGCTGTTTCACTGAAAGACAA GTAAGTAGTAAATTTGTGGAAGTTAAAAAATTTTTTCAGATAA CCTGTGAAAACAGTTACTATCAAACTGGTCAACAGCACATC ATTGTATAAGAACTGTAAAAAGCTACTACTGGAGAACAATAAA AACCCAACGATAAAGAAGAACGCCGAGTTTGAAGATCAGGGG TATTACTCCTGCGTGCATTTCTTCATCATAATGGAAAACCTATT TAATATCACAAAACCTTCAATATAACAATAGTGGAAAGATCGC AGTAATATAGTTCCGGTTCTTCTTGGACCAAAGCTTAACCATGT TGCAGTGAATTAGGAAAAAACGTAAGGCTCAACTGCTCTGCT TTGCTGAATGAAGAGGATGTAATTTATTGGATGTTCCGGGAAG AAAATGGATCGGATCCTAATATACATGAAGAGAAAGAAATGA GAATTATGACTCCAGAAGGCAAATGGCATGCTTCAAAAGTATT GAGAATTGAAAATATTGGTGAAAGCAATCTAAATGTTTTATAT AATTGCACTGTGGCCAGCACGGGAGGCACAGACACCAAAAGC TTCATCTTGGTGAGAAAAGCAGACATGGCTGATATCCCAGGCC ACGTCTTCACAAGAGGAATGATCATAGCTGTTTTGATCTTGGT GGCAGTAGTGTGCCTAGTGACTGTGTGTGTCATTTATAGAGTT GACTTGGTTCTATTTTATAGACATTTAACGAGAAGAGATGAAA CATTACAGATGGAAAAACATATGATGCTTTTGTGTCTTACCT AAAAGAATGCCGACCTGAAAATGGAGAGGAGCACACCTTTGC

			TGTGGAGATTTTGCCCAGGGTGTGGAGAAACATTTTGGGTAT AAGTTATGCATATTTGAAAGGGATGTAGTGCCTGGAGGAGCTG TTGTTGATGAAATCCACTCACTGATAGAGAAAAGCCGAAGACT AATCATTGTCTAAGTAAAAGTTATATGTCTAATGAGGTCAGG TATGAACTTGAAAGTGGACTCCATGAAGCATTGGTGGAAAGAA AAATTTAAATAATCTTAATTGAATTTACACCTGTTACTGACTTC ACATTCTTGCCCCAATCACTAAAGCTTTTGAAATCTCACAGAGT TCTGAAGTGGAAGGCCGATAAATCTCTTTCTTATAACTCAAGG TTCTGGAAGAACCTTCTTTACTTAATGCCTGCAAAAACAGTCA AGCCAGGTAGAGACGAACCGGAAGTCTTGCTGTTCTTTCCGA GTCTTAATCTTCAGAAACAGTGAACGCCAAAAAGAACTCAAGA TATTCTGGGGACTGAGCATATGAACCTGTTTATAACAAAGGCT GTGACTCGAAATAATTAACTTTGTCAAAATCCTGCTCACAATTT GAAGATGAACTTGTCAATTAGGTTGGCGGGAATGAGACTAAA GATTGCGCTGTGGGCTGTGGTCACGTGCTCCCAGAAGACCTGG AATTCAAAAGAAATGGAGCTATTCTTTTTCTCCCTCTTTCATAA CTGGATGCAGCTGCTCATACTCAATCCCATATTCAGCAAGTGT GAAGCTGGACGTGATGCAAAATAACCGATGCCCTACAAAAG GCGCATCTTTAAGAGTTTTAATGCCAGTGCTTAATTCGAATG AGGGGATTTTAAGTGTCTGAAGAGGCATTTTCTAGGGACCAGT GGGTGACTGAGTAACTGAAATGCTGCTTTCACTCCCTAACACC ATGGATCTGGTTGTGCATAGGATGTGGGAGGAGGGGCTGGCA GGGCCGCCTTCAGAGGCTGCAGGGCCTCAGCCTCAGGATGCAT TTAATGTATCCTGGCCACAGTTGCAGCCAACGGTTCTTGAAAG CTCGGTAAGGCCCTGCAACGCAGAGCCTGCTTATGTGGATCTA TTTATGGGAACTTCTTAAAAGGACCCAGAATAGCTCTTTATCT TTCACAAGAGACACAAATTCTAATTGAGTTAATTATCTGGGCC TTTCACTTTGGATGCTCTGAAACATTTGTTGATTTTGTGTGAAT GTTTATATCAAAATGTTTGCCAGGTTGTATTAGCCATTGAATAG CAAAAAAGTATAGTTACTTGCTTGTTTTTAAAAATTACATAT TAAAAATGCCCTTGGCATAAGGCAGCATGGTGTGGCAGTTAAG AGATGGGCTGTGCAGCCCATCCTGAGCTCCAGTCTTGAGTTTG CTACTTACTTCTGTGGCCTCTGGAACCTTATCCAACCTCTTGGT GCTTCAGTTTCCTCATCTGTGAAATTAGAATTTATAATAATTGC ACCTACCTCCCAGGGGTAATAATGAATAAATAATAAAAGT ACTTACAGTGGTTCCTGACACAGACTCAGCACTCCGTCAGTGT TGCCATGACTATTTTTATTATCATTATTAATGATTACTTAGATC AATTATTTAGCAGTGGACTAATGGAAGCTACAGAGCAGGGAA GGAAGCAGATCTAGGGAGGAAGGCAGTTTGTATTTGAGGAG GTTTGCACATGTAGAGAAGCATACTGGAGAAGCATATCCAGAG GGCGAAAGATATCTCTCCATTGTGCATCTGCCTCTTTTGACGTT GGAAGACACATGTCTTACTCCCCAAAGGGAGCCCAGCACTGGG AGCCTTCTTGATGATCTCAAAAATAATAGCTATTCAAGAAAAT CACCAAGTGACTGTGAAACCGTCAGTTCGGAAGGCTGGTTAGA ACATGTGGGAGCAACATGAATGTTCTACAAAAGTTTAAAGCAG AGATTGTTTCAAATGGGTGTAGTAGATATTACTGAAAACCAAA AAAGAGTGAGATTGTCAAGTGAAGAATGTGATTTAATGTTTGT AGTGCTTACAATTTTGTGTACCAACTGGATGACTAAAAAGAGT AAAATAATTTAATTAATAGCTCATATTTTATGTGTGAAAACAT GTTAGTGAACATATATAATCAAAATAGATTTTCATTGCTATTGC ATAGTCTCTAATACATAGAATGATTTTGCTTTTCTCTTTTATTAT ACTTGCTTTAAAATACTTGAAATATATTTTGCATTAAATGCATT TCAAGTTAAATGTCTTAAATGTATACATTAGATGTGTGTTTAA AATGCATAAAACACGTTGAAATACATTAATGAACCATT TCAGGAGGCGGAGATCGCTGCTTCTCACCTACTTTCTGAACTTG
11	NM	2	TCAGGAGGCGGAGATCGCTGCTTCTCACCTACTTTCTGAACTTG

0012 8239 9.1		GCCTCCGCAGTCGCGACCTGGCGTGAAGGAGGAGCTGCCGCCC CCGCCCCAGCCTCGGGGACGCCTCTCTGAAGAGAAGCCATTG AAGCAGAATCCAAACCATGAATTGTAGAGAATTACCCTTGACC CTTTGGGTGCTTATATCTGTAAGCACTGCAGAAATTATACTCAG AAATGGAAATTAATGTTCATCAGAAGAAATAAACACAGCTGTT TCACTGAAAGACAAGTAAGTAGTAAAATTGTGGAAGTTAAAA AATTTTTTCAGATAACCTGTGAAAACAGTTACTATCAAACACT GGTCAACAGCACATCATTGTATAAGATAGGACCACCTATTTGC AGGAAAACAAGCTCAGGGCTCCACTGATTCTACATTATGAACT GTAAAAAGCTACTACTGGAGAACAATAAAAAACCAACGATAA AGAAGAACGCCGAGTTTGAAGATCAGGGGTATTACTCCTGCGT GCATTTCTTCATCATAATGGAAAACACTATTTAATATCACCAA ACCTTCAATATAACAATAGTGGAAGATCGCAGTAATATAGTTC CGGTTCTTCTTGACCAAAGCTTAACCATGTTGCAGTGGAATT AGGAAAAAACGTAAGGCTCAACTGCTCTGCTTTGCTGAATGAA GAGGATGTAATTTATTGGATGTTTCGGGGAAGAAAATGGATCGG ATCCTAATATACATGAAGAGAAAAGAAATGAGAATTATGACTCC AGAAGGCAAATGGCATGCTTCAAAAGTATTGAGAATTGAAAA TATTGGTGAAAGCAATCTAAATGTTTTATATAATTGCACTGTGG CCAGCACGGGAGGCACAGACACCAAAAGCTTCATCTTGGTGA GAAAAGACATGGCTGATATCCCAGGCCACGTCTTCACAAGAGG AATGATCATAGCTGTTTTGATCTTGGTGGCAGTAGTGTGCCTAG TGACTGTGTGTGTCATTTATAGAGTTGACTTGGTTCTATTTTAT AGACATTTAACGAGAAGAGATGAAACATTAACAGATGGAAAA ACATATGATGCTTTTGTGTCTTACCTAAAAGAATGCCGACCTG AAAATGGAGAGGAGCACACCTTTGCTGTGGAGATTTTGCCAG GGTGTGGAGAAACATTTTGGGTATAAGTTATGCATATTTGAA AGGGATGTAGTGCTGGAGGAGCTGTTGTTGATGAAATCCACT CACTGATAGAGAAAAGCCGAAGACTAATCATTGTCTAAGTAA AAGTTATATGTCTAATGAGGTCAGGTATGAACCTGAAAAGTGA CTCCATGAAGCATTGGTGGAAGAAAAATTAATAATCTTAA TTGAATTTACACCTGTTACTGACTTCACATTCTTGCCCCAATCA CTAAAGCTTTTGAAATCTCACAGAGTTCTGAAGTGGAAGGCCG ATAAATCTCTTTCTTATAACTCAAGGTTCTGGAAGAACCTTCTT TACTTAATGCCTGCAAAAACAGTCAAGCCAGGTAGAGACGAA CCGGAAGTCTTGCTGTTCTTTCCGAGTCTTAATCTTCAGAAAC AGTGAACGCCAAAAAGAAGTCAAGATATTCTGGGGACTGAGC ATATGAACCTGTTTATAACAAAGGCTGTGACTCGAAATAATTA ACTTTGTCAAAATCCTGCTCACAATTTGAAGATGAACTTGTC ATTAGGTTGGCGGGAATGAGACTAAAGATTGCGCTGTGGGCTG TGGTCACGTGCTCCAGAAGACCTGGAATTCAAAAGAAATGGA GCTATTCTTTTTCTCCCTCTTTCATAACTGGATGCAGCTGCTCAT ACTCAATCCCATATTCAGCAAGTGTGAAGCTGGACGTGATGCA AAATAACCGATGCCCTACAAAAAGGGCGCATCTTTAAGAGTTT TAATGCCAGTGCTTAATTCGAATGAGGGGATTTTAAGTGTCTG AAGAGGCATTTTCTAGGGACCAGTGGGTGACTGAGTAACTGAA ATGCTGCTTTCACTCCCTAACACCATGGATCTGGTTGTGCATAG GATGTGGGAGGAGGGGCTGGCAGGGCCGCCTTCAGAGGCTGC AGGGCCTCAGCCTCAGGATGCATTTAATGTATCCTGGCCACAG TTGCAGCCAACGGTTCTTGAAAGCTCGGTAAGGCCCTGCAACG CAGAGCCTGCTTATGTGGATCTATTTATGGGAACCTTCTAAAA GGACCCAGAAATAGCTCTTTATCTTTCACAAGAGACACAAATT CTAATTGAGTTAATTATCTGGGCCTTTCACCTTTGGATGCTCTGA AACATTTGTTGATTTTGTGTGAATGTTTATATCAAAATGTTTGC CAGGTTGTATTAGCCATTGAATAGCAAAAAACTGATAGTTACT

			TGCTTGTTTTTTAAAAATTACATATTAATAATGCCCTTGGCATA AGGCAGCATGGTGTGGCAGTTAAGAGATGGGCTGTGCAGCCC ATCCTGAGCTCCAGTCCTGAGTTTGCTACTTACTTCTGTGGCCT CTGGAACCTTATCCAACCTCTTGGTGCTTCAGTTTCCTCATCTG TGAAATTAGAATTTATAATAATTGCACCTACCTCCCAGGGGTA ACTAAATGAATAAATAATAATAAGTACTTACAGTGGTTCCTGA CACAGACTCAGCACTCCGTCAGTGTTGCCATGACTATTTTTATT ATCATTATTAATGATTACTTAGATCAATTATTTAGCAGTGGACT AATGGAAGCTACAGAGCAGGGAAGGGAAGCAGATCTAGGGAG GAAGGCAGTTTTGATTTGAGGAGGTTTGCACATGTAGAGAAGC ATACTGGAGAAGCATATCCAGAGGGCGAAAGATATCTCTCCAT TGTGCATCTGCCTCTTTTGACGTTGGAAGACACATGTCTTACTC CCCAAAGGGAGCCCAGCACTGGGAGCCTTCTTGATGATCTCAA AAATAATAGCTATTCAAGAAAATCACCAAGTGACTGTGAAACC GTCAGTTCGGAAGGCTGGTTAGAACATGTGGGAGCAACATGA ATGTTCTACAAAAGTTTAAAGCAGAGATTGTTTCAAATGGGTG TAGTAGATATTACTGAAAACCAAAAAAGAGTGAGATTGTCAGT GTAAGAATGTGATTTAATGTTTGTAGTGCTTACAATTTTGTGTA CCAAGTGGATGACTAAAAAGAGTAAATAATTTAATTAATAGC TCATATTTTATGTGTGAAAACATGTTAGTGAACATATATAATCA AAATAGATTTTCATTGCTATTGCATAGTCTCTAATACATAGAATG ATTTTGCTTTTCTCTTTTATTATACTTGCTTTAAAATACTTGAAA TATATTTTGCATTAAATGCATTTCAAGTTAAATGTCTTAAATGT ATACATTAGATGTGTGTTTTTAAATGCATAAAACACGTTGAAA TACATTAATGAACCATT

Table 9. IL18R1 Protein Sequences

SE Q ID NO.	NCB I Ref. No.	Isoform	Sequence
8	NP_003846.1	1	MNCRELPLTLWVLISVSTAESCTSRPHITVVEGEPFYLKHCSCSLA HEIETTTKSWYKSSGSQEHVELNPRSSSRIALHDCVLEFWPVELND TGSYFFQMKNYTQKWKLNVIRRNKHSCFTEQVTSKIVEVKKFF QITCENSYYQTLVNSTSLYKNCKKLLLENNKNPTIKKNAEFEDQG YYSCVHFLHHNGKLFNITKTFNITIVEDRSNIVPVLLGPKLNHVAV ELGKNVRLNCSALLNEEDVIYWMFGEENGSDPNIHEEKEMRIMTP EGKWHASKVLRIENIGESNLNVLYNCTVASTGGTDTKSFILVRKA DMADIPGHVFTRGMIIAVLILVAVVCLVTVCVIYRVLDLVLFYRHL TRRDETLDGKTYDAFVSYLKECRPENGEETFAVEILPRVLEKH FGYKLCIFERDVVPGGAVVDEIHSLEKSRRLIIVLSKSYMSNEVRY ELESGLHEALVERKIKIILIEFTPVTDFTFPLQSLKLLKSHRVLKWK ADKSLSYNSRFWKNLLYLMPAKTVKPGRDEPEVLPVLSSES
9	NP_001269328.1	2	MNCKKLLLENNKNPTIKKNAEFEDQGYYSVHFLHHNGKLFNIT KTFNITIVEDRSNIVPVLLGPKLNHVAVELGKNVRLNCSALLNEED VIYWMFGEENGSDPNIHEEKEMRIMTPGKWHASKVLRIENIGES NLNVLYNCTVASTGGTDTKSFILVRKDMADIPGHVFTRGMIIAVLI LVAVVCLVTVCVIYRVLDLVLFYRHLTRRDETLDGKTYDAFVSY LKECRPENGEETFAVEILPRVLEKHFGYKLCIFERDVVPGGAVV DEIHSLEKSRRLIIVLSKSYMSNEVRYELESGLHEALVERKIKIILIE FTPVTDFTFPLQSLKLLKSHRVLKWKADKSLSYNSRFWKNLLYL MPAKTVKPGRDEPEVLPVLSSES

Table 10. Other Sequences

SEQ ID NO.	Type of Sequence	Sequence
1	Nucleic Acid	ACTTCTTAAT TCTGTCCATA AGATTGAAA GAGGACTTAA AAATTGATGA N TTTTGTCTG GTAGCCATAG GCACTAGCTG AAATACCTTA AAAGTACTCA
2	Nucleic Acid	AAAACAGATT CAGCCAAAGC TTCAAACAA AAGTGTGCCT ATCTTATGAA N GTTTAAAAAT CTTCTGGCAC ACAGATTTTT AAAAAACAA CCTAGAAGAT
3	Nucleic Acid	TCTGTGTGTA CATTTCCCTC TACCTTCATT TCTTCATCTC TATCATTGAA AA N TATCCCTTTT GTATCCCCTT CCTTCTTAGT TGATTTTCGTT CTAAAATTT
4	Nucleic Acid	TAATAGACCC TGAAGTTTCC CACATCCTAC TCCTGAGTTC CTGTGAATAC N ATATGTTACA TGGCAAAAGG AACCTCTAGG TGTGATTAAA TTAAGGATCT
5	Nucleic Acid	CAAACTGTA ACAAATTA GAAAAAGCTG GTTCAATGAG CTTAGATTCT N TGAGATTAAAT CTGAAAAGGG AGAGTAGTTA TGAGAAGTCT TAAAAAGTG
6	Nucleic Acid	AAAACAGATT CAGCCAAAGC TTCAAACAA AAGTGTGCCT ATCTTATGAA N GTTTAAAAAT CTTCTGGCAC ACAGATTTTT AAAAAACAA CCTAGAAGAT
7	Nucleic Acid	CTCTCAAATG CCTCCTGAAT CACTGGGATT CCTTTGAGGA AAAAAGAAAA N GCCTTCTTTC CCCTTTTGCC TCCTCTGTCC TCTCTTACA GATGGGTAAT

[00289] While preferred embodiments of the present examples have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is

intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

ADDITIONAL EMBODIMENTS

1. A method of treating or preventing a disease or condition in a subject, the method comprising administering a modulator of Interleukin 18 Receptor 1(IL18R1) activity or expression to the subject, provided a genotype is detected in a sample obtained the subject.
2. A method of reducing or ablating activity or expression of Interleukin 18 Receptor 1(IL18R1) in a subject, the method comprising administering a modulator of IL18R1 to the subject, provided a genotype is detected in a sample obtained from the subject.
3. A method of treating or preventing a disease or condition in a subject, the method comprising:
 - a) obtaining a sample from a subject;
 - b) detecting a presence or an absence of a genotype in the sample obtained from the subject; and
 - c) administering to the subject a modulator of Interleukin 18 Receptor 1(IL18R1) activity or expression to the subject, provided the presence of the genotype is detected in the sample obtained from the subject.
4. A method of reducing, ablating, increasing, or activating, an activity or expression of Interleukin 18 Receptor 1 (IL18R1) in a subject, the method comprising:
 - a) obtaining a sample from a subject;
 - b) detecting a presence or an absence of a genotype in the sample obtained from the subject; and
 - c) administering to the subject a modulator of IL18R1 activity or expression to the subject, provided the presence of the genotype is detected in the sample obtained from the subject.
5. The method of any one or claims 1-4, wherein the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof.
6. The method of any one of claims 1-5, wherein the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1.
7. The method of any one of claims 1-5, wherein the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1.
8. The method of claim 6 or 7, wherein the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule.
9. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises an inverse agonist.
10. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM).
11. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM).

12. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both.
13. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both.
14. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide.
15. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9.
16. The method of any one of claims 6-7, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide.
17. The method of any one of claims 6-16, wherein the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both
18. The method of any one of claims 6-17, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling.
19. The method of any one of claims 6-18, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding.
20. The method of any one of claims 1-19, wherein the genotype is homozygous or heterozygous.
21. The method of any one or claims 1-19, wherein the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition.
22. The method of claim 21, wherein the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cihrosis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis.
23. The method of any one or claims 1-22, wherein the sample comprises whole blood, plasma, serum, or biopsy tissue.
24. The method of any one of claims 1-23, wherein subject is mammal.
25. The method of any one or claims 1-24, wherein the subject is human.
26. The method of any one of claims 1-25 wherein the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment.

27. The method of any one of claims 21-26, wherein the inflammatory, fibrostenotic, and/or fibrotic disease is refractory.
28. The method of any one of claims 1-27, wherein the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof.
29. The method of claim 28, wherein the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
30. The method of claim 28, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some cases, the SNP is rs10213846 and comprises a "G" or a "T" allele.
31. The method of claim 28, wherein the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP.
32. The method of claim 28, wherein the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
33. The method of claim 28, wherein the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
34. The method of claim 28, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
35. The method of claim 28, wherein the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
36. The method of claim 28 or 29, wherein the Indel at rs1921622 is within SEQ ID NO: 1.
37. The method of claim 28 or 30, wherein the SNP at rs2287037 is within SEQ ID NO: 2.
38. The method of claim 28 or 31, wherein the SNP at rs1974675 is within SEQ ID NO: 3.
39. The method of claim 28 or 32, wherein the SNP at rs2041739 is within s SEQ ID NO: 4.
40. The method of claim 28 or 33, wherein the SNP at rs76362690 is within SEQ ID NO: 5.
41. The method of claim 28 or 34, wherein the SNP at rs2287037 is within SEQ ID NO: 6.
42. The method of claim 28 or 35, wherein the SNP at rs80256362 is within SEQ ID NO: 7.
43. The method of any one of claims 28-42, where LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0.
44. The method of any one of claims 1-43, wherein the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .

45. The method of any one of claims 1-43, wherein the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
46. The method of claim 45, wherein the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes.
47. The method of any one or claims 1-46, wherein the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.
48. A method of diagnosing a disease or condition in a subject, the method comprising:
- a) obtaining a sample from a subject;
 - b) detecting a presence or an absence of a genotype in the sample obtained from the subject; and
 - c) diagnosing the disease or condition in the subject, provided the presence of the genotype is detected in the sample obtained from the subject.
49. A method of determining whether a subject is at risk for developing a disease or condition, in a subject, the method comprising:
- a) obtaining a sample from a subject;
 - b) detecting a presence or an absence of a genotype in the sample obtained from the subject; and
 - c) determining the subject is at risk for developing the disease or condition, provided the presence of the genotype is detected in the sample obtained from the subject.
50. A method of determining whether a subject is suitable for treatment of a disease or condition with a modulator of Interleukin 18 Receptor 1 (IL18R1) activity or expression, the method comprising:
- a) obtaining a sample from a subject;
 - b) detecting a presence or an absence of a genotype in the sample obtained from the subject; and
 - c) determining the subject is suitable for treatment of the disease or condition with a modulator of IL18R1, provided the presence of the genotype is detected in the sample obtained from the subject.
51. The method of any one or claims 48-50, wherein the genotype is detected with an assay comprising polymerase chain reaction (PCR), quantitative reverse-transcription PCR (qPCR), automated sequencing, genotype array, or a combination thereof.
52. The method of any one of claims 48-51, further comprising administering to the subject a modulator or IL18R1 activity or expression.

53. The method of claim 52, wherein the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1.
54. The method of claim 52, wherein the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1.
55. The method of any one of claims 52-54, wherein the agonist or partial agonist comprises an antibody or antigen-binding fragment, peptide, small molecule.
56. The method of any one of claims 52-55, wherein the modulator of IL18R1 activity or expression comprises an inverse agonist.
57. The method of any one of claims 52-56, wherein the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM).
58. The method of any one of claims 52-56, wherein the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM).
59. The method of any one of claims 52-58, wherein the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both.
60. The method of any one of claims 52-58, wherein the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both.
61. The method of any one of claims 52-58, wherein the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide.
62. The method of any one of claims 52-58, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9.
63. The method of any one of claims 52-58, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide.
64. The method of any one of claims 52-63, wherein the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both
65. The method of any one of claims 52-64, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling.
66. The method of any one of claims 52-64, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding.
67. The method of any one of claims 48-66, wherein the genotype is homozygous or heterozygous.

68. The method of any one or claims 48-67, wherein the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition.
69. The method of claim 68, wherein the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cholangitis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis.
70. The method of any one or claims 48-69, wherein the sample comprises whole blood, plasma, serum, or biopsy tissue.
71. The method of any one of claims 48-70, wherein subject is mammal.
72. The method of any one or claims 48-71, wherein the subject is human.
73. The method of any one of claims 48-72, wherein the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment.
74. The method of any one of claims 48-73, wherein the inflammatory, fibrostenotic, and/or fibrotic disease is refractory.
75. The method of any one of claims 48-74, wherein the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof.
76. The method of claim 75, wherein the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
77. The method of claim 75, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some cases, the SNP is rs10213846 and comprises a "G" or a "T" allele.
78. The method of claim 75, wherein the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP.
79. The method of claim 75, wherein the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
80. The method of claim 75, wherein the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
81. The method of claim 75, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
82. The method of claim 75, wherein the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
83. The method of claim 75 or 76, wherein the Indel at rs1921622 is within SEQ ID NO: 1.
84. The method of claim 75 or 77, wherein the SNP at rs2287037 is within SEQ ID NO: 2.

85. The method of claim 75 or 78, wherein the SNP at rs1974675 is within SEQ ID NO: 3.
86. The method of claim 75 or 79, wherein the SNP at rs2041739 is within s SEQ ID NO: 4.
87. The method of claim 75 or 80, wherein the SNP at rs76362690 is within SEQ ID NO: 5.
88. The method of claim 75 or 81, wherein the SNP at rs2287037 is within SEQ ID NO: 6.
89. The method of claim 75 or 82, wherein the SNP at rs80256362 is within SEQ ID NO: 7.
90. The method of any one of claims 75-89, where LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0.
91. The method of any one of claims 48-90, wherein the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
92. The method of any one of claims 48-90, wherein the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
93. The method of claim 92, wherein the subclinical phenotype comprises stricturing, penetrating, stricturing and penetrating, disease phenotypes.
94. The method of any one or claims 48-93, wherein the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.
95. A method for processing or analyzing a sample obtained from a subject, the method comprising:
 - a) obtaining a sample from a subject;
 - b) subjecting the sample to an assay by sequencing, genotype array, and/or nucleic acid amplification, to yield a data set comprising data corresponding to a presence or an absence of a genotype;
 - c) in a programmed computer, inputting said data from (b) to a trained algorithm to determine whether the subject is at risk of developing, a disease or disorder, wherein the trained algorithm is trained with a plurality of training samples, and wherein said sample is independent of said plurality of training samples; and
 - d) electronically outputting a report comprising the determination for the subject.
96. A method for processing or analyzing a sample obtained from a subject, the method comprising:

- a) obtaining a sample from a subject;
 - b) subjecting the sample to an assay by sequencing, genotype array, and/or nucleic acid amplification, to yield a data set comprising data corresponding to a presence or an absence of a genotype;
 - c) in a programmed computer, inputting said data from (b) to a trained algorithm to determine a likelihood that the subject is suitable for treatment of a disease or disorder with an agonist of IL18R1, wherein the trained algorithm is trained with a plurality of training samples, and wherein said sample is independent of said plurality of training samples; and
 - d) electronically outputting a report comprising the determination for the subject.
97. The method of any one or claims 95-96, wherein (c) comprises calculating a polygenic risk score (PRS), and the PRS comprises a normalized weighted sum of a number of risk alleles within the genotype present in the subject with weights proportional to a beta value of association between the genotype with the disease or condition.
98. The method of any one of any one or claims 95-97, wherein the data set of (b) further comprises data corresponding to a presence or an absence of a surrogate genotype, provided an absence of a genotype is detected.
99. The method of claim 98, wherein the surrogate genotype is in linkage disequilibrium with the absent genotype as determined by an r^2 value of at least about, 0.8, about 0.85, about 0.90, about 0.95, or about 1.0.
100. The method of any one of claims 95-99, wherein the report is configured to display the determination of the subject on a user interface of an electronic device.
101. The method of claim 100, wherein the electronic device comprises a personal electronic device belonging to the subject.
102. The method of any one of claims 95-102, further comprising administering to the subject a modulator of IL18R1 activity or expression, provided the subject is determined to be at risk of having, or developing, the disease or condition.
103. The method of 102, wherein the modulator of IL18R1 activity or expression comprises an agonist or a partial agonist of IL18R1.
104. The method of claim 102, wherein the modulator of IL18R1 activity or expression comprises an antagonist or partial antagonist of IL18R1.
105. The method of any one of claims 102-104, wherein the modulator of IL18R1 activity or expression comprises an antibody or antigen-binding fragment, peptide, small molecule.
106. The method of any one of claims 102-105, wherein the modulator of IL18R1 activity or expression comprises an inverse agonist.
107. The method of any one of claims 102-105, wherein the modulator of IL18R1 activity or expression comprises a positive allosteric modulator (PAM).

108. The method of any one of claims 102-105, wherein the modulator of IL18R1 activity or expression comprises a negative allosteric modulator (NAM).
109. The method of any one of claims 102-108, wherein the modulator of IL18R1 activity or expression comprises a small molecule that binds to IL18R1 or IL18, or both.
110. The method of any one of claims 102-108, wherein the modulator of IL18R1 activity or expression comprises an antibody or antigen binding fragment that binds to IL18R1 or IL18, or both.
111. The method of any one of claims 102-108, wherein the modulator of IL18R1 activity or expression comprises recombinant IL18R1 peptide, or a recombinant IL18 peptide.
112. The method of any one of claims 102-108, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9.
113. The method of any one of claims 102-108, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide.
114. The method of any one of claims 102-113, wherein the modulator of IL18R1 activity or expression comprises a fusion, a conjugate, or both
115. The method of any one of claims 102-114, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18 signaling.
116. The method of any one of claims 102-115, wherein the modulator of IL18R1 activity or expression comprises an agonist or an antagonist of IL18-IL18R1 binding.
117. The method of any one of claims 95-116, wherein the genotype is homozygous or heterozygous.
118. The method of any one or claims 95-117, wherein the disease or condition comprises and inflammatory, fibrostenotic, and/or fibrotic disease or condition.
119. The method of claim 118, wherein the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cholangitis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis.
120. The method of any one or claims 95-119, wherein the sample comprises whole blood, plasma, serum, or biopsy tissue.
121. The method of any one of claims 95-120, wherein subject is mammal.

122. The method of any one of claims 95-121, wherein the subject is human.
123. The method of any one of claims 95-122, wherein the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment.
124. The method of any one of claims 118-123, wherein the inflammatory, fibrostenotic, and/or fibrotic disease is refractory.
125. The method of any one of claims 95-124, wherein the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs1921622, rs2287037, rs1974675, rs2041739, rs76362690, rs2287037, or rs80256362, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof.
126. The method of claim 125, wherein the SNP at rs1921622 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
127. The method of claim 125, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP. In some cases, the SNP is rs10213846 and comprises a "G" or a "T" allele.
128. The method of claim 125, wherein the SNP at rs1974675 comprises a "C" or a "T" on a reverse DNA strand encoding the SNP.
129. The method of claim 125, wherein the SNP at rs2041739 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
130. The method of claim 125, wherein the SNP at rs76362690 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
131. The method of claim 125, wherein the SNP at rs2287037 comprises an "A" or a "G" on a reverse DNA strand encoding the SNP.
132. The method of claim 125, wherein the SNP at rs80256362 comprises an "A" or a "G" on a forward DNA strand encoding the SNP.
133. The method of claim 125 or 126, wherein the Indel at rs1921622 is within SEQ ID NO: 1.
134. The method of claim 125 or 127, wherein the SNP at rs2287037 is within SEQ ID NO: 2.
135. The method of claim 125 or 128, wherein the SNP at rs1974675 is within SEQ ID NO: 3.
136. The method of claim 125 or 129, wherein the SNP at rs2041739 is within s SEQ ID NO: 4.
137. The method of claim 125 or 130, wherein the SNP at rs76362690 is within SEQ ID NO: 5.
138. The method of claim 125 or 131, wherein the SNP at rs2287037 is within SEQ ID NO: 6.

139. The method of claim 125 or 132, wherein the SNP at rs80256362 is within SEQ ID NO: 7.
140. The method of any one of claims 125-139, where LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0.
141. The method of any one of claims 125-140, wherein the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
142. The method of any one of claims 125-141, wherein the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
143. The method of claim 142 wherein the subclinical phenotype comprises stricturing, penetrating, stricturing and penetrating, disease phenotypes.
144. The method of any one or claims 125-143, wherein the genotype comprises one or more SNPs in linkage disequilibrium with rs1921622 as determined by an r^2 value of at least about 0.80, about 0.85, about 0.90, about 0.95, or about 1.0.
145. The method of any one of claims 125-144, wherein the genotype comprises at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14, single nucleotide polymorphism (SNP) or indels.
146. A method of treating a subject in need thereof with a modulator of interleukin 18 receptor 1 (IL18R1) activity or expression, wherein the subject has moderate to severe Crohn's disease (CD), and wherein the subject has a genotype characterized by the presence of one or more SNPs.
147. The method of claim 146, wherein the one or more SNPs comprises a SNP listed in Table 1.
148. The method of claim 146, wherein the single nucleotide polymorphism is associated with structuring.
149. The method of claim 148, wherein the stricturing is isolated to an ileocolonic region of an intestine.
150. The method of claim 148 or 149, wherein the one or more SNPs comprises a SNP listed in Table 2.

151. The method of claim 146, wherein the single nucleotide polymorphism is associated with a risk of a subject developing morphological defects in ileal Paneth cells.
152. The method of claim 151, wherein the one or more SNPs comprises a SNP listed in Table 3.
153. A method of treating a subject in need thereof with a modulator of interleukin 18 receptor 1 (IL18R1) activity or expression, wherein the subject has moderate to severe inflammatory bowel disease (IBD), and wherein the subject has a genotype characterized by the presence of one or more SNPs.
154. The method of claim 153, wherein the one or more SNPs comprises a SNP listed in Table 4.
155. A method of treating a subject in need thereof with a modulator of interleukin 18 receptor 1 (IL18R1) activity or expression, wherein the subject has moderate to severe ulcerative colitis, and wherein the subject has a genotype characterized by the presence of one or more SNPs.
156. The method of claim 155, wherein the one or more SNPs comprises a SNP listed in Table 5.

CLAIMS

What is claimed is

1. A method of treating or preventing a disease or condition in a subject, the method comprising administering a modulator of Interleukin 18 Receptor 1(IL18R1) activity or expression to the subject, provided a genotype is detected in a sample obtained the subject.
2. A method of treating or preventing a disease or condition in a subject, the method comprising:
 - a. obtaining a sample from a subject;
 - b. detecting a presence or an absence of a genotype in the sample obtained from the subject; and
 - c. administering to the subject a modulator of Interleukin 18 Receptor 1(IL18R1) activity or expression to the subject, provided the presence of the genotype is detected in the sample obtained from the subject.
3. The method of claim 1 or claim 2, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9.
4. The method of claim 1 or claim 2, wherein the modulator of IL18R1 activity or expression comprises a recombinant peptide comprising an amino acid sequence that is about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 8 or SEQ ID NO: 9, and wherein the amino acid sequence is truncated at the N-terminal and/or C-terminal ends of the peptide.
5. The method of claim 1 or claim 2, wherein the disease or condition comprises an inflammatory, fibrostenotic, and/or fibrotic disease or condition.
6. The method of claim 5, wherein the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises inflammatory bowel disease (IBD), Crohn's disease (CD), perianal CD, ulcerative colitis (UC), multiple sclerosis (MS), rheumatoid arthritis (RA), primary sclerosing cholangitis (PSC), Pancolitis, primary biliary cihrosis, asthma, Proctitis, Iritis, intestinal fibrosis, pulmonary fibrosis, or intestinal fibrostenosis.
7. The method of claim 6, wherein the inflammatory, fibrostenotic, and/or fibrotic disease or condition comprises IBD.
8. The method of claim 1 or claim 2, wherein the subject is non-responsive to an induction of anti-Tumor Necrosis Factor (TNF) therapy, or lost response to the anti-TNF therapy after a period of time during treatment.
9. The method of claim 5, wherein the inflammatory, fibrostenotic, and/or fibrotic disease is refractory.
10. The method of claim 1 or claim 2, wherein the genotype comprises one or more single nucleotide polymorphisms (SNPs) or indels at rs76362690, rs80256362, rs1921622,

- rs2287037, rs1974675, or rs2041739, a SNP in linkage disequilibrium (LD) therewith, or any combination thereof.
11. The method of claim 10, comprising the SNP at rs76362690, wherein the SNP at rs76362690 is within SEQ ID NO: 5.
 12. The method of claim 10, comprising the SNP at rs80256362, wherein the SNP at rs80256362 is within SEQ ID NO: 7.
 13. The method of claim 10, comprising the Indel at rs1921622, wherein the Indel at rs1921622 is within SEQ ID NO: 1.
 14. The method of claim 10, comprising the SNP at rs1974675, wherein the SNP at rs1974675 is within SEQ ID NO: 3.
 15. The method of claim 10, comprising the SNP at rs2041739, wherein the SNP at rs2041739 is within s SEQ ID NO: 4.
 16. The method of claim 10, comprising the SNP at rs2287037, wherein the SNP at rs2287037 is within SEQ ID NO: 2.
 17. The method of claim 10, where LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0.
 18. The method of claim 1 or claim 2, wherein the genotype is associated with a risk that a subject has, or will develop, inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC), as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
 19. The method of claim 1 or claim 2, wherein the genotype is associated with a risk that the subject has, or will develop, a subclinical phenotype of the disease or condition as determined by a P value of at most about 1.0×10^{-6} , about 1.0×10^{-7} , about 1.0×10^{-8} , about 1.0×10^{-9} , about 1.0×10^{-10} , about 1.0×10^{-20} , about 1.0×10^{-30} , about 1.0×10^{-40} , about 1.0×10^{-50} , about 1.0×10^{-60} , about 1.0×10^{-70} , about 1.0×10^{-80} , about 1.0×10^{-90} , or about 1.0×10^{-100} .
 20. The method of claim 19, wherein the subclinical phenotype comprises stricturing, penetrating, or stricturing and penetrating, disease phenotypes.

FIG. 1A

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. Ctrl	imm_2_10230 5468	rs130013 25	3.98E-31	A	94040	0.123564 214	10293903 6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232 4148	rs142010 1	6.93E-31	A	94080	0.123034 419	10295771 6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 5593	rs124792 10	1.16E-30	A	94088	0.122583 046	10294916 1	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 8994	rs950880	5.12E-30	A	94092	0.121212 221	10293256 2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 8258	rs130205 53	6.50E-30	G	94088	0.121288 712	10293182 6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 7254	rs130190 81	2.26E-28	C	91372	0.120586 459	10295082 2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 9499	rs127121 41	1.13E-27	A	94101	0.111190 719	10295306 7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 5460	rs228703 7	2.12E-27	A	90448	0.1117902 413	10297902 8	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 5251	rs142010 2	2.63E-27	G	94059	0.110446 109	10294881 9	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 5371	rs124663 80	3.92E-27	A	94097	0.110032 167	10294893 9	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231 7505	rs199746 7	4.14E-27	A	94088	0.109983 326	10295107 3	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 7982	rs155861 9	4.35E-27	C	94094	0.109929 235	10293155 0	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10230 5866	rs142008 8	4.47E-27	A	94092	0.109908 721	10293943 4	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 0561	rs129993 64	5.26E-27	A	94085	0.113865 41	10297412 9	intronic	NA	NA	NA	NA

FIG. 1B

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	CD vs. Ctrl	imm_2_10230_3914	rs414213_2	6.18E-27	G	94098	0.109604_092	10293748_2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234_1768	rs129879_77	6.74E-27	C	94101	0.113620_038	10297533_6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10230_2563	rs116904_43	6.86E-27	T	94088	0.109505_304	10293613_1	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231_8230	rs136235_0	8.45E-27	G	93070	0.110388_707	10295179_8	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_8234	rs129965_05	9.27E-27	A	94097	0.109228_496	10293180_2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232_2115	rs873022	1.15E-26	A	94097	0.124457_072	10295568_3	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10230_3413	rs974389	1.19E-26	G	94098	0.108990_523	10293698_1	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232_2292	rs377117_7	1.20E-26	A	94098	0.124413_258	10295586_0	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232_3964	rs373212_9	1.31E-26	G	94095	0.124314_251	10295753_2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231_8792	rs170269_74	1.31E-26	A	94079	0.124311_81	10295236_0	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10230_6844	rs670684_4	1.76E-26	A	94078	0.108620_14	10294041_2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_8358	rs130207_93	1.85E-26	G	94087	0.108564_498	10293192_6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_3518	rs116854_80	2.30E-26	G	94076	0.108358_768	10292708_6	upstream	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_6579	rs155862_2	2.51E-26	G	94067	0.108313_872	10293014_7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_8679	rs101833_88	2.62E-26	G	94099	0.108202_123	10293224_7	intronic	NA	NA	NA	NA

FIG. 1C

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	CD vs. Ctrl	imm_2_10229_7380	rs12712135	3.19E-26	A	94095	0.108059473	102930948	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_7313	rs10189711	3.37E-26	A	94093	0.107994887	102930881	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_3413	rs11685424	3.83E-26	G	94097	0.107871445	102926981	upstream	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_6812	rs10189202	3.92E-26	A	94101	0.107847588	102930380	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_7089	rs10191914	3.99E-26	A	94098	0.107830935	102930657	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10230_1669	rs11123918	4.42E-26	A	93761	0.108096706	102935237	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_9984	rs1968171	4.68E-26	NA	NA	0.112079141	102933552	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_5444	rs6733174	4.75E-26	A	94099	0.107665708	102929012	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232_0622	rs59247511	5.13E-26	G	88756	0.110154423	102954190	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_7827	rs1558620	6.31E-26	A	89819	0.108787339	102931395	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_2499	rs1921622	1.31E-25	G	94090	0.107035619	102966067	intronic	MAP4K4	0.049614781	0.016696387	0
CD	CD vs. Ctrl	rs12998521	rs12998521	1.98E-25	A	92721	0.111649081	102974417	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_1174	rs13017455	1.67E-24	A	91754	0.110331899	102964742	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231_8404	rs1362349	3.32E-24	C	87425	0.107123202	102951972	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_4276	rs11123923	4.86E-24	A	94070	0.106807654	102967844	intronic	NA	NA	NA	NA

FIG. 1D

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Chr2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	CD vs. Ctrl	imm_2_10236_0488	rs10190555	7.63E-24	A	93178	0.119781385	102994056	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10238_6351	rs1035127	1.13E-23	A	94060	0.118936913	103019919	intergenic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10238_2350	rs17027087	1.52E-23	A	94100	0.116534161	103015918	downstream	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10236_1452	rs2080289	1.77E-23	A	94058	0.116352042	102995020	intronic	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10237_2819	rs4851570	2.17E-23	G	94084	0.116121872	103006387	intronic	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10237_3999	rs17027060	2.80E-23	G	94097	0.115824168	103007567	intronic	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10237_5142	rs12712145	2.98E-23	A	94090	0.117766457	103008710	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10235_0711	rs1420098	3.32E-23	G	86682	0.108389949	102984279	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10238_4509	rs3732123	3.42E-23	G	94095	0.115858448	103018077	intergenic	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10237_7020	rs2287034	3.46E-23	A	94095	0.115581024	103010588	intronic	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10237_4055	rs3860444	3.79E-23	A	94084	0.11722169	103007623	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10236_3304	rs3821203	3.83E-23	A	94040	0.115500401	102996872	intronic	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10236_5744	rs56258475	3.97E-23	G	94064	0.115420327	102999312	intronic	IL1RL1	0.067250733	0.043692753	0

FIG. 1E

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. Ctrl	imm_2_10235 8511	rs227029 8	4.46E-23	G	94101	0.115283 316	10299207 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. Ctrl	imm_2_10239 1170	rs485100 6	4.56E-23	A	93111	0.116386 348	10302473 8	intergenic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 3969	rs671088 5	4.62E-23	G	87495	0.107812 145	10297753 7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10238 1128	rs156868 1	5.03E-23	G	94078	0.116926 782	10301469 6	UTR3	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10236 9475	rs224111 7	5.08E-23	A	94101	0.116827 15	10300304 3	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10236 1316	rs170270 37	5.59E-23	G	94084	0.115021 314	10299488 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. Ctrl	imm_2_10235 9107	rs227029 7	5.83E-23	A	94087	0.116663 736	10299267 5	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10235 9593	rs675371 7	5.99E-23	A	94088	0.116670 554	10299316 1	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10236 8827	rs375527 4	6.47E-23	A	94096	0.116541 176	10300239 5	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10237 9106	rs170270 71	6.71E-23	A	94100	0.114758 595	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. Ctrl	imm_2_10236 1146	rs675002 0	6.78E-23	G	94092	0.116522 658	10299471 4	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 1764	rs170270 06	7.62E-23	C	94096	0.114970 653	10296533 2	intronic	IL1RL1	0.066330 072	0.040946 538	IL1RL1
CD	CD vs. Ctrl	imm_2_10236 3237	rs116837 00	8.08E-23	A	94100	0.114588 773	10299680 5	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. Ctrl	imm_2_10235 1856	rs205862 2	8.18E-23	A	94099	0.116579 805	10298542 4	intronic	NA	NA	NA	NA

FIG. 1F

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE	eqtl beta	eqtl p	priority
CD	CD vs. Ctrl	imm_2_10239_1245	rs4851007	8.31E-23	A	94090	0.116246065	103024813	intergenic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10238_0394	rs3732126	9.72E-23	C	89806	0.116181764	103013962	UTR3	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10239_9579	rs1807782	9.97E-23	G	94057	0.115913928	103033147	intergenic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_2303	rs12469506	1.75E-22	A	94099	0.113949647	102965871	intronic	IL1RL1	0.065931376	0.047728888	IL1RL1
CD	CD vs. Ctrl	imm_2_10239_1635	rs4851575	1.94E-22	G	93053	0.116419901	103025203	intergenic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10235_2244	rs3771172	3.12E-22	A	94093	0.11292591	102985812	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10236_4165	rs11465633	3.16E-22	A	93025	0.113858529	102997733	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10238_0734	rs1135354	3.38E-22	C	94075	0.11270546	103014302	UTR3	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10235_1116	rs1558627	4.23E-22	G	92154	0.116576628	102984684	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_1293	rs55927292	4.24E-22	A	94066	0.112854191	102964861	intronic	IL1RL1	0.06998232	0.030542666	IL1RL1
CD	CD vs. Ctrl	imm_2_10235_2382	rs3771171	6.45E-22	G	93096	0.113194321	102985950	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_8297	rs13015714	7.03E-22	C	94091	0.113978172	102971865	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10235_2586	rs2160202	7.53E-22	A	93116	0.112969681	102986154	intronic	NA	NA	NA	NA

FIG. 1G

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Chr2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	CD vs. Ctrl	imm_2_10239_0763	rs55883125	9.51E-22	A	89792	0.113245606	103024331	intergenic	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. Ctrl	imm_2_10235_6166	rs2041740	4.49E-21	A	89771	0.112845426	102989734	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10236_7834	rs1035130	4.22E-20	A	87767	0.110084818	103001402	exonic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10231_5064	rs1420103	2.86E-19	A	94095	0.105029003	102948632	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_6239	rs67723747	4.42E-19	NA	NA	0.108931442	102969807	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229_4158	rs6543116	2.73E-18	A	94078	0.102041477	102927726	upstream	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10238_2648	rs55664618	3.63E-17	A	94101	0.086522084	103016216	downstream	IL1RL1	0.055883857	0.041785706	0
CD	Paneth-D5 phenotype	imm_2_10234_1343	rs76721133	1.46E-15	C	155	3.19	102974911	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10237_7984	rs4851005	3.43E-12	A	94039	0.07515371	103011552	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10233_2499	rs1921622	5.72E-07	G	7967	1.202	102966067	intronic	MAP4K4	0.049614781	0.016696387	0
CD	CD vs. Ctrl	imm_2_10237_3483	rs17027056	2.65E-06	A	94095	0.105207576	103007051	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10235_1116	rs1558627	7.09E-06	G	6053	1.402	102984684	intronic	NA	NA	NA	NA

FIG. 1H

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs B1	imm_2_10235 2412	rs3771170	9.37E-06	A	6063	1.396	102985980	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10235 1856	rs2058622	9.44E-06	A	6064	1.395	102985424	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10233 8297	rs13015714	1.89E-05	C	6062	1.38	102971865	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10235 9107	rs2270297	2.55E-05	A	6064	1.371	102992675	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10235 9593	rs6753717	2.55E-05	A	6064	1.371	102993161	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10236 0488	rs10190555	2.55E-05	A	6064	1.371	102994056	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10236 1146	rs6750020	2.55E-05	G	6064	1.371	102994714	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10236 8827	rs3755274	2.55E-05	A	6064	1.371	103002395	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10236 9475	rs224117	2.55E-05	A	6064	1.371	103003043	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10238 1128	rs1568681	2.84E-05	G	6064	1.369	103014696	UTR3	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10237 5142	rs12712145	2.87E-05	A	6062	1.369	103008710	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10237 4055	rs3860444	2.93E-05	A	6064	1.368	103007623	intronic	NA	NA	NA	NA

FIG. 1I

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs B1	imm_2_10238 2476	rs111239 26	2.96E-05	C	6064	1.368	10301604 4	downstream	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10239 9579	rs180778 2	3.33E-05	G	6064	1.365	10303314 7	intergenic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10239 1245	rs485100 7	3.35E-05	A	6063	1.365	10302481 3	intergenic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10234 0561	rs129993 64	3.74E-05	A	7967	0.8526	10297412 9	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10234 1768	rs129879 77	3.74E-05	C	7967	0.8526	10297533 6	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10234 5460	rs228703 7	4.11E-05	A	7965	0.8533	10297902 8	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10238 6351	rs103512 7	4.14E-05	A	6061	1.36	10301991 9	intergenic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10232 4148	rs142010 1	4.15E-05	A	7966	0.8529	10295771 6	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	rs12998521	rs129985 21	4.61E-05	A	7965	0.8541	10297441 7	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 4158	rs654311 6	4.62E-05	A	6064	1.354	10292772 6	upstream	NA	NA	NA	NA

FIG. 1J

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs B1	imm_2_10231_5064	rs1420103	4.74E-05	A	6064	1.354	102948632	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10233_4276	rs11123923	5.09E-05	A	7967	0.855	102967844	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10230_5468	rs13001325	5.50E-05	A	7967	0.8551	102939036	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10231_5593	rs12479210	5.67E-05	A	7967	0.8553	102949161	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229_8258	rs13020553	5.89E-05	G	7966	0.8556	102931826	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229_8994	rs950880	6.07E-05	A	7967	0.8559	102932562	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10235_1116	rs1558627	7.57E-05	G	7956	1.184	102984684	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10235_2412	rs3771170	8.17E-05	A	7966	1.183	102985980	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10235_1856	rs2058622	8.33E-05	A	7967	1.183	102985424	intronic	NA	NA	NA	NA

FIG. 1K

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. Ctrl	imm_2_10230 4821	rs142008 9	0.0001065 73	G	94092	0.065270 37	10293838 9	intronic	IL1R2, IL1RL2	0.231497 33812603 4, 0.122966 17855485 1	0.040373 08383166 27, 0.045654 18745379 71	0, 0
CD	CD vs. non-IBD Controls	imm_2_10233 8297	rs130157 14	0.000114	C	7964	1.179	10297186 5	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10235 9107	rs227029 7	0.0001521	A	7967	1.174	10299267 5	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10235 9593	rs675371 7	0.0001521	A	7967	1.174	10299316 1	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10236 0488	rs101905 55	0.0001521	A	7967	1.174	10299405 6	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10236 1146	rs675002 0	0.0001521	G	7967	1.174	10299471 4	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10236 8827	rs375527 4	0.0001521	A	7967	1.174	10300239 5	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10236 9475	rs224111 7	0.0001521	A	7967	1.174	10300304 3	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232 6078	rs621526 61	0.0001604 86	G	94094	0.063639 504	10295964 6	intronic	IL1R2, IL1RL2	0.231497 33812603	0.040373 08383166	0, 0

FIG. 1L

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
											4, 0.122966 17855485 1	27, 0.045654 18745379 71	
CD	CD vs. non-IBD Controls	imm_2_10237 5142	rs127121 45	0.0001926	A	7965	1.172	10300871 0	intronic	NA	NA	NA	NA
											0.083853 43352003 65, 0.118117 25329138 , 0.231864 78857383 6, 0.170724 36416156 9,- 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	
CD	CD vs. Ctrl	imm_2_10237 9334	rs142009 5	0.0001931 31	G	94076	0.069120 743	10301290 2	intronic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31			0, 0, 0, 0, 0, 0, 0, 0
CD	CD vs. non-IBD Controls	imm_2_10237 4055	rs386044 4	0.0001956	A	7967	1.172	10300762 3	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10238 1128	rs156868 1	0.0002071	G	7967	1.171	10301469 6	UTR3	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10236 9466	rs560300 66	0.0002128 47	C	94101	0.068801 294	10300303 4	intronic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138	0.003724 27407991 006, 0.020080 42083512	0, 0, 0, 0, 0, 0, 0, 0

FIG. 1M

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											, - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	
											0.083853 43352003 65, 0.118117 25329138 32, 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	
CD	CD vs. Ctrl	imm_2_10239 9158	rs621527 14	0.0002161 21	G	94099	0.066768 011	10303272 6	intergenic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, IL18R AP, 0, 0, 0
CD	CD vs. Ctrl	imm_2_10233 1585	rs176963 76	0.0002222 46	A	94096	0.062522 074	10296515 3	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0

FIG. 1N

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. non-IBD Controls	imm_2_10238 2476	rs111239 26	0.0002239	C	7967	1.17	10301604 4	downstrea m	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10239 1245	rs485100 7	0.0002642	A	7965	1.168	10302481 3	intergenic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10231 5064	rs142010 3	0.0002682	A	7967	1.166	10294863 2	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229 4158	rs654311 6	0.0002693	A	7967	1.166	10292772 6	upstream	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10239 9579	rs180778 2	0.0002766	G	7967	1.167	10303314 7	intergenic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10238 6351	rs103512 7	0.0003218	A	7962	1.165	10301991 9	intergenic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 0654	rs121058 08	0.0003719 99	T	94095	0.060364 666	10297422 2	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
CD	CD vs. Ctrl	imm_2_10233 5102	rs782486 80	0.0004399 03	G	94094	0.059911 774	10296867 0	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74,	0.040680 45960476 85,	0, 0, 0

FIG. 10

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Chr2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
											0.237344 37839605 6, 0.126970 25442693 9	0.043046 34381681 61, 0.046936 06576706 77	
CD	CD vs. Ctrl	imm_2_10237 7761	rs561510 44	0.0004786 22	A	94074	0.062538 132	10301132 9	intronic	TMEM182	0.214216 334	0.038091 085	0
											0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	
CD	CD vs. Ctrl	imm_2_10232 8773	rs621526 62	0.0005410 83	A	93166	0.059153 293	10296234 1	intronic	IL1R1, IL1R2, IL1RL2	0.049614 781	0.016696 387	0, 0, 0
CD	L3 B2a+B2b vs B1	imm_2_10233 2499	rs192162 2	0.0005652 A		6064	0.7923	10296606 7	intronic	MAP4K4	0.049614 781	0.016696 387	0
CD	CD vs. Ctrl	imm_2_10236 8082	rs176514 85	0.0006964 68	A	94085	0.060688 718	10300165 0	intronic	TMEM182	0.214216 334	0.038091 085	0
CD	CD vs. non-IBD Controls	imm_2_10231 8792	rs170269 74	0.0007921 A		7967	0.8639	10295236 0	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10232 2115	rs873022	0.0009816 A		7967	0.8662	10295568 3	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10232 3964	rs373212 9	0.0009816 G		7967	0.8662	10295753 2	intronic	NA	NA	NA	NA

FIG. 1P

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	CD vs. non-IBD Controls	imm_2_10232292	rs3771177	0.001002	A	7966	0.8664	102955860	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102345460	rs2287037	0.001095	A	6061	0.7899	102979028	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_102360963	rs115532730	0.001321	G	297	7.788	102994531	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102340561	rs12999364	0.001435	A	6064	0.7947	102974129	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102341768	rs12987977	0.001435	C	6064	0.7947	102975336	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_102363606	rs3771162	0.001447	A	7965	0.8705	102997174	intronic	IL1RL1	0.067250733	0.043692753	0
											0.0841962068519057, 0.0522514054377319, 0.182483696156476, 0.0715996057128788	0.0202861227094196, 0.0335291660561106, 0.0445364127496054, 0.0461409912270284	
CD	CD vs. Ctrl	imm_2_102346655	rs11465572	0.00148993	A	94088	0.052334173	102980223	intronic	MAP4K4, TMEM182, RPL31, RPL31			0, 0, 0, 0
CD	L3 B2a+B2b vs B1	rs12998521	rs12998521	0.001494	A	6063	0.7953	102974417	intronic	NA	NA	NA	NA

FIG. 1Q

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. non-IBD Controls	imm_2_10236 1452	rs208028 9	0.001602	A	7965	0.8711	10299502 0	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10235 8511	rs227029 8	0.00171	G	7967	0.8719	10299207 9	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10236 3304	rs382120 3	0.00171	A	7967	0.8719	10299687 2	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10236 5744	rs562584 75	0.00171	G	7967	0.8719	10299931 2	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10237 2819	rs485157 0	0.00171	G	7967	0.8719	10300638 7	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10237 3999	rs170270 60	0.00171	G	7967	0.8719	10300756 7	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	L3 B2a+B2b vs B1	imm_2_10233 4276	rs111239 23	0.001745	A	6064	0.798	10296784 4	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10237 7020	rs228703 4	0.001778	A	7967	0.8723	10301058 8	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10233 7597	rs563865 07	0.00178	A	7967	0.8724	10297116 5	intronic	IL1RL1	- 0.067510 094	0.037554 638	IL1RL1

FIG. 1R

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
CD	CD vs. non-IBD Controls	imm_2_10235_2244	rs3771172	0.001793	A	7967	0.8724	102985812	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10238_2350	rs17027087	0.001796	A	7967	0.8724	103015918	downstream	IL1RL1	0.067250733	0.043692753	0
CD	CD vs. non-IBD Controls	imm_2_10236_1316	rs17027037	0.001827	G	7967	0.8726	102994884	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L2 colonic	imm_2_10234_4891	rs3755276	0.001835	A	2162	0.7812	102978459	intronic	IL1RL1	0.053336426	0.042506604	0
CD	L2 colonic	imm_2_10234_6056	rs9308857	0.001835	A	2162	0.7812	102979624	intronic	IL1RL1	0.053336426	0.042506604	0
CD	L2 colonic	imm_2_10235_2654	rs3771166	0.001835	A	2162	0.7812	102986222	intronic	IL1RL1	0.053336426	0.042506604	0
CD	L2 colonic	imm_2_10235_2807	rs1974675	0.001835	A	2162	0.7812	102986375	intronic	IL1RL1	0.053336426	0.042506604	0
CD	CD vs. non-IBD Controls	imm_2_10233_1764	rs17027006	0.001851	C	7967	0.8728	102965332	intronic	IL1RL1	0.066330072	0.040946538	IL1RL1
CD	L2 colonic	imm_2_10234_1482	rs10173193	0.001935	A	2162	0.7823	102975050	intronic	IL1RL1	0.053336426	0.042506604	0
CD	CD vs. non-IBD Controls	imm_2_10233_2303	rs12469506	0.001948	A	7967	0.8733	102965871	intronic	IL1RL1	0.065931376	0.047728888	IL1RL1
CD	CD vs. Ctrl	imm_2_10232_8361	rs1946131	0.002011885	A	94026	0.051004271	102961929	intronic	MAP4K4, TMEM182, RPL31, RPL31	0.0841962068519057, 0.0522514054377319,	0.0202861227094196, 0.0335291660561106,	0, 0, 0, 0

FIG. 1S

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.182483 69615647 6, 0.071599 60571287 88	0.044536 41274960 54, 0.046140 99122702 84	
CD	CD vs. non-IBD Controls	imm_2_10236 3237	rs116837 00	0.002031	A	7967	0.8738	10299680 5	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10233 6345	rs116885 59	0.002041	A	2162	0.7831	10296991 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L2_colonic	imm_2_10233 6537	rs116956 27	0.002041	G	2162	0.7831	10297010 5	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L2_colonic	imm_2_10233 7738	rs980845 3	0.002041	A	2162	0.7831	10297130 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L2_colonic	imm_2_10233 3863	rs670456 5	0.002041	A	2162	0.7831	10296743 1	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L2_colonic	imm_2_10233 4290	rs675248 2	0.002041	G	2162	0.7831	10296785 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L2_colonic	imm_2_10233 4360	rs498895 5	0.002041	G	2162	0.7831	10296792 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	CD vs. non-IBD Controls	imm_2_10238 0734	rs113535 4	0.002055	C	7964	0.874	10301430 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10238 4509	rs373212 3	0.002062	G	7967	0.874	10301807 7	intergenic	IL1RL1	0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10233 3668	rs134240 06	0.002156	G	2162	0.7842	10296723 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L2_colonic	imm_2_10233 3845	rs675196 7	0.002156	G	2162	0.7842	10296741 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L2_colonic	imm_2_10233 9231	rs485156 6	0.002187	C	2162	0.7846	10297279 9	intronic	IL1RL1	0.053336 426	0.042506 604	0

FIG. 1T

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	Paneth-D1 phenotype	imm_2_10238 7498	rs112139 796	0.002267	G	297	1.967	10302106 6	intergenic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10237 9106	rs170270 71	0.002554	A	7967	0.8766	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. Ctrl	imm_2_10232 9171	rs129891 97	0.0026732 05	A	94078	0.049471 679	10296273 9	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
CD	CD vs. Ctrl	imm_2_10231 8649	rs375527 8	0.0027702 82	G	94095	0.052429 306	10295221 7	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	CD vs. non-IBD Controls	imm_2_10237 7984	rs485100 5	0.002864	A	7967	0.8858	10301155 2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232 9504	rs654311 9	0.0029089 05	A	93081	0.031785 47	10296307 2	intronic	NA	NA	NA	NA
CD	Paneth-D1234 phenotype	imm_2_10231 3976	rs771271 14	0.003062	A	297	6.711	10294754 4	intronic	IL1RL1, MAP4K4, IL18RAP, CNOT11, MAP4K4	0.154006 31456082 4, 0.052797 13115951 81, - 0.135420	0.006657 33914116 06, 0.010799 75270327 78, 0.023225	IL1RL1, 0, 0, 0, 0

FIG. 1U

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											47625685 3, 0.203509 01597676 2, 0.097682 68462740 83	60255846 7, 0.037112 34476033 54, 0.043278 92676263 28	
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
CD	CD vs. Ctrl	imm_2_10232 7798	rs130140 44	0.0032215 34	G	94081	0.048452 556	10296136 6	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0
											0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	
CD	CD vs. Ctrl	imm_2_10231 4613	rs176956 48	0.0032286 66	G	94101	0.051660 235	10294818 1	intronic	MAP4K4, TMEM18 2			0, 0
											0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	
CD	CD vs. Ctrl	imm_2_10230 4398	rs129877 82	0.0032497 81	A	94095	0.051527 863	10293796 6	intronic	MAP4K4, TMEM18 2			0, 0
											0.154006 31456082 4, 0.052797 13115951 81,- 0.135420	0.006657 33914116 06, 0.010799 75270327 78, 0.023225	
CD	Paneth-D0 phenotype	imm_2_10231 3976	rs771271 14	0.003279 A	A	297	-6.659	10294754 4	intronic	IL1RL1, MAP4K4, IL18RAP, CNOT11, MAP4K4			IL1RL1 , 0, 0, 0, 0

FIG. 1V

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
											476256853, 0.203509 01597676 2, 0.097682 68462740 83	602558467, 0.037112 34476033 54, 0.043278 92676263 28	
CD	CD vs. non-IBD Controls	imm_2_10231_9499	rs12712141	0.003334	A	7967	1.116	102953067	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10233_1293	rs55927292	0.003376	A	7966	0.88	102964861	intronic	IL1RL1	0.06998232	0.030542666	IL1RL1
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
CD	CD vs. Ctrl	imm_2_10233_0381	rs13028993	0.003376708	G	94098	0.048192276	102963949	intronic	RPL31, RPL31, TMEM182	NA	NA	0, 0, 0
CD	L3 B2a+B2b vs B1	imm_2_10231_9499	rs12712141	0.003482	G	6064	0.8195	102953067	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10231_7505	rs1997467	0.003522	G	6059	0.8195	102951073	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232_8782	rs1054096	0.003620482	G	93915	0.047843116	102962350	intronic	NA	NA	NA	NA

FIG. 1W

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs B1	imm_2_10231 7899	rs199746 6	0.003698	C	6064	0.8204	10295146 7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 0060	rs129960 97	0.0037096 32	A	94077	- 0.047709 003	10296362 8	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
CD	CD vs. Ctrl	imm_2_10233 7795	rs130146 44	0.0038728 71	A	86188	- 0.049541 771	10297136 3	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 0.071599 60571287 88	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140 99122702 84	0, 0, 0, 0
CD	CD vs. Ctrl	imm_2_10232 2694	rs130227 99	0.0039288 31	G	94090	- 0.050335 024	10295626 2	intronic	RPL31, TMEM18 2	0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	0, 0
CD	L2 colonic	imm_2_10235 3891	rs654312 4	0.004054	A	2162	0.7956	10298745 9	intronic	IL1RL1	0.053489 519	0.039961 127	0
CD	L3 B2a+B2b vs B1	imm_2_10229 7982	rs155861 9	0.004421	A	6064	0.8237	10293155 0	intronic	NA	NA	NA	NA

FIG. 1X

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs B1	imm_2_10231 5251	rs142010 2	0.004552	A	6064	0.8241	10294881 9	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 3518	rs116854 80	0.004565	A	6064	0.8242	10292708 6	upstream	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 6579	rs155862 2	0.004565	A	6064	0.8242	10293014 7	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 6812	rs101892 02	0.004565	G	6064	0.8242	10293038 0	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 8358	rs130207 93	0.004565	A	6064	0.8242	10293192 6	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 8679	rs101833 88	0.004566	G	6063	1.213	10293224 7	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 8234	rs129965 05	0.004567	A	6064	1.213	10293180 2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 1824	rs129995 42	0.0045745 83	C	94100	0.046574 589	10296539 2	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
CD	L3 B2a+B2b vs B1	imm_2_10230 5866	rs142008 8	0.004591	G	6064	0.8243	10293943 4	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10231 5371	rs124663 80	0.004592	G	6063	0.8243	10294893 9	intronic	NA	NA	NA	NA

FIG. 1Y

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
CD	Paneth-D4 phenotype	imm_2_10236_9466	rs56030066	0.004594	C	297	2.295	103003034	intronic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	
CD	L3 B2a+B2b vs B1	imm_2_10231_7494	rs12712140	0.004596	A	6064	0.8245	102951062	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229_7089	rs10191914					102930657	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10230_3914	rs4142132	0.00463	G	6064	0.8245	102937482	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10230_2563	rs11690443	0.004647	A	6063	0.8245	102936131	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229_8258	rs13020553	0.004713	A	6063	0.8247	102931826	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10230_5468	rs13001325	0.00501	G	6063	0.8175	102939036	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229_8994	rs950880	0.005257	A	6064	0.8186	102932562	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1			0.005284	A	6064	0.8187		intronic	NA	NA	NA	NA

FIG. 1Z

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	CD vs. Ctrl L3	imm_2_10232_5512	rs13016771	0.005319493	A	94095	0.048571576	102959080	intronic	RPL31, TMEM182	0.0801136510989988, 0.0546502830572637	0.0285133800383803, 0.0292598586431115	0, 0
CD	B2a+B2b vs B1	imm_2_10231_5593	rs12479210	0.005324	A	6064	0.8188	102949161	intronic	NA	NA	NA	NA
CD	i2 CD vs. i2 Ctrl	imm_2_10234_3118	rs76022452	0.005471	A	1792	3.273	102976686	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10237_9334	rs1420095	0.005664	G	297	2.222	103012902	intronic	IL1RL1, IL18RAP, RPL31, IL1RL2, RPL31	0.0838534335200365, 0.11811725329138, -0.231864788573836, 0.170724364161569, -0.2634020.033428	0.00372427407991006, 0.0200804208351232, 0.0239002404371004, 0.0257519329018087, 0.0334284392287019	0, 0, 0, 0, 0
CD	Time to First Surgery	imm_2_10234_5460	rs2287037	0.00586388	A	1091	1.13142	102979028	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229_7380	rs12712135	0.006258	A	6064	1.205	102930948	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229_3413	rs11685424	0.006379	G	6064	1.204	102926981	upstream	NA	NA	NA	NA

FIG. 1AA

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs B1	imm_2_10229 5444	rs6733174	0.006379	A	6064	1.204	102929012	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10229 7313	rs10189711	0.006379	A	6064	1.204	102930881	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10230 3413	rs9743389	0.006437	G	6064	1.204	102936981	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 6297	rs13005049	0.006452321	A	94100	0.047949538	102929865	intronic	MAP4K4, TMEM182	0.089477 14269207 61, 05, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	L3 B2a+B2b vs B1	imm_2_10230 6844	rs6706844	0.006526	A	6064	1.204	102940412	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10233 4276	rs11123923	0.00658011	A	1091	1.12932	102967844	intronic	NA	NA	NA	NA
CD	Time to Second Surgery	imm_2_10239 1933	rs80256362	0.00669707	G	181	1.6083	103025501	intergenic	IL1RL1, MAP4K4, IL18RAP, TMEM182	0.116880 84727671 7, 0.038239 94346461 23,- 0.098743 01937070 37, 0.041825 39104075 5	0.002027 76557373 782, 0.005753 84548298 579, 0.013336 51636585 45, 60340416 81	0, 0, IL18R AP, 0
CD	L2_colonic	imm_2_10236 0765	rs2041739	0.006737	G	2162	1.224	102994333	intronic	IL1RL1	0.059172591	0.01708069	0

FIG. 1BB

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs B1	imm_2_10232_4148	rs1420101	0.006961	A	6063	0.8242	102957716	intronic	NA	NA	NA	NA
		imm_2_10234_0561	rs12999364	0.00696491	A	1091	1.12836	102974129	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10234_1768	rs12987977	0.00696491	C	1091	1.12836	102975336	intronic	NA	NA	NA	NA
		rs12998521	rs12998521	0.00696491	A	1091	1.12836	102974417	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10239_9158	rs62152714	0.007143	G	297	2.106	103032726	intergenic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138 ,- 0.231864 78857383 6, 0.170724 36416156 9,- 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	0, IL18R AP, 0, 0, 0
		imm_2_10234_7408	rs11465575	0.007322252	G	93110	0.092078874	102980976	intronic	NA	NA	NA	NA
CD	L2_colonic	imm_2_10235_7220	rs10439410	0.007423	C	2162	1.221	102990788	intronic	IL1RL1	0.059172591	0.01708069	0
		imm_2_10235_7801	rs6758936	0.007423	G	2162	1.221	102991369	intronic	IL1RL1	0.059172591	0.01708069	0

FIG. 1CC

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
CD	L2_colonic	imm_2_10236_2777	rs10208196	0.007423	G	2162	1.221	102996345	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_10236_4152	rs75556917	0.007423	C	2162	1.221	102997720	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_10236_4711	rs3213732	0.007423	A	2162	1.221	102998279	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_10236_5406	rs10204757	0.007423	A	2162	1.221	102998974	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_10236_6384	rs6760621	0.007423	A	2162	1.221	102999952	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_10236_7300	rs11465641	0.007423	A	2162	1.221	103000868	intronic	IL1RL1	0.059172591	0.01708069	0
CD	CD vs. Ctrl	imm_2_10235_3645	rs11465597	0.007586902	G	94099	0.043792977	102987213	intronic	RPL31, MAP4K4, CNOT11, TMEM182, RPL31	0.183805835083763, 0.0728465666462062, 0.137933540238369, 0.0442693164786652, 0.0637731216907573	0.0251565704541081, 0.0266971299490349, 0.0380904843071586, 0.0469275673644461, 0.0498599952723028	0, 0, 0, 0, 0
CD	Time to Frst Surgery	imm_2_10229_8234	rs12996505	0.00789343	A	1091	0.894727	102931802	intronic	NA	NA	NA	NA

FIG. 1DD

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	Time to Fris Surgery	imm_2_10229 8679	rs101833 88	0.0078934 3	G	1091	0.894727	10293224 7	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10231 7505	rs199746 7	0.008024	A	7962	1.104	10295107 3	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10238 6571	rs211066 2	0.008409	T	2162	1.217	10302013 9	intergenic	IL1RL1	0.060162 739	0.014743 734	0
CD	CD vs. Ctrl	imm_2_10236 3606	rs377116 2	0.0084702 16	A	94076	0.030572 037	10299717 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	B2a+B2b vs B1	imm_2_10237 3483	rs170270 56	0.008606	A	6064	0.6001	10300705 1	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10235 1116	rs155862 7	0.008743	G	1048	1.295	10298468 4	intronic	NA	NA	NA	NA
CD	Smoking_S tatus	imm_2_10232 0808	rs985523	0.008895	A	603	1.778	10295437 6	intronic	IL1RL1, MAP4K4	0.097133 46836259 56, 0.030462 06039871 91	0.009923 07563826 999, 0.026953 59831841 94	IL1RL1, 0
CD	Smoking_S tatus	imm_2_10232 4668	rs671913 0	0.008895	A	603	1.778	10295823 6	intronic	IL1RL1, MAP4K4	0.097133 46836259 56, 0.030462 06039871 91	0.009923 07563826 999, 0.026953 59831841 94	IL1RL1, 0
CD	CD vs. non-IBD Controls	imm_2_10231 7899	rs199746 6	0.008895	G	7967	1.102	10295146 7	intronic	NA	NA	NA	NA

FIG. 1EE

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
CD	L2_colonic	imm_2_102371390	rs3771159	0.009215	A	2162	1.214	103004958	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102371762	rs11903946	0.009215	A	2162	1.214	103005330	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102372880	rs6749014	0.009215	G	2162	1.214	103006448	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102375146	rs12712146	0.009215	G	2162	1.214	103008714	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102375969	rs4851004	0.009215	G	2162	1.214	103009537	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102376094	rs6732138	0.009215	G	2162	1.214	103009662	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102377669	rs2287033	0.009215	A	2162	1.214	103011237	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102382119	rs1420094	0.009215	G	2162	1.214	103015687	downstream	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102384484	rs3732124	0.009215	G	2162	1.214	103018052	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102385432	rs4851571	0.009215	G	2162	1.214	103019000	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102386217	rs1035129	0.009215	A	2162	1.214	103019785	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	L2_colonic	imm_2_102390110	rs6710034	0.009215	G	2162	1.214	103023678	intergenic	IL1RL1	0.059172591	0.01708069	0

FIG. 1FF

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L2 colonic	imm_2_10239 1092	rs758914 2	0.009215	A	2162	1.214	10302466 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L2 colonic	imm_2_10239 4083	rs102009 52	0.009215	A	2162	1.214	10302765 1	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L2 colonic	imm_2_10239 8001	rs159245 9	0.009215	A	2162	1.214	10303156 9	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	CD vs. non-IBD Controls	imm_2_10231 7494	rs127121 40	0.009265	C	7967	1.102	10295106 2	intronic	NA	NA	NA	NA
CD	Smoking_S tatus	imm_2_10235 3525	rs114655 96	0.009279	A	603	1.813	10298709 3	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 98393204 15	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	0, 0, 0
CD	i2 CD vs. i2 Ctrl	imm_2_10229 7959	rs114275 869	0.0093	G	1792	3.063	10293152 7	intronic	NA	NA	NA	NA
CD	i2 CD vs. i2 Ctrl	imm_2_10232 0927	rs788419 71	0.0093	G	1792	3.063	10295449 5	intronic	NA	NA	NA	NA
CD	i2 CD vs. i2 Ctrl	imm_2_10230 1640	rs785355 98	0.009515	A	1792	3.053	10293520 8	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10237 7344	rs142009 6	0.009599	G	2161	1.213	10301091 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	CD vs. non-IBD Controls	imm_2_10231 5371	rs124663 80	0.009601	A	7966	1.101	10294893 9	intronic	NA	NA	NA	NA

FIG. 1GG

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. non-IBD Controls	imm_2_10230 5866	rs142008 8	0.009604	A	7967	1.101	10293943 4	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10237 2536	rs670600 2	0.00962	A	2162	1.213	10300610 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Smoking_S tatus	imm_2_10231 9876	rs176392 15	0.009627	A	603	1.81	10295344 4	intronic	IL1RL1, MAP4K4	0.107679 30429227 7, 0.035460 38514225 5	0.005065 12943857 112, 0.011522 77515793 16	IL1RL1 ,0
CD	CD vs. non-IBD Controls	imm_2_10230 3914	rs414213 2	0.009829	G	7966	1.101	10293748 2	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10231 5251	rs142010 2	0.009873	G	7967	1.101	10294881 9	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10231 8230	rs136235 0	0.01004	G	2252	1.194	10295179 8	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229 3518	rs116854 80	0.01005	G	7967	1.101	10292708 6	upstream	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229 6579	rs155862 2	0.01005	G	7967	1.101	10293014 7	intronic	NA	NA	NA	NA

FIG. 1HH

Population	PHENOTYPE	Marker	dbSNP	p_value	AI	n_miss	OR_Z_B	base_pair r Chr2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
CD	CD vs. non-IBD Controls	imm_2_10229 6812	rs10189202	0.01005	A	7967	1.101	102930380	intronic	NA	NA	NA	NA
		imm_2_10229 8358	rs13020793	0.01005	G	7967	1.101	102931926	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229 7089	rs10191914	0.01024	A	7967	1.1	102930657	intronic	NA	NA	NA	NA
CD	Paneth-D2 phenotype	imm_2_10231 3976	rs77127114	0.0103	A	297	3.593	102947544	intronic	ILIRL1, MAP4K4, IL18RAP, CNOT11, MAP4K4	0.154006 31456082 4,06, 0.052797 13115951 81,- 0.135420 0.023225 47625685 3,7, 0.203509 0.037112 01597676 2,34476033 54, 0.043278 0.097682 68462740 83,28	0.006657 33914116 06, 0.010799 75270327 78, 0.023225 60255846 7, 0.037112 34476033 54, 0.043278 92676263 28	ILIRL1 ,0,0,0, 0
CD	L3 B2a+B2b vs B1	imm_2_10234 6655	rs11465572	0.01031	A	6064	0.7543	102980223	intronic	MAP4K4, TMEM18 2,RPL31, RPL31	0.084196 20685190 57,96, 0.033529 40543773 19,06, 0.182483 69615647 6,54,	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54,	0,0,0, 0

FIG. 1II

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.071599 60571287 88	0.046140 99122702 84	
CD	CD vs. non-IBD Controls	imm_2_10229 7982	rs155861 9	0.01033	C	7967	1.1	10293155 0	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 1343	rs767211 33	0.0103538 07	C	94099	0.133995 884	10297491 1	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10230 1669	rs111239 18	0.01042	A	7966	1.1	10293523 7	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10230 2563	rs116904 43	0.01045	T	7962	1.1	10293613 1	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10235 9471	rs114656 23	0.0107466 71	A	NA	0.072502 824	10299303 9	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10232 4163	rs781971 97	0.01086	A	2321	3.372	10295773 1	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10235 1856	rs205862 2	0.01109	A	1051	1.284	10298542 4	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10235 2412	rs377117 0	0.01109	A	1051	1.284	10298598 0	intronic	NA	NA	NA	NA
CD	Smoking_S tatus	imm_2_10235 2903	rs672894 5	0.01112	G	603	1.748	10298647 1	intronic	IL1RL1, MAP4K4, IL18RAP,	0.106197 01173231 9, 0.033425	0.004748 52757225 921, 0.015104	0, 0, 0, 0

FIG. 1JJ

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
										TMEM182	2711234699, -0.0892665435028165, 0.209496447273056	4158781986, 0.0241395694282341, 0.0345736924968317	
CD	Time to First Surgery	imm_2_102297380	rs12712135	0.0113158	A	1091	0.899139	102930948	intronic	NA	NA	NA	NA
CD	B2	imm_2_102360765	rs2041739	0.01166	G	2170	1.186	102994333	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 B1 vs non-IBD ctrl	imm_2_102361452	rs2080289	0.01177	A	2905	0.6266	102995020	intronic	IL1RL1	0.067250733	0.043692753	0
CD	B2	imm_2_102357220	rs10439410	0.01192	C	2170	1.186	102990788	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_102357801	rs6758936	0.01192	G	2170	1.186	102991369	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_102362777	rs10208196	0.01192	G	2170	1.186	102996345	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_102364152	rs7556917	0.01192	C	2170	1.186	102997720	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_102364711	rs3213732	0.01192	A	2170	1.186	102998279	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_102365406	rs10204757	0.01192	A	2170	1.186	102998974	intronic	IL1RL1	0.059172591	0.01708069	0

FIG. 1KK

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair	snp location	cis_eGE	eqtl beta	eqtl p	priority
CD	B2	imm_2_102366384	rs6760621	0.01192	A	2170	1.186	102999952	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_102367300	rs11465641	0.01192	A	2170	1.186	103000868	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Smoking_S tatus	imm_2_102347450	rs10515921	0.01217	C	603	1.775	102981018	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814314103196, 0.0384489604471703,- 0.0967129839320415	0.00228301835533339, 0.00601483658512599, 0.0165484385905364	0, 0, 0
CD	Smoking_S tatus	imm_2_102349061	rs11465584	0.01217	A	603	1.775	102982629	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814314103196, 0.0384489604471703,- 0.0967129839320415	0.00228301835533339, 0.00601483658512599, 0.0165484385905364	0, 0, 0
CD	Time to Frist Surgery	imm_2_102302563	rs11690443	0.0125327	T	1088	0.900264	102936131	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_102317494	rs12712140	0.0125653	C	1091	0.90033	102951062	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_102318404	rs1362349	0.01259	C	2252	0.8424	102951972	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_102381128	rs1568681	0.01266	G	1421	1.763	103014696	UTR3	NA	NA	NA	NA

FIG. 1LL

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	Pyoderma G	imm_2_10238_2476	rs111239_26	0.01266	C	1421	1.763	10301604_4	downstream	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10239_9579	rs180778_2	0.01266	G	1421	1.763	10303314_7	intergenic	NA	NA	NA	NA
	L3 B2a+B2b vs non-IBD ctrl												
CD		imm_2_10235_9107	rs227029_7	0.01271	A	1051	1.275	10299267_5	intronic	NA	NA	NA	NA
	L3 B2a+B2b vs non-IBD ctrl												
CD		imm_2_10235_9593	rs675371_7	0.01271	A	1051	1.275	10299316_1	intronic	NA	NA	NA	NA
	L3 B2a+B2b vs non-IBD ctrl												
CD		imm_2_10236_0488	rs101905_55	0.01271	A	1051	1.275	10299405_6	intronic	NA	NA	NA	NA
	L3 B2a+B2b vs non-IBD ctrl												
CD		imm_2_10236_1146	rs675002_0	0.01271	G	1051	1.275	10299471_4	intronic	NA	NA	NA	NA
	L3 B2a+B2b vs non-IBD ctrl												
CD		imm_2_10236_8827	rs375527_4	0.01271	A	1051	1.275	10300239_5	intronic	NA	NA	NA	NA
	L3 B2a+B2b vs non-IBD ctrl												
CD		imm_2_10236_9475	rs224111_7	0.01271	A	1051	1.275	10300304_3	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10239_1245	rs485100_7	0.0128	A	1420	1.761	10302481_3	intergenic	NA	NA	NA	NA
	CD vs. Ctrl												
CD		imm_2_10237_0141	rs114656_50	0.0129587_06	A	NA	0.070137_747	10300370_9	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10237_4055	rs386044_4	0.01298	A	1421	1.76	10300762_3	intronic	NA	NA	NA	NA

FIG. 1MM

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	AI	n_miss	OR_Z_B	base_pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	Pyoderma G	imm_2_10237 5142	rs127121 45	0.01298	A	1421	1.76	10300871 0	intronic	NA	NA	NA	NA
	L3	imm_2_10235 3645	rs114655 97	0.01304	G	6064	0.7664	10298721 3	intronic	RPL31, MAP4K4, CNOT11, TMEM18 2, RPL31	0.183805 83508376 3, 0.072846 56664620 62, 0.137933 54023836 9, 0.044269 31647866 52, 0.063773 0.049859 99527230 28	0.025156 57045410 81, 0.026697 12994903 49, 0.038090 48430715 86, 0.046927 56736444 61, 0.049859 99527230 28	0, 0, 0, 0, 0, 0,
CD	Time to Frist Surgery	imm_2_10231 9499	rs127121 41	0.0131031	G	1091	1.10969	10295306 7	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10229 3518	rs116854 80	0.0132364	G	1091	0.90114	10292708 6	upstream	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10229 6579	rs155862 2	0.0132364	G	1091	0.90114	10293014 7	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10229 6812	rs101892 02	0.0132364	A	1091	0.90114	10293038 0	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10229 7089	rs101919 14	0.0132364	A	1091	0.90114	10293065 7	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10229 8358	rs130207 93	0.0132364	G	1091	0.90114	10293192 6	intronic	NA	NA	NA	NA

FIG. 1NN

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	Time to Frist Surgery	imm_2_10230 1669	rs111239 18	0.0132364	A	1091	0.90114	10293523 7	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10229 7827	rs155862 0	0.0133071	A	1090	0.901135	10293139 5	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10233 1293	rs559272 92	0.01336	A	2906	0.635	10296486 1	intronic	IL1RL1	0.069982 32	0.030542 666	IL1RL1
CD	CD vs. Ctrl	imm_2_10239 0028	rs781785 97	0.0133761 66	A	89466	0.031428 416	10302359 6	intergenic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10235 6166	rs204174 0	0.01359	A	1421	1.755	10298973 4	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10235 9107	rs227029 7	0.01359	A	1421	1.755	10299267 5	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10235 9593	rs675371 7	0.01359	A	1421	1.755	10299316 1	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10236 0488	rs101905 55	0.01359	A	1421	1.755	10299405 6	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10236 1146	rs675002 0	0.01359	G	1421	1.755	10299471 4	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10236 8827	rs375527 4	0.01359	A	1421	1.755	10300239 5	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10236 9475	rs224111 7	0.01359	A	1421	1.755	10300304 3	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10230 3914	rs414213 2	0.0136092	G	1091	0.901449	10293748 2	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10230 5866	rs142008 8	0.0136092	A	1091	0.901449	10293943 4	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10231 5371	rs124663 80	0.0136092	A	1091	0.901449	10294893 9	intronic	NA	NA	NA	NA

FIG. 100

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B2	imm_2_10237 1390	rs377115 9	0.01365	A	2170	1.182	10300495 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10237 1762	rs119039 46	0.01365	A	2170	1.182	10300533 0	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10237 2880	rs674901 4	0.01365	G	2170	1.182	10300644 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10237 5146	rs127121 46	0.01365	G	2170	1.182	10300871 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10237 5969	rs485100 4	0.01365	G	2170	1.182	10300953 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10237 6094	rs673213 8	0.01365	G	2170	1.182	10300966 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10237 7669	rs228703 3	0.01365	A	2170	1.182	10301123 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10238 2119	rs142009 4	0.01365	G	2170	1.182	10301568 7	downstrea m	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10238 4484	rs373212 4	0.01365	G	2170	1.182	10301805 2	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10238 5432	rs485157 1	0.01365	G	2170	1.182	10301900 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10238 6217	rs103512 9	0.01365	A	2170	1.182	10301978 5	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	B2	imm_2_10239 0110	rs671003 4	0.01365	G	2170	1.182	10302367 8	intergenic	IL1RL1	0.059172 591	0.017080 69	0

FIG. 1PP

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	B2	imm_2_10239_1092	rs7589142	0.01365	A	2170	1.182	103024660	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_10239_4083	rs10200952	0.01365	A	2170	1.182	103027651	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	B2	imm_2_10239_8001	rs1592459	0.01365	A	2170	1.182	103031569	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	L1 B1 vs non-IBD ctrl	imm_2_10233_1764	rs17027006	0.01379	C	2906	0.6365	102965332	intronic	IL1RL1	0.066330072	0.040946538	IL1RL1
CD	Time to Frst Surgery	imm_2_10231_7505	rs1997467	0.0138153	A	1091	0.90159	102951073	intronic	NA	NA	NA	NA
CD	Time to Frst Surgery	imm_2_10231_7899	rs1997466	0.0138153	G	1091	0.90159	102951467	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10231_5064	rs1420103	0.01385	A	1421	1.771	102948632	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10233_7597	rs56386507	0.01398	A	2906	0.6371	102971165	intronic	IL1RL1	0.067510094	0.037554638	IL1RL1
CD	Pyoderma G	imm_2_10229_4158	rs6543116	0.01413	A	1421	1.768	102927726	upstream	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10232_8361	rs1946131	0.01414	A	6063	0.7642	102961929	intronic	MAP4K4, TMEM182, RPL31, RPL31	0.0841962068519057, 0.0522514054377319, 0.182483696156476, 0.07159900715990	0.0202861227094196, 0.0335291660561106, 0.0445364127496054, 0.046140	0, 0, 0, 0

FIG. 1QQ

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
											6057128788	9912270284	
CD	Asca CD vs. Asca Ctrl	imm_2_102324148	rs1420101	0.01424	A	2252	0.8557	102957716	intronic	NA	NA	NA	NA
CD	B2	imm_2_102377344	rs1420096	0.01431	G	2169	1.18	103010912	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 B1 vs non-IBD ctrl	imm_2_102332303	rs12469506	0.01443	A	2906	0.6384	102965871	intronic	IL1RL1	0.065931376	0.047728888	IL1RL1
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_102374055	rs3860444	0.01446	A	1051	1.269	103007623	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_102375142	rs12712145	0.01446	A	1051	1.269	103008710	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_102381128	rs1568681	0.01446	G	1051	1.269	103014696	UTR3	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_102382476	rs11123926	0.01446	C	1051	1.269	103016044	downstream	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_102391245	rs4851007	0.01446	A	1051	1.269	103024813	intergenic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_102399579	rs1807782	0.01446	G	1051	1.269	103033147	intergenic	NA	NA	NA	NA

FIG. 1RR

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B2	imm_2_10237 2536	rs670600 2	0.01448	A	2170	1.18	10300610 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Time to Frist Surgery	imm_2_10229 7982	rs155861 9	0.0144941	C	1091	0.902519	10293155 0	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10232 0622	rs592475 11	0.0146	G	2252	0.8457	10295419 0	intronic	NA	NA	NA	NA
CD	i2 CD vs. i2 Ctrl	imm_2_10239 2402	rs115715 837	0.01465	A	1792	2.888	10302597 0	intergenic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10233 8297	rs130157 14	0.01479	C	1051	1.272	10297186 5	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10235 2244	rs377117 2	0.01481	A	2906	0.6397	10298581 2	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229 8679	rs101833 88	0.01481	G	7966	1.095	10293224 7	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229 8234	rs129965 05	0.01484	A	7967	1.095	10293180 2	intronic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	imm_2_10232 9504	rs654311 9	0.01487	A	2252	0.8486	10296307 2	intronic	NA	NA	NA	NA
CD	Time to Frist Surgery	imm_2_10231 5251	rs142010 2	0.0148989	G	1091	0.902831	10294881 9	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10236 3606	rs377116 2	0.01497	A	2905	0.6414	10299717 4	intronic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1SS

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B2	imm_2_10238 6571	rs211066 2	0.01511	T	2170	1.178	10302013 9	intergenic	IL1RL1	0.060162 739	0.014743 734	0
CD	Pyoderma G	imm_2_10238 6351	rs103512 7	0.01534	A	1419	1.746	10301991 9	intergenic	NA	NA	NA	NA
	L3												
CD	B2a+B2b vs non-IBD ctrl	imm_2_10238 6351	rs103512 7	0.01541	A	1050	1.266	10301991 9	intergenic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10237 5401	rs669196 07	0.0155023 89	C	89822	0.028549 259	10300896 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
	L1 B1 vs non-IBD ctrl	imm_2_10237 9106	rs170270 71	0.01561	A	2906	0.6421	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_10238 0734	rs113535 4	0.01565	C	2906	0.642	10301430 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_10238 2350	rs170270 87	0.01565	A	2906	0.642	10301591 8	downstrea m	IL1RL1	0.067250 733	0.043692 753	0
CD	anti-TNF time to loss of response	imm_2_10231 7909	rs763626 90	0.0158195	G	243	-2.41305	10295147 7	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
CD	L1 B1 vs non-IBD ctrl	imm_2_10237 7984	rs485100 5	0.01591	A	2906	0.6781	10301155 2	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10235 8511	rs227029 8	0.01593	G	2906	0.6428	10299207 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_10236 1316	rs170270 37	0.01593	G	2906	0.6428	10299488 4	intronic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1TT

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	L1 B1 vs non-IBD ctrl	imm_2_102363304	rs3821203	0.01593	A	2906	0.6428	102996872	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_102365744	rs56258475	0.01593	G	2906	0.6428	102999312	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_102372819	rs4851570	0.01593	G	2906	0.6428	103006387	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_102373999	rs17027060	0.01593	G	2906	0.6428	103007567	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_102377020	rs2287034	0.01593	A	2906	0.6428	103010588	intronic	IL1RL1	0.067250733	0.043692753	0
CD	Smoking_S tatus	imm_2_102317614	rs11891827	0.01613	G	603	1.743	102951182	intronic	IL1RL1, MAP4K4	0.11719167059551, 0.0353788545524176	0.00350722414540951, 0.0160981230619359	IL1RL1, 0
CD	Smoking_S tatus	imm_2_102317909	rs76362690	0.01613	G	603	1.743	102951477	intronic	IL1RL1, MAP4K4	0.11719167059551, 0.0353788545524176	0.00350722414540951, 0.0160981230619359	IL1RL1, 0
CD	CD vs. non-IBD Controls	imm_2_102293413	rs11685424	0.01635	G	7967	1.094	102926981	upstream	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_102295444	rs6733174	0.01635	A	7967	1.094	102929012	intronic	NA	NA	NA	NA

FIG. 1UU

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	CD vs. non-IBD Controls	imm_2_10229_7313	rs10189711	0.01635	A	7967	1.094	102930881	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10236_3237	rs11683700	0.01636	A	2906	0.644	102996805	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B1 vs non-IBD ctrl	imm_2_10238_4509	rs3732123	0.01648	G	2906	0.6445	103018077	intergenic	IL1RL1	0.067250733	0.043692753	0
CD	L1 ileal	imm_2_10233_9231	rs4851566	0.01671	C	2162	1.192	102972799	intronic	IL1RL1	0.053336426	0.042506604	0
	L1 B2a+B2b vs non-IBD ctrl	imm_2_10236_1452	rs2080289	0.01685	A	575	1.625	102995020	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10231_5064	rs1420103	0.01708	A	1051	1.263	102948632	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10230_3413	rs974389	0.01722	G	7967	1.093	102936981	intronic	NA	NA	NA	NA
	Paneth-D2 phenotype	imm_2_10235_3793	rs7579737	0.01739	G	297	1.544	102987361	intronic	IL1RL1, IL1R1	0.0625934262778242, 0.0337453937432971	0.0204389804110964, 0.0373191165184261	0, 0
CD	B3	imm_2_10236_0765	rs2041739	0.01745	G	2170	0.8487	102994333	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L3 B2a+B2b vs B1	imm_2_10231_8649	rs3755278	0.01757	G	6064	0.7637	102952217	intronic	MAP4K4, TMEM182	0.0894771426920761,	0.0182080516619405,	0, 0

FIG. 1VV

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
											0.060198 97220702 9	0.018871 92869050 61	
CD	CD vs. non-IBD Controls	imm_2_102306844	rs6706844	0.01763	A	7967	1.093	102940412	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_102338297	rs13015714	0.01785	C	1420	1.732	102971865	intronic	NA	NA	NA	NA
CD	Cbcr CD vs. Cbcr Ctrl	imm_2_102329504	rs6543119	0.01787	A	2321	0.8528	102963072	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_102331293	rs55927292	0.01822	A	576	1.608	102964861	intronic	IL1RL1	0.069982 - 32	0.030542 666	IL1RL1
CD	Smoking_S tatus	imm_2_102299246	rs79144324	0.01841	A	603	1.714	102932814	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
CD	L3 B2a+B2b vs B1	imm_2_102296297	rs13005049	0.01865	A	6064	0.7656	102929865	intronic	MAP4K4, TMEM182	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	L3 B2a+B2b vs B1	imm_2_102314613	rs17695648	0.01865	G	6064	0.7656	102948181	intronic	MAP4K4, TMEM182	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	Pyoderma G	imm_2_102351856	rs2058622	0.01873	A	1421	1.723	102985424	intronic	NA	NA	NA	NA

FIG. 1WW

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	Pyoderma G	imm_2_10235_2412	rs3771170	0.01873	A	1421	1.723	10298598	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10232_2115	rs873022	0.01894	A	2906	0.6521	10295568	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10232_3964	rs3732129	0.01894	G	2906	0.6521	10295753	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10235_1116	rs1558627	0.01904	G	1420	1.721	10298468	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10232_2292	rs3771177	0.01908	A	2905	0.6525	10295586	intronic	NA	NA	NA	NA
CD	Time to Frst Surgery	imm_2_10230_3413	rs974389	0.0191732	G	1091	0.906004	10293698	intronic	NA	NA	NA	NA
CD	Time to Frst Surgery	imm_2_10230_6844	rs6706844	0.0191732	A	1091	0.906004	10294041	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10231_8792	rs17026974	0.0194	A	2906	0.6532	10295236	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10238_6571	rs2110662	0.01992	T	2162	0.8474	10302013	intergenic	IL1RL1	0.060162739	0.014743734	0
CD	Time to Frst Surgery	imm_2_10229_3413	rs11685424	0.0200564	G	1091	0.906733	10292698	upstream	NA	NA	NA	NA
CD	Time to Frst Surgery	imm_2_10229_5444	rs6733174	0.0200564	A	1091	0.906733	10292901	intronic	NA	NA	NA	NA
CD	Time to Frst Surgery	imm_2_10229_7313	rs10189711	0.0200564	A	1091	0.906733	10293088	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10233_3668	rs13424006	0.02021	G	2162	1.186	10296723	intronic	IL1RL1	0.053336426	0.042506604	IL1RL1

FIG. 1XX

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Chr2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	L1 ileal	imm_2_10233 3845	rs675196 7	0.02021	G	2162	1.186	10296741 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Asca CD vs. Asca Ctrl	imm_2_10230 5468	rs130013 25	0.02056	A	2252	0.8628	10293903 6	intronic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	imm_2_10231 5593	rs124792 10	0.02056	A	2252	0.8628	10294916 1	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 6537	rs116956 27	0.0206329 42	G	93766	0.024350 62	10297010 5	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Time to Frst Surgery	imm_2_10229 8994	rs950880 06	0.0207958	A	1091	1.1096	10293256 2	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 3668	rs134240 06	0.0207999 55	G	94093	0.024233 9	10296723 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Time to Frst Surgery	imm_2_10229 8258	rs130205 53	0.0209411	G	1090	1.10949	10293182 6	intronic	NA	NA	NA	NA
CD	i2 CD vs. i2 Ctrl	imm_2_10231 8230	rs136235 0	0.02099	C	1792	0.8448	10295179 8	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10233 7597	rs563865 07	0.02105	A	576	1.593	10297116 5	intronic	IL1RL1	0.067510 094	0.037554 638	IL1RL1
CD	L1 ileal	imm_2_10233 6345	rs116885 59	0.02108	A	2162	1.184	10296991 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L1 ileal	imm_2_10233 6537	rs116956 27	0.02108	G	2162	1.184	10297010 5	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L1 ileal	imm_2_10233 7738	rs980845 3	0.02108	A	2162	1.184	10297130 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L1 ileal	imm_2_10233 3863	rs670456 5	0.02108	A	2162	1.184	10296743 1	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L1 ileal	imm_2_10233 4290	rs675248 2	0.02108	G	2162	1.184	10296785 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L1 ileal	imm_2_10233 4360	rs498895 5	0.02108	G	2162	1.184	10296792 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1

FIG. 1YY

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L1 ileal	imm_2_10237 2536	rs670600 2	0.02117	A	2162	0.8487	10300610 4	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10237 7344	rs142009 6	0.02117	G	2161	0.8486	10301091 2	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10236 4152	rs755691 7	0.02124	A	6064	0.8552	10299772 0	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10236 4711	rs321373 2	0.02139	G	6059	0.8554	10299827 9	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10236 7300	rs114656 41	0.02139	C	6063	0.8554	10300086 8	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10234 1482	rs101731 93	0.0214	A	2162	1.184	10297505 0	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10237 7984	rs485100 5	0.02145	A	576	1.518	10301155 2	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10235 7220	rs104394 10	0.02146	C	2162	0.8488	10299078 8	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10235 7801	rs675893 6	0.02146	G	2162	0.8488	10299136 9	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10236 2777	rs102081 96	0.02146	G	2162	0.8488	10299634 5	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10236 4152	rs755691 7	0.02146	C	2162	0.8488	10299772 0	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10236 4711	rs321373 2	0.02146	A	2162	0.8488	10299827 9	intronic	IL1RL1	- 0.059172 591	0.017080 69	0

FIG. 1ZZ

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	L1 ileal	imm_2_10236_5406	rs10204757	0.02146	A	2162	0.8488	102998974	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_10236_6384	rs6760621	0.02146	A	2162	0.8488	102999952	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_10236_7300	rs11465641	0.02146	A	2162	0.8488	103000868	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Time to Frst Surgery	imm_2_10230_5468	rs13001325	0.0215244	A	1091	1.10895	102939036	intronic	NA	NA	NA	NA
CD	Time to Frst Surgery	imm_2_10231_5593	rs12479210	0.0215244	A	1091	1.10895	102949161	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10235_7220	rs10439410	0.02157	A	6064	0.8556	102990788	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L3 B2a+B2b vs B1	imm_2_10235_7801	rs6758936	0.02157	A	6064	0.8556	102991369	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L3 B2a+B2b vs B1	imm_2_10236_2777	rs10208196	0.02157	A	6064	0.8556	102996345	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L3 B2a+B2b vs B1	imm_2_10236_6384	rs6760621	0.02157	G	6064	0.8556	102999952	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2 colonic	imm_2_10230_5468	rs13001325	0.02165	A	2162	1.199	102939036	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10231_5593	rs12479210	0.02165	A	2162	1.199	102949161	intronic	NA	NA	NA	NA
CD	Cbcr CD vs. Cbcr Ctrl	imm_2_10235_1116	rs1558627	0.02196	G	2321	1.164	102984684	intronic	NA	NA	NA	NA

FIG. 1AAA

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	L1 ileal	imm_2_102371390	rs3771159	0.02212	A	2162	0.8497	103004958	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102371762	rs11903946	0.02212	A	2162	0.8497	103005330	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102372880	rs6749014	0.02212	G	2162	0.8497	103006448	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102375146	rs12712146	0.02212	G	2162	0.8497	103008714	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102375969	rs4851004	0.02212	G	2162	0.8497	103009537	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102376094	rs6732138	0.02212	G	2162	0.8497	103009662	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102377669	rs2287033	0.02212	A	2162	0.8497	103011237	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102382119	rs1420094	0.02212	G	2162	0.8497	103015687	downstream	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102384484	rs3732124	0.02212	G	2162	0.8497	103018052	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102385432	rs4851571	0.02212	G	2162	0.8497	103019000	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102386217	rs1035129	0.02212	A	2162	0.8497	103019785	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	L1 ileal	imm_2_102390110	rs6710034	0.02212	G	2162	0.8497	103023678	intergenic	IL1RL1	0.059172591	0.01708069	0

FIG. 1BBB

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L1 ileal	imm_2_10239 1092	rs758914 2	0.02212	A	2162	0.8497	10302466 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10239 4083	rs102009 52	0.02212	A	2162	0.8497	10302765 1	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10239 8001	rs159245 9	0.02212	A	2162	0.8497	10303156 9	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	IGA Asca CD vs. IGA Asca Ctrl	imm_2_10230 5468	rs130013 25	0.02224	A	2252	0.8577	10293903 6	intronic	NA	NA	NA	NA
CD	IGA Asca CD vs. IGA Asca Ctrl	imm_2_10231 5593	rs124792 10	0.02224	A	2252	0.8577	10294916 1	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10238 6571	rs211066 2	0.02227	A	6064	0.8563	10302013 9	intergenic	IL1RL1	0.060162 739	0.014743 734	0
CD	B3	imm_2_10238 0394	rs373212 6	0.02228	C	2168	0.8187	10301396 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10235 8511	rs227029 8	0.02234	G	576	1.582	10299207 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10236 1316	rs170270 37	0.02234	G	576	1.582	10299488 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10236 3237	rs116837 00	0.02234	A	576	1.582	10299680 5	intronic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1CCC

Population	PHENOTYPE	Marker	dbSNP	p_value	AI	n_miss	OR_Z_B	base_pair Chr2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10236 3304	rs3821203	0.02234	A	576	1.582	102996872	intronic	IL1RL1	0.067250733	0.043692753	0
	L1 B2a+B2b vs non-IBD ctrl	imm_2_10236 3606	rs3771162	0.02234	A	576	1.582	102997174	intronic	IL1RL1	0.067250733	0.043692753	0
	L1 B2a+B2b vs non-IBD ctrl	imm_2_10236 5744	rs56258475	0.02234	G	576	1.582	102999312	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10237 2819	rs4851570	0.02234	G	576	1.582	103006387	intronic	IL1RL1	0.067250733	0.043692753	0
	L1 B2a+B2b vs non-IBD ctrl	imm_2_10237 3999	rs17027060	0.02234	G	576	1.582	103007567	intronic	IL1RL1	0.067250733	0.043692753	0
	L1 B2a+B2b vs non-IBD ctrl	imm_2_10237 7020	rs2287034	0.02234	A	576	1.582	103010588	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10237 9106	rs17027071	0.02234	A	576	1.582	103012674	intronic	IL1RL1	0.067250733	0.043692753	0
	L1 B2a+B2b vs non-IBD ctrl	imm_2_10238 0734	rs1135354	0.02234	C	576	1.582	103014302	UTR3	IL1RL1	0.067250733	0.043692753	0
	L1 B2a+B2b vs non-IBD ctrl	imm_2_10238 2350	rs17027087	0.02234	A	576	1.582	103015918	downstream	IL1RL1	0.067250733	0.043692753	0

FIG. 1DDD

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10238 4509	rs373212 3	0.02234	G	576	1.582	10301807 7	intergenic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 ileal	imm_2_10234 4891	rs375527 6	0.02235	A	2162	1.182	10297845 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L1 ileal	imm_2_10234 6056	rs930885 7	0.02235	A	2162	1.182	10297962 4	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L1 ileal	imm_2_10235 2654	rs377116 6	0.02235	A	2162	1.182	10298622 2	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L1 ileal	imm_2_10235 2807	rs197467 5	0.02235	A	2162	1.182	10298637 5	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L3 B2a+B2b vs B1	imm_2_10236 5406	rs102047 57	0.02239	C	6064	0.8564	10299897 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Asca CD vs. Asca Ctrl	imm_2_10229 8994	rs950880	0.02242	A	2252	0.8646	10293256 2	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10229 4158	rs654311 6	0.0225	A	1051	1.25	10292772 6	upstream	NA	NA	NA	NA
CD	L2 colonic	imm_2_10229 8258	rs130205 53	0.02253	G	2161	1.198	10293182 6	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 0328	rs759732 38	0.0226649 57	A	93789	0.132810 49	10296389 6	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10229 8994	rs950880	0.0228	A	2162	1.198	10293256 2	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10233 1764	rs170270 06	0.02281	C	576	1.582	10296533 2	intronic	IL1RL1	0.066330 072	0.040946 538	IL1RL1
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10235 2244	rs377117 2	0.02281	A	576	1.582	10298581 2	intronic	NA	NA	NA	NA

FIG. 1EEE

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	Asca CD vs. Asca Ctrl	imm_2_10229 8258	rs130205 53	0.02289	G	2252	0.8651	10293182 6	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10232 7798	rs130140 44	0.02229	G	6064	0.7807	10296136 6	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
CD	L3 B2a+B2b vs B1	imm_2_10232 9171	rs129891 97	0.02229	A	6064	0.7807	10296273 9	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
CD	L3 B2a+B2b vs B1	imm_2_10233 0060	rs129960 97	0.02229	A	6064	0.7807	10296362 8	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
CD	L3 B2a+B2b vs B1	imm_2_10233 0381	rs130289 93	0.02229	G	6064	0.7807	10296394 9	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8,	0.013815 65927969 22, 0.026913 52129718 4,	0, 0, 0

FIG. 1FFF

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.047501 78772048 85	0.048534 58524677 78	
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
CD	L3 B2a+B2b vs B1	imm_2_10233 1824	rs129995 42	0.0229	C	6064	0.7807	10296539 2	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0
CD	CD vs. Ctrl	imm_2_10233 7738	rs980845 3	0.0229247 66	A	94016	0.023865 438	10297130 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	anti-TNF time to loss of response	imm_2_10239 2402	rs115715 837	0.0231869	A	243	2.27034	10302597 0	intergenic	NA	NA	NA	NA
											0.117191 67059551	0.003507 22414540	
CD	anti-TNF time to loss of response	imm_2_10229 9246	rs791443 24	0.0233052	A	243	-2.26839	10293281 4	intronic	IL1RL1, MAP4K4	0.035378 85455241 76	0.016098 12306193 59	IL1RL1 ,0
											0.117191 67059551	0.003507 22414540	
CD	anti-TNF time to loss of response	imm_2_10231 7614	rs118918 27	0.0233052	G	243	-2.26839	10295118 2	intronic	IL1RL1, MAP4K4	0.035378 85455241 76	0.016098 12306193 59	IL1RL1 ,0
	L3 B2a+B2b vs B1	imm_2_10237 1390	rs377115 9	0.02334	G	6064	0.8573	10300495 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10237 1762	rs119039 46	0.02334	G	6064	0.8573	10300533 0	intronic	IL1RL1	0.059172 591	0.017080 69	0

FIG. 1GGG

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L3 B2a+B2b vs B1	imm_2_10237 2880	rs674901 4	0.02334	A	6064	0.8573	10300644 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10237 5146	rs127121 46	0.02334	A	6064	0.8573	10300871 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10237 5969	rs485100 4	0.02334	A	6064	0.8573	10300953 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10237 6094	rs673213 8	0.02334	A	6064	0.8573	10300966 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10238 2119	rs142009 4	0.02334	A	6064	0.8573	10301568 7	downstrea m	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10237 7669	rs228703 3	0.02335	G	6063	0.8573	10301123 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	i2 CD vs. i2 Ctrl	imm_2_10231 8404	rs136234 9	0.02336	C	1792	0.8471	10295197 2	intronic	NA	NA	NA	NA
CD	OMPC CD vs. OMPC Ctrl	imm_2_10229 5877	rs654311 7	0.02347	G	2281	4.364	10292944 5	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10239 4083	rs102009 52	0.02366	C	6063	0.8576	10302765 1	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10235 7220	rs104394 10	0.02367	C	2170	0.8551	10299078 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10235 7801	rs675893 6	0.02367	G	2170	0.8551	10299136 9	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10236 2777	rs102081 96	0.02367	G	2170	0.8551	10299634 5	intronic	IL1RL1	0.059172 591	0.017080 69	0

FIG. 1HHH

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B3	imm_2_10236 4152	rs755691 7	0.02367	C	2170	0.8551	10299772 0	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10236 4711	rs321373 2	0.02367	A	2170	0.8551	10299827 9	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10236 5406	rs102047 57	0.02367	A	2170	0.8551	10299897 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10236 6384	rs676062 1	0.02367	A	2170	0.8551	10299995 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10236 7300	rs114656 41	0.02367	A	2170	0.8551	10300086 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10236 0765	rs204173 9	0.02371	G	2162	0.8515	10299433 3	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10238 6217	rs103512 9	0.02382	G	6064	0.8578	10301978 5	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	CD vs. Ctrl	imm_2_10233 4360	rs498895 5	0.0239849 2	G	94077	0.023674 412	10296792 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	L3 B2a+B2b vs B1	imm_2_10237 2536	rs670600 2	0.02399	G	6064	0.858	10300610 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10238 5432	rs485157 1	0.02399	A	6063	0.8579	10301900 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	i2 CD vs. i2 Ctrl	imm_2_10232 0622	rs592475 11	0.02399	G	1792	0.8479	10295419 0	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10232 4148	rs142010 1	0.02401	A	2252	0.8597	10295771 6	intronic	NA	NA	NA	NA

FIG. 1III

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L3 B2a+B2b vs B1	imm_2_10237 7344	rs142009 6	0.02405	A	6063	0.858	10301091 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10239 8001	rs159245 9	0.02405	G	6064	0.858	10303156 9	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10233 2303	rs124695 06	0.02409	A	576	1.578	10296587 1	intronic	IL1RL1	0.065931 376	0.047728 888	IL1RL1
CD	L2_colonic	imm_2_10234 0760	rs561790 05	0.02414	A	2162	0.7832	10297432 8	intronic	IL18R1	0.041927 743	0.040233 926	IL18R1
CD	L2_colonic	imm_2_10234 8465	rs728236 69	0.02414	A	2162	0.7832	10298203 3	intronic	IL18R1	0.041927 743	0.040233 926	IL18R1
CD	L3 B2a+B2b vs B1	imm_2_10238 4484	rs373212 4	0.02427	A	6063	0.8582	10301805 2	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	Cbir CD vs. Cbir Ctrl	imm_2_10235 1856	rs205862 2	0.02434	A	2321	1.161	10298542 4	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10235 2412	rs377117 0	0.02434	A	2321	1.161	10298598 0	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10232 2115	rs873022	0.02439	A	2162	0.8151	10295568 3	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10232 2292	rs377117 7	0.02439	A	2162	0.8151	10295586 0	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10232 3964	rs373212 9	0.02439	G	2162	0.8151	10295753 2	intronic	NA	NA	NA	NA
CD	IGA Asca CD vs. IGA Asca Ctrl	imm_2_10229 8994	rs950880	0.02475	A	2252	0.8601	10293256 2	intronic	NA	NA	NA	NA

FIG. 1JJJ

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	B3	imm_2_102380734	rs1135354	0.02479	C	2169	0.8221	103014302	UTR3	IL1RL1	0.067250733	0.043692753	0
CD	Paneth-D4 phenotype L3	imm_2_102382648	rs55664618	0.02487	A	297	-0.9566	103016216	downstream	IL1RL1	0.055883857	0.041785706	0
CD	B2a+B2b vs B1	imm_2_102391092	rs7589142	0.02494	G	6064	0.8588	103024660	intergenic	IL1RL1	0.059172591	0.01708069	0
	IGG Asca CD vs. IGA Asca Ctrl	imm_2_102298258	rs13020553	0.02512	G	2252	0.8604	102931826	intronic	NA	NA	NA	NA
CD	B3	imm_2_102382350	rs17027087	0.02519	A	2170	0.8223	103015918	downstream	IL1RL1	0.067250733	0.043692753	0
CD	B3	imm_2_102384509	rs3732123	0.02519	G	2170	0.8223	103018077	intergenic	IL1RL1	0.067250733	0.043692753	0
	Paneth high (>20%) vs low (<20%) abnormal paneth phenotype	imm_2_102352903	rs6728945	0.02549	G	297	1.844	102986471	intronic	IL1RL1, MAP4K4, IL18RAP, TMEM182	0.106197011732319, 0.0334250334252711234699, -0.08926600241395435028165, 0.209496034573447273056	0.00474852757225921, 0.0151044158781986, 0.0241395694282341, 0.0345736924968317	0, 0, 0, 0
CD	L1 ileal	imm_2_102352244	rs3771172	0.02578	A	2162	0.8167	102985812	intronic	NA	NA	NA	NA
CD	B3	imm_2_102390763	rs55883125	0.02584	A	2169	0.8231	103024331	intergenic	IL1RL1	0.067250733	0.043692753	0

FIG. 1KKK

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	CD vs. non-IBD Controls	imm_2_102297380	rs12712135	0.02586	A	7967	1.087	102930948	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_102360765	rs2041739	0.02592	A	6064	0.8597	102994333	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L2 colonic	imm_2_102320049	rs3771180	0.02593	A	2162	0.7851	102953617	intronic	IL18R1	0.041927743	0.040233926	0
CD	L2 colonic	imm_2_102320645	rs72823646	0.02593	A	2162	0.7851	102954213	intronic	IL18R1	0.041927743	0.040233926	0
CD	L2 colonic	imm_2_102323780	rs10173081	0.02593	A	2162	0.7851	102957348	intronic	IL18R1	0.041927743	0.040233926	0
CD	Cb1r CD vs. Cb1r Ctrl	imm_2_102338297	rs13015714	0.02593	C	2321	1.159	102971865	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_102343628	rs6543123	0.026022295	A	85515	0.024412423	102977196	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_102338096	rs9807962	0.026235964	G	93067	0.023555575	102971664	intronic	NA	NA	NA	NA
CD	B3	imm_2_102358511	rs2270298	0.02663	G	2170	0.8239	102992079	intronic	IL1RL1	0.067250733	0.043692753	0
CD	B3	imm_2_102361316	rs17027037	0.02663	G	2170	0.8239	102994884	intronic	IL1RL1	0.067250733	0.043692753	0
CD	B3	imm_2_102363237	rs11683700	0.02663	A	2170	0.8239	102996805	intronic	IL1RL1	0.067250733	0.043692753	0
CD	B3	imm_2_102363304	rs3821203	0.02663	A	2170	0.8239	102996872	intronic	IL1RL1	0.067250733	0.043692753	0

FIG. 1LLL

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B3	imm_2_10236 5744	rs562584 75	0.02663	G	2170	0.8239	10299931 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	B3	imm_2_10237 2819	rs485157 0	0.02663	G	2170	0.8239	10300638 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	B3	imm_2_10237 3999	rs170270 60	0.02663	G	2170	0.8239	10300756 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	B3	imm_2_10237 7020	rs228703 4	0.02663	A	2170	0.8239	10301058 8	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 ileal	imm_2_10231 8792	rs170269 74	0.02669	A	2162	0.8174	10295236 0	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10239 8798	rs760220 7	0.0267046 6	C	88754	0.025031 494	10303236 6	intergenic	NA	NA	NA	NA
CD	B3	imm_2_10238 6571	rs211066 2	0.02722	T	2170	0.8586	10302013 9	intergenic	IL1RL1	0.060162 739	0.014743 734	0
CD	Asca CD vs. Asca Ctrl	imm_2_10234 0561	rs129993 64	0.02724	A	2252	0.8701	10297412 9	intronic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	imm_2_10234 1768	rs129879 77	0.02724	C	2252	0.8701	10297533 6	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10230 4398	rs129877 82	0.02737	A	6063	0.7809	10293796 6	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	Asca CD vs. Asca Ctrl	imm_2_10234 5460	rs228703 7	0.02747	A	2252	0.8703	10297902 8	intronic	NA	NA	NA	NA

FIG. 1MM

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B3	imm_2_10237 5401	rs669196 07	0.02748	C	2169	0.8248	10300896 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	B3	imm_2_10236 1452	rs208028 9	0.02752	A	2169	0.8249	10299502 0	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. Ctrl	imm_2_10235 2654	rs377116 6	0.0275466 36	A	94075	0.023119 762	10298622 2	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	B3	imm_2_10237 2536	rs670600 2	0.02846	A	2170	0.8596	10300610 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10237 7344	rs142009 6	0.02851	G	2169	0.8595	10301091 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Pyoderma G	imm_2_10237 7984	rs485100 5	0.02853	A	1421	0.5131	10301155 2	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10232 9504	rs654311 9	0.02853	A	2252	0.8559	10296307 2	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10231 7494	rs127121 40	0.02855	C	2252	1.151	10295106 2	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10231 7505	rs199746 7	0.02857	A	2252	1.151	10295107 3	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10231 7899	rs199746 6	0.02857	G	2252	1.151	10295146 7	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10232 2694	rs130227 99	0.02859	G	6064	0.7814	10295626 2	intronic	RPL31, TMEM18 2	0.080113 65109899 88, 0.054650	0.028513 38003838 03, 0.029259	0, 0

FIG. 1NNN

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											28305726 37	85864311 15	
											0.080113 65109899 88,	0.028513 38003838 03,	
CD	L3 B2a+B2b vs B1	imm_2_10232 5512	rs130167 71	0.02859	A	6064	0.7814	10295908 0	intronic	RPL31, TMEM18 2	0.054650 28305726 37	0.029259 85864311 15	0, 0
	Asca CD vs. Asca Ctrl	imm_2_10233 1174	rs130174 55	0.02869	A	2252	0.8364	10296474 2	intronic	NA	NA	NA	NA
	L3 B2a+B2b vs B1	imm_2_10239 0110	rs671003 4	0.02885	A	6063	0.8621	10302367 8	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs B1	imm_2_10232 8782	rs105409 6	0.02885	G	6058	0.788	10296235 0	intronic	NA	NA	NA	NA
	Asca CD vs. Asca Ctrl	rs12998521	rs129985 21	0.02896	A	2252	0.8714	10297441 7	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10231 8792	rs170269 74	0.02913	A	2162	1.216	10295236 0	intronic	NA	NA	NA	NA
	CD vs. Ctrl	imm_2_10235 3891	rs654312 4	0.0291709 36	A	94026	0.022918 809	10298745 9	intronic	IL1RL1	0.053489 519	0.039961 127	0
CD	L2 colonic	imm_2_10237 5844	rs116791 46	0.02955	G	2162	0.7886	10300941 2	intronic	IL18R1	0.046361 422	0.019212 446	IL18R1
	B3	imm_2_10237 9106	rs170270 71	0.02964	A	2170	0.8271	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 ileal	imm_2_10235 3891	rs654312 4	0.02969	A	2162	1.173	10298745 9	intronic	IL1RL1	0.053489 519	0.039961 127	0
	B3	imm_2_10237 1390	rs377115 9	0.02971	A	2170	0.8605	10300495 8	intronic	IL1RL1	0.059172 591	0.017080 69	0

FIG. 1000

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	B3	imm_2_10237_1762	rs11903946	0.02971	A	2170	0.8605	103005330	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10237_2880	rs6749014	0.02971	G	2170	0.8605	103006448	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10237_5146	rs12712146	0.02971	G	2170	0.8605	103008714	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10237_5969	rs4851004	0.02971	G	2170	0.8605	103009537	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10237_6094	rs6732138	0.02971	G	2170	0.8605	103009662	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10237_7669	rs2287033	0.02971	A	2170	0.8605	103011237	intronic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10238_2119	rs1420094	0.02971	G	2170	0.8605	103015687	downstream	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10238_4484	rs3732124	0.02971	G	2170	0.8605	103018052	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10238_5432	rs4851571	0.02971	G	2170	0.8605	103019000	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10238_6217	rs1035129	0.02971	A	2170	0.8605	103019785	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10239_0110	rs6710034	0.02971	G	2170	0.8605	103023678	intergenic	IL1RL1	0.059172591	0.01708069	0
CD	B3	imm_2_10239_1092	rs7589142	0.02971	A	2170	0.8605	103024660	intergenic	IL1RL1	0.059172591	0.01708069	0

FIG. 1PPP

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B3	imm_2_10239 4083	rs102009 52	0.02971	A	2170	0.8605	10302765 1	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	B3	imm_2_10239 8001	rs159245 9	0.02971	A	2170	0.8605	10303156 9	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	Time to Frist Surgery	imm_2_10232 4148	rs142010 1	0.0297696	A	1091	1.10258	10295771 6	intronic	NA	NA	NA	NA
CD	IGA Asca Ctrl	imm_2_10231 5251	rs142010 2	0.02989	G	2252	1.149	10294881 9	intronic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	imm_2_10239 0511	rs621527 11	0.02995	A	2252	2.478	10302407 9	intergenic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	imm_2_10233 4276	rs111239 23	0.02996	A	2252	0.8722	10296784 4	intronic	NA	NA	NA	NA
CD	i2 CD vs. i2 Ctrl	imm_2_10239 0028	rs781785 97	0.03015	A	1792	1.217	10302359 6	intergenic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10231 8649	rs375527 8	0.03018	G	7967	0.8756	10295221 7	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	IGA Asca Ctrl	imm_2_10230 3413	rs974389	0.03038	G	2252	1.149	10293698 1	intronic	NA	NA	NA	NA
CD	IGA Asca Ctrl	imm_2_10230 6844	rs670684 4	0.03038	A	2252	1.149	10294041 2	intronic	NA	NA	NA	NA

FIG. 1QQQ

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L2 colonic	imm_2_10238 0734	rs113535 4	0.03054	C	2161	1.213	10301430 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
CD	Pyoderma G	imm_2_10229 7380	rs127121 35	0.03065	A	1421	1.673	10293094 8	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10234 6056	rs930885 7	0.0308155 28	A	94093	0.022656 017	10297962 4	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L1 ileal	imm_2_10236 3606	rs377116 2	0.03141	A	2162	0.8233	10299717 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L3 B2a+B2b vs B1	imm_2_10235 3793	rs757973 7	0.03147	G	6064	0.8547	10298736 1	intronic	IL1RL1, IL1R1	0.062593 42627782 42, 0.033745 39374329 71	0.020438 98041109 64, 0.037319 11651842 61	0, 0
CD	CD vs. Ctrl	imm_2_10234 1482	rs101731 93	0.0315543 16	A	94058	0.022564 502	10297505 0	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10230 3914	rs414213 2	0.03162	G	2252	1.148	10293748 2	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10230 5866	rs142008 8	0.03162	A	2252	1.148	10293943 4	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10231 5371	rs124663 80	0.03162	A	2252	1.148	10294893 9	intronic	NA	NA	NA	NA
CD	Paneth high (>20%) vs low (<20%) abnormal	imm_2_10232 0808	rs985523	0.03213	A	297	1.798	10295437 6	intronic	IL1RL1, MAP4K4	0.097133 46836259 56, 0.030462 06039871 91	0.009923 07563826 999, 0.026953 59831841 94	IL1RL1 , 0

FIG. 1RRR

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
	paneth phenotype												
CD	Paneth high (>20%) vs low (<20%) abnormal paneth phenotype	imm_2_102324668	rs6719130	0.03213	A	297	1.798	102958236	intronic	IL1RL1, MAP4K4	0.0971334683625956, 0.0304620603987191	0.00992307563826999, 0.0269535983184194	IL1RL1, 0
CD	Paneth-D4 phenotype	imm_2_102293413	rs11685424	0.03217	A	297	-0.8889	102926981	upstream	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_102295444	rs6733174	0.03217	G	297	-0.8889	102929012	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_102297313	rs10189711	0.03217	G	297	-0.8889	102930881	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_102303413	rs974389	0.03217	A	297	-0.8889	102936981	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_102306844	rs6706844	0.03217	G	297	-0.8889	102940412	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_102298044	rs72823635	0.03224	G	2162	0.793	102931612	intronic	IL18R1	0.041927743	0.040233926	0
CD	L2 colonic	imm_2_102298944	rs950881	0.03224	A	2162	0.793	102932512	intronic	IL18R1	0.041927743	0.040233926	0
CD	L2 colonic	imm_2_102301406	rs10179458	0.03224	A	2162	0.793	102934974	intronic	IL18R1	0.041927743	0.040233926	0

FIG. 1SSS

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L2 colonic	imm_2_10230 3976	rs101891 54	0.03224	A	2162	0.793	10293754 4	intronic	IL18R1	0.041927 743	0.040233 926	0
CD	L2 colonic	imm_2_10230 4315	rs101895 26	0.03224	A	2162	0.793	10293788 3	intronic	IL18R1	0.041927 743	0.040233 926	0
CD	Cb1r CD vs. Cb1r Ctrl	rs12998521	rs129985 21	0.03226	A	2321	0.8749	10297441 7	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10237 7761	rs561510 44	0.03229	A	6064	0.7903	10301132 9	intronic	TMEM18 2	0.214216 334	0.038091 085	0
CD	L2 colonic	imm_2_10235 2244	rs377117 2	0.03232	A	2162	1.21	10298581 2	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10232 2115	rs873022 7	0.03248	A	2162	1.21	10295568 3	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10232 2292	rs377117 7	0.03248	A	2162	1.21	10295586 0	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10232 3964	rs373212 9	0.03248	G	2162	1.21	10295753 2	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10235 1116	rs155862 7	0.03267	G	5991	1.19	10298468 4	intronic	NA	NA	NA	NA
CD	PDM	imm_2_10237 7984	rs485100 5	0.03279	A	2093	1.17	10301155 2	intronic	NA	NA	NA	NA
CD	IGA Asca CD vs. IGA Asca Ctrl	imm_2_10229 7827	rs155862 0	0.03294	A	2252	1.146	10293139 5	intronic	NA	NA	NA	NA
CD	B3	imm_2_10235 2244	rs377117 2	0.03304	A	2170	0.8306	10298581 2	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10230 5468	rs130013 25	0.03304	A	6002	0.8518	10293903 6	intronic	NA	NA	NA	NA

FIG. 1TTT

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	CD vs. non-IBD Controls	imm_2_10236_9697	rs2241116	0.03307	A	7967	0.9031	103003265	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10229_8258	rs13020553	0.03307	G	6002	0.8518	102931826	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10229_8994	rs950880	0.03307	A	6002	0.8518	102932562	intronic	NA	NA	NA	NA
	IGG Asca												
CD	CD vs. IGA Asca Ctrl	imm_2_10229_7982	rs1558619	0.03311	C	2252	1.146	102931550	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10235_2807	rs1974675	0.033164814	A	94096	0.022347585	102986375	intronic	IL1RL1	0.053336426	0.042506604	0
	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237_7761	rs56151044	0.03321	A	1051	0.7466	103011329	intronic	TMEM182	0.214216334	0.038091085	0
	Cbir CD vs. Cbir Ctrl	imm_2_10229_7754	rs75452014	0.03322	A	2321	1.908	102931322	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10231_5593	rs12479210	0.03333	A	6002	0.852	102949161	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229_7380	rs12712135	0.03342	G	297	-0.8688	102930948	intronic	NA	NA	NA	NA
	Paneth high (>20%) vs low (<20%) abnormal paneth phenotype									IL1RL1, MAP4K4, IL18RAP, TMEM182	0.106760025100458, 0.0334140.0142424892443608, -0.091611	0.00417049321545419, 0.0142424892443608, 0.019477	0, 0, 0, 0

FIG. 1UUU

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											83632137 71, 0.228371 77265979	80551913 42, 0.019898 45717528 45	
CD	Asca CD vs. Asca Ctrl	imm_2_10235 6117	rs114656 08	0.03358	G	2252	0.2554	10298968 5	intronic	NA	NA	NA	NA
CD	B3	imm_2_10236 3606	rs377116 2			2170	0.8318	10299717 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10234 0561	rs129993 64	0.03368	A	2162	1.181	10297412 9	intronic	NA	NA	NA	NA
CD	L2_colonic	imm_2_10234 1768	rs129879 77	0.03373	A	2162	1.181	10297533 6	intronic	NA	NA	NA	NA
CD	L2_colonic	rs12998521	rs129985 21	0.03373	A	2162	1.181	10297441 7	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10237 9106	rs170270 71	0.03375	A	2162	0.8247	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	Cbir CD vs. Cbir Ctrl	imm_2_10234 0561	rs129993 64	0.03397	A	2321	0.8761	10297412 9	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10234 1768	rs129879 77	0.03397	C	2321	0.8761	10297533 6	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10236 1452	rs208028 9	0.03401	A	2161	0.8248	10299502 0	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	CD vs. non-IBD Controls	imm_2_10231 4613	rs176956 48			7967	0.8782	10294818 1	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0

FIG. 1VVV

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	i2 CD vs. i2 Ctrl	imm_2_10232_1514	rs13408661	0.03469	A	1792	1.976	102955082	intronic	NA	NA	NA	NA
CD	Paneth-D5 phenotype	imm_2_10238_6571	rs2110662	0.03471	T	155	0.1364	103020139	intergenic	IL1RL1	0.060162739	0.014743734	0
CD	Paneth-D5 phenotype	imm_2_10235_7220	rs10439410	0.03472	C	155	0.1376	102990788	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10235_7801	rs6758936	0.03472	G	155	0.1376	102991369	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10236_0765	rs2041739	0.03472	G	155	0.1376	102994333	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10236_2777	rs10208196	0.03472	G	155	0.1376	102996345	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10236_4152	rs7556917	0.03472	C	155	0.1376	102997720	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10236_4711	rs3213732	0.03472	A	155	0.1376	102998279	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10236_5406	rs10204757	0.03472	A	155	0.1376	102998974	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10236_6384	rs6760621	0.03472	A	155	0.1376	102999952	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10236_7300	rs11465641	0.03472	A	155	0.1376	103000868	intronic	IL1RL1	0.059172591	0.01708069	0
CD	Paneth-D5 phenotype	imm_2_10237_1390	rs3771159	0.03472	A	155	0.1376	103004958	intronic	IL1RL1	0.059172591	0.01708069	0

FIG. 1WWW

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	Paneth-D5 phenotype	imm_2_10237 1762	rs119039 46	0.03472	A	155	0.1376	10300533 0	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10237 2536	rs670600 2	0.03472	A	155	0.1376	10300610 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10237 2880	rs674901 4	0.03472	G	155	0.1376	10300644 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10237 5146	rs127121 46	0.03472	G	155	0.1376	10300871 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10237 5969	rs485100 4	0.03472	G	155	0.1376	10300953 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10237 6094	rs673213 8	0.03472	G	155	0.1376	10300966 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10237 7344	rs142009 6	0.03472	G	155	0.1376	10301091 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10237 7669	rs228703 3	0.03472	A	155	0.1376	10301123 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10238 2119	rs142009 4	0.03472	G	155	0.1376	10301568 7	downstrea m	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10238 4484	rs373212 4	0.03472	G	155	0.1376	10301805 2	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10238 5432	rs485157 1	0.03472	G	155	0.1376	10301900 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10238 6217	rs103512 9	0.03472	A	155	0.1376	10301978 5	intergenic	IL1RL1	0.059172 591	0.017080 69	0

FIG. 1XXX

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	Paneth-D5 phenotype	imm_2_10239 0110	rs671003 4	0.03472	G	155	0.1376	10302367 8	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10239 1092	rs758914 2	0.03472	A	155	0.1376	10302466 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10239 4083	rs102009 52	0.03472	A	155	0.1376	10302765 1	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	Paneth-D5 phenotype	imm_2_10239 8001	rs159245 9	0.03472	A	155	0.1376	10303156 9	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L1 ileal	imm_2_10238 0394	rs373212 6	0.03478	C	2161	0.8257	10301396 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10229 3518	rs116854 80	0.035	G	2252	1.145	10292708 6	upstream	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10229 6579	rs155862 2	0.035	G	2252	1.145	10293014 7	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10229 6812	rs101892 02	0.035	A	2252	1.145	10293038 0	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10229 8358	rs130207 93	0.035	G	2252	1.145	10293192 6	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10238 0734	rs113535 4	0.03505	C	2161	0.8261	10301430 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1YY

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10230 2563	rs116904 43	0.03505	T	2252	1.145	10293613 1	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10234 5460	rs228703 7	0.03514	A	2162	1.18	10297902 8	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 7913	rs485156 5	0.0354108 07	A	84124	0.023248 715	10297148 1	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10238 2350	rs170270 87	0.03548	A	2162	0.8263	10301591 8	downstrea m	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 ileal	imm_2_10238 4509	rs373212 3	0.03548	G	2162	0.8263	10301807 7	intergenic	IL1RL1	0.067250 733	0.043692 753	0
CD	Pyoderma G	imm_2_10229 8234	rs129965 05	0.03567	A	1421	1.648	10293180 2	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 8679	rs101833 88	0.03567	G	1421	1.648	10293224 7	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10231 8404	rs136234 9	0.03579	C	2321	0.8726	10295197 2	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10236 8082	rs176514 85	0.03585	A	1050	0.7487	10300165 0	intronic	TMEM18 2	0.214216 334	0.038091 085	0
CD	L1 ileal	imm_2_10239 0763	rs558831 25	0.03609	A	2161	0.8268	10302433 1	intergenic	IL1RL1	0.067250 733	0.043692 753	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10229 8234	rs129965 05	0.03632	A	1051	1.208	10293180 2	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10229 8679	rs101833 88	0.03632	G	1051	1.208	10293224 7	intronic	NA	NA	NA	NA

FIG. 1ZZZ

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	OMPC CD vs. OMPC Ctrl	imm_2_10238 6038	rs115528 884	0.03652	A	2281	2.436	10301960 6	intergenic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10229 6297	rs130050 49	0.03656	A	7967	0.8797	10292986 5	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	Cbir CD vs. Cbir Ctrl	imm_2_10234 5460	rs228703 7	0.03663	A	2321	0.8777	10297902 8	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10233 4276	rs111239 23	0.03672	A	2162	1.178	10296784 4	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10229 7754	rs754520 14	0.0369154 53	A	94051	0.104882 034	10293132 2	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10229 7380	rs127121 35	0.03714	A	1051	1.208	10293094 8	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10229 7089	rs101919 14	0.0372	A	2252	1.143	10293065 7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 9231	rs485156 6	0.0372061 62	C	92717	0.022117 383	10297279 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	Cbir CD vs. Cbir Ctrl	imm_2_10233 4276	rs111239 23	0.03727	A	2321	0.8782	10296784 4	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10235 8511	rs227029 8	0.03728	G	2162	0.8278	10299207 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 ileal	imm_2_10236 1316	rs170270 37	0.03728	G	2162	0.8278	10299488 4	intronic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1A AAA

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	L1 ileal	imm_2_10236_3237	rs11683700	0.03728	A	2162	0.8278	102996805	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 ileal	imm_2_10236_3304	rs3821203	0.03728	A	2162	0.8278	102996872	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 ileal	imm_2_10236_5744	rs56258475	0.03728	G	2162	0.8278	102999312	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 ileal	imm_2_10237_2819	rs4851570	0.03728	G	2162	0.8278	103006387	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 ileal	imm_2_10237_3999	rs17027060	0.03728	G	2162	0.8278	103007567	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 ileal	imm_2_10237_7020	rs2287034	0.03728	A	2162	0.8278	103010588	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L2 colonic	imm_2_10238_2350	rs17027087	0.0373	A	2162	1.205	103015918	downstream	IL1RL1	0.067250733	0.043692753	0
CD	L2 colonic	imm_2_10238_4509	rs3732123	0.0373	G	2162	1.205	103018077	intergenic	IL1RL1	0.067250733	0.043692753	0
CD	Asca CD vs. Asca Ctrl	imm_2_10235_2153	rs11465594	0.03731	C	2252	0.3417	102985721	intronic	NA	NA	NA	NA
CD	IGA Asca Ctrl	imm_2_10229_3413	rs11685424	0.03737	G	2252	1.143	102926981	upstream	NA	NA	NA	NA
CD	IGA Asca Ctrl	imm_2_10229_5444	rs6733174	0.03737	A	2252	1.143	102929012	intronic	NA	NA	NA	NA

FIG. 1BBBB

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10229_7313	rs10189711	0.03737	A	2252	1.143	102930881	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10234_5903	NA	0.03747	G	2252	1.287	102979471	intronic	IL1R1, IL1R2, IL1RL2	0.072683 27965234 32, 0.306742 0.023505 01255030 8, 0.161597 69485878 6	0.009288 01154136 09, 0.023505 27678191 85, 0.028541 82938325 35	0, 0, 0
CD	Paneth-D4 phenotype	imm_2_10229_3518	rs11685480	0.03761	A	297	-0.8545	102927086	upstream	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229_6579	rs1558622	0.03761	A	297	-0.8545	102930147	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229_6812	rs10189202	0.03761	G	297	-0.8545	102930380	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229_7089	rs10191914	0.03761	G	297	-0.8545	102930657	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229_7827	rs1558620	0.03761	G	297	-0.8545	102931395	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229_7982	rs1558619	0.03761	A	297	-0.8545	102931550	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229_8358	rs13020793	0.03761	A	297	-0.8545	102931926	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10230_1669	rs11123918	0.03761	G	297	-0.8545	102935237	intronic	NA	NA	NA	NA

FIG. 1CCCC

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	Paneth-D4 phenotype	imm_2_10230_2563	rs116904_43	0.03761	A	297	-0.8545	10293613	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10230_3914	rs414213_2	0.03761	A	297	-0.8545	10293748	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10230_5866	rs142008_8	0.03761	G	297	-0.8545	10293943	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10231_5251	rs142010_2	0.03761	A	297	-0.8545	10294881	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10231_5371	rs124663_80	0.03761	G	297	-0.8545	10294893	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10231_7494	rs127121_40	0.03761	A	297	-0.8545	10295106	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10231_7899	rs199746_6	0.03761	C	297	-0.8545	10295146	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10233_1293	rs559272_92	0.03783	A	2162	0.8289	10296486	intronic	IL1RL1	0.06998232	0.030542666	IL1RL1
CD	L2 colonic	imm_2_10233_2303	rs124695_06	0.03793	A	2162	1.204	10296587	intronic	IL1RL1	0.065931376	0.047728888	IL1RL1
CD	Paneth-D4 phenotype	imm_2_10231_7505	rs199746_7	0.03793	G	296	-0.8545	10295107	intronic	NA	NA	NA	NA
CD	B2a+B2b vs B1	imm_2_10235_2412	rs377117_0	0.03802	A	6001	1.184	10298598	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10238_0394	rs373212_6	0.03806	C	2161	1.204	10301396	UTR3	IL1RL1	0.067250733	0.043692753	0

FIG. 1DDDD

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	L1	imm_2_10235 1856	rs205862 2	0.03818	A	6002	1.184	10298542 4	intronic	NA	NA	NA	NA
	L2 B1 vs non-IBD ctrl	imm_2_10237 3483	rs170270 56	0.03821	A	3008	1.546	10300705 1	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10237 5401	rs669196 07	0.03831	C	2161	0.8287	10300896 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	Time to Second Surgery	imm_2_10234 7450	rs105159 21	0.0383349	C	181	1.42917	10298101 8	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 98393204 15	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	0, 0, 0
		imm_2_10234 9061	rs114655 84	0.0383349	A	181	1.42917	10298262 9	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 98393204 15	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	0, 0, 0
CD	Time to Second Surgery	imm_2_10235 3525	rs114655 96	0.0383349	A	181	1.42917	10298709 3	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 98393204 15	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	0, 0, 0

FIG. 1EEEE

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	L1 B2a+B2b vs B1	imm_2_10233 2499	rs192162 2	0.0384	A	6002	0.8636	10296606 7	intronic	MAP4K4	0.049614 781	0.016696 387	0
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10231 8792	rs170269 74	0.03842	A	576	1.511	10295236 0	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10232 2115	rs873022	0.03842	A	576	1.511	10295568 3	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10232 2292	rs377117 7	0.03842	A	576	1.511	10295586 0	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs non-IBD ctrl	imm_2_10232 3964	rs373212 9	0.03842	G	576	1.511	10295753 2	intronic	NA	NA	NA	NA
CD	B3	imm_2_10231 8792	rs170269 74	0.03863	A	2170	0.8354	10295236 0	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs B1	imm_2_10236 8082	rs176514 85	0.03873	A	6062	0.7965	10300165 0	intronic	TMEM18 2	0.214216 334	0.038091 085	0
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10229 7380	rs127121 35	0.03874	A	2252	1.142	10293094 8	intronic	NA	NA	NA	NA
CD	anti-TNF time to loss of response	imm_2_10233 2499	rs192162 2	0.0388444	A	243	-2.06583	10296606 7	intronic	MAP4K4	0.049614 781	0.016696 387	0
CD	Paneth-D4 phenotype	imm_2_10229 8234	rs129965 05	0.03901	G	297	-0.8349	10293180 2	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10229 8679	rs101833 88	0.03901	A	297	-0.8349	10293224 7	intronic	NA	NA	NA	NA

FIG. 1FFFF

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	Uveitis	imm_2_10233 6345	rs116885 59	0.03912	A	1426	0.4877	10296991 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 6537	rs116956 27	0.03912	G	1426	0.4877	10297010 5	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 7738	rs980845 3	0.03912	A	1426	0.4877	10297130 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 3668	rs134240 06	0.03912	G	1426	0.4877	10296723 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 3845	rs675196 7	0.03912	G	1426	0.4877	10296741 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 3863	rs670456 5	0.03912	A	1426	0.4877	10296743 1	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 4290	rs675248 2	0.03912	G	1426	0.4877	10296785 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 4360	rs498895 5	0.03912	G	1426	0.4877	10296792 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	Uveitis	imm_2_10233 9231	rs485156 6	0.03917	C	1426	0.4884	10297279 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L2_colonic	imm_2_10238 4560	rs129917 37	0.0392	T	2162	0.8167	10301812 8	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	L2_colonic	imm_2_10239 1706	rs101817 85	0.0392	A	2162	0.8167	10302527 4	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	L2_colonic	imm_2_10239 2170	rs116877 68	0.0392	G	2162	0.8167	10302573 8	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	L2_colonic	imm_2_10239 4498	rs758698 3	0.0392	A	2162	0.8167	10302806 6	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	B3	imm_2_10238 4560	rs129917 37	0.03935	T	2170	1.191	10301812 8	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	B3	imm_2_10239 1706	rs101817 85	0.03935	A	2170	1.191	10302527 4	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1

FIG. 1GGGG

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	B3	imm_2_10239 2170	rs116877 68	0.03935	G	2170	1.191	10302573 8	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	B3	imm_2_10239 4498	rs758698 3	0.03935	A	2170	1.191	10302806 6	intergenic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	L2 colonic	imm_2_10236 3483	rs728236 77	0.03943	A	2162	0.7998	10299705 1	intronic	IL18R1	0.046361 422	0.019212 446	IL18R1
CD	Pyoderma G	imm_2_10230 3413	rs974389 rs670684 4	0.03967	G	1421	1.632	10293698 1	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10230 6844	rs670684 4	0.03967	A	1421	1.632	10294041 2	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10230 4398	rs129877 82	0.03977	A	7966	0.8822	10293796 6	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
CD	L2_colonic	imm_2_10233 7597	rs563865 07	0.03978	A	2162	1.201	10297116 5	intronic	IL1RL1	0.067510 094	0.037554 638	IL1RL1
CD	PDM	imm_2_10236 3606	rs377116 2	0.03979	A	2093	1.176	10299717 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	Uveitis	imm_2_10235 2654	rs377116 6	0.03997	A	1426	0.4895	10298622 2	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L1 ileal	imm_2_10233 2303	rs124695 06	0.04008	A	2162	0.8304	10296587 1	intronic	IL1RL1	0.065931 376	0.047728 888	IL1RL1
CD	Paneth high (>20%) vs low (<20%) abnormal paneth phenotype	imm_2_10231 3976	rs771271 14	0.04018	A	297	2.308	10294754 4	intronic	IL1RL1, MAP4K4, IL18RAP, CNOT11, MAP4K4	0.154006 31456082 4, 0.052797 13115951 81,- 0.135420	0.006657 33914116 06, 0.010799 75270327 78, 0.023225	IL1RL1 , 0, 0, 0, 0

FIG. 1HHHH

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											47625685 3, 0.203509 01597676 2, 0.097682 68462740 83	60255846 7, 0.037112 34476033 54, 0.043278 92676263 28	
CD	L2 colonic IGG Asca CD vs. IGA Asca Ctrl	imm_2_10232 4148	rs142010 1	0.04024	A	2162	1.176	10295771 6	intronic	NA	NA	NA	NA
CD		imm_2_10229 8234	rs129965 05	0.04029	A	2252	1.141	10293180 2	intronic	NA	NA	NA	NA
CD		imm_2_10229 8679	rs101833 88	0.04029	G	2252	1.141	10293224 7	intronic	NA	NA	NA	NA
CD	L2 colonic L1 B2a+B2b vs B1	imm_2_10239 0763	rs558831 25	0.04034	A	2161	1.201	10302433 1	intergenic	IL1RL1	0.067250 733	0.043692 753	0
CD		imm_2_10234 5460	rs228703 7	0.04039	A	5999	0.8575	10297902 8	intronic	NA	NA	NA	NA
CD	Uveitis	imm_2_10234 1482	rs101731 93	0.04056	A	1426	0.4907	10297505 0	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	Uveitis	imm_2_10234 4891	rs375527 6	0.04056	A	1426	0.4907	10297845 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	Uveitis	imm_2_10234 6056	rs930885 7	0.04056	A	1426	0.4907	10297962 4	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	Uveitis	imm_2_10235 2807	rs197467 5	0.04056	A	1426	0.4907	10298637 5	intronic	IL1RL1	0.053336 426	0.042506 604	0
CD	L1 ileal	imm_2_10233 1764	rs170270 06	0.04075	C	2162	0.8309	10296533 2	intronic	IL1RL1	0.066330 072	0.040946 538	IL1RL1

FIG. 1III

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L2 colonic	imm_2_10237 0393	rs377116 1	0.04082	A	2162	0.8181	10300396 1	intronic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	L2 colonic	imm_2_10237 6326	rs377115 8	0.04082	G	2162	0.8181	10300989 4	intronic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	L2 colonic	imm_2_10238 0182	rs373212 7	0.04082	C	2162	0.8181	10301375 0	UTR3	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	Arthralgias	imm_2_10237 7761	rs561510 44	0.04089	A	1624	1.32	10301132 9	intronic	TMEM18 2	0.214216 334	0.038091 085	0
CD	IGA Asca Ctrl	imm_2_10231 9499	rs127121 41	0.04095	A	2252	1.14	10295306 7	intronic	NA	NA	NA	NA
CD	L1 ileal	imm_2_10233 7597	rs563865 07	0.04118	A	2162	0.8314	10297116 5	intronic	IL1RL1	0.067510 094	0.037554 638	IL1RL1
CD	Pyoderma G	imm_2_10229 3413	rs116854 24	0.0414	G	1421	1.626	10292698 1	upstream	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 5444	rs673317 4	0.0414	A	1421	1.626	10292901 2	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 7313	rs101897 11	0.0414	A	1421	1.626	10293088 1	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10238 2648	rs556646 18	0.04151	A	1421	0.5953	10301621 6	downstrea m	IL1RL1	0.055883 857	0.041785 706	0
CD	CD vs. non-IBD Controls	imm_2_10231 7614	rs118918 27	0.04189	G	7966	0.8937	10295118 2	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0

FIG. 1JJJ

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pair Chr2	snp location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	Cbir CD vs. Cbir Ctrl	imm_2_10232_0622	rs59247511	0.04218	G	2321	0.8766	102954190	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233_4290	rs6752482	0.042300165	G	94074	0.021400723	102967858	intronic	IL1RL1	0.053336426	0.042506604	IL1RL1
CD	L2 colonic L1	imm_2_10235_7080	rs17027029	0.04246	G	2162	0.8206	102990648	intronic	IL18R1	0.04036643	0.035376172	IL18R1
CD	B2a+B2b vs B1	imm_2_10233_4276	rs11123923	0.04249	A	6002	0.8589	102967844	intronic	NA	NA	NA	NA
CD	i2 CD vs. i2 Ctrl	imm_2_10232_1488	rs13408569	0.04257	C	1792	0.8152	102955056	intronic	NA	NA	NA	NA
CD	L2 colonic L1	imm_2_10236_4316	rs3213733	0.0426	A	2162	0.8195	102997884	intronic	IL18R1	0.04036643	0.035376172	IL18R1
CD	B2a+B2b vs B1	imm_2_10234_0561	rs12999364	0.0426	A	6002	0.859	102974129	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10234_1768	rs12987977	0.0426	C	6002	0.859	102975336	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10232_9659	rs17696274	0.042978792	G	93836	0.060548072	102963227	intronic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	rs1420103	rs1420103	0.04302	A	2252	9.963	102948632	intronic;intronic	NA	NA	NA	NA
CD	Arthralgias	imm_2_10236_8082	rs17651485	0.04307	A	1623	1.318	103001650	intronic	TMEM182	0.214216334	0.038091085	0
CD	B3	imm_2_10232_2115	rs873022	0.04333	A	2170	0.8394	102955683	intronic	NA	NA	NA	NA
CD	B3	imm_2_10232_2292	rs3771177	0.04333	A	2170	0.8394	102955860	intronic	NA	NA	NA	NA

FIG. 1KKKK

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	B3	imm_2_10232_3964	rs3732129	0.04333	G	2170	0.8394	102957532	intronic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10237_5401	rs66919607	0.0435	C	2161	1.198	103008969	intronic	IL1RL1	0.067250733	0.043692753	0
CD	B3	imm_2_10236_4316	rs3213733	0.04356	A	2170	1.187	102997884	intronic	IL18R1	0.04036643	0.035376172	IL18R1
CD	L2 colonic	imm_2_10236_1452	rs2080289	0.04366	A	2161	1.198	102995020	intronic	IL1RL1	0.067250733	0.043692753	0
CD	L1 B2a+B2b vs B1	rs12998521	rs12998521	0.04375	A	6001	0.8596	102974417	intronic	NA	NA	NA	NA
CD	IGA Asca Ctrl	imm_2_10234_0561	rs12999364	0.04403	A	2252	0.8749	102974129	intronic	NA	NA	NA	NA
CD	IGA Asca Ctrl	imm_2_10234_1768	rs12987977	0.04403	C	2252	0.8749	102975336	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10231_9499	rs12712141	0.04411	G	6002	0.8656	102953067	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10235_7220	rs10439410	0.0442	A	1051	0.8392	102990788	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10235_7801	rs6758936	0.0442	A	1051	0.8392	102991369	intronic	IL1RL1	0.059172591	0.01708069	0
CD	L3 B2a+B2b	imm_2_10236_2777	rs10208196	0.0442	A	1051	0.8392	102996345	intronic	IL1RL1	0.059172591	0.01708069	0

FIG. 1LLLL

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
	vs non-IBD ctrl												
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10236 4152	rs755691 7	0.0442	A	1051	0.8392	10299772 0	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10236 4711	rs321373 2	0.0442	G	1051	0.8392	10299827 9	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10236 5406	rs102047 57	0.0442	C	1051	0.8392	10299897 4	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10236 6384	rs676062 1	0.0442	G	1051	0.8392	10299995 2	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10236 7300	rs114656 41	0.0442	C	1051	0.8392	10300086 8	intronic	IL1RL1	- 0.059172 591	0.017080 69	0
CD	CD vs. Ctrl	imm_2_10233 3845	rs675196 7	0.0442730 01	G	94098	0.021096 118	10296741 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	CD vs. Ctrl	imm_2_10234 4162	rs102048 37	0.0443474 94	A	84062	0.022417 807	10297773 0	intronic	NA	NA	NA	NA
CD	L2_colonic	imm_2_10235 8511	rs227029 8	0.0446	G	2162	1.197	10299207 9	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10236 1316	rs170270 37	0.0446	G	2162	1.197	10299488 4	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10236 3237	rs116837 00	0.0446	A	2162	1.197	10299680 5	intronic	IL1RL1	- 0.067250 733	0.043692 753	0

FIG. 1MMMM

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L2_colonic	imm_2_10236 3304	rs382120 3	0.0446	A	2162	1.197	10299687 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10236 5744	rs562584 75	0.0446	G	2162	1.197	10299931 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10237 2819	rs485157 0	0.0446	G	2162	1.197	10300638 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10237 3999	rs170270 60	0.0446	G	2162	1.197	10300756 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L2_colonic	imm_2_10237 7020	rs228703 4	0.0446	A	2162	1.197	10301058 8	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	L1 B2a+B2b vs B1	imm_2_10238 1128	rs156868 1	0.04462	G	6002	1.177	10301469 6	UTR3	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10232 4148	rs142010 1	0.04465	A	6001	0.8599	10295771 6	intronic	NA	NA	NA	NA
CD	Time to Second Surgery	imm_2_10236 9697	rs224111 6	0.0447271	A	181	0.740343	10300326 5	intronic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	imm_2_10233 8096	rs980796 2	0.04483	G	2252	1.141	10297166 4	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10230 2563	rs116904 43	0.04487	A	1420	0.6205	10293613 1	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10237 5142	rs127121 45	0.04493	A	6000	1.177	10300871 0	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10237 4055	rs386044 4	0.04539	A	6002	1.176	10300762 3	intronic	NA	NA	NA	NA

FIG. 1NNNN

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L1 B2a+B2b vs B1	imm_2_10238 2476	rs111239 26	0.04559	C	6002	1.176	10301604 4	downstrea m	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10233 4276	rs111239 23	0.04561	A	2906	0.7488	10296784 4	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 7982	rs155861 9	0.04562	A	1421	0.6218	10293155 0	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10231 5251	rs142010 2	0.04562	A	1421	0.6218	10294881 9	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 7827	rs155862 0	0.04564	G	1420	0.6217	10293139 5	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10231 7909	rs763626 90	0.04571	G	7967	0.8954	10295147 7	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
CD	B3	imm_2_10237 0393	rs377116 1	0.04578	A	2170	1.185	10300396 1	intronic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	B3	imm_2_10237 6326	rs377115 8	0.04578	G	2170	1.185	10300989 4	intronic	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	B3	imm_2_10238 0182	rs373212 7	0.04578	C	2170	1.185	10301375 0	UTR3	IL18R1	0.040366 43	0.035376 172	IL18R1
CD	Asca CD vs. Asca Ctrl	imm_2_10234 4162	rs102048 37	0.04583	A	2252	1.164	10297773 0	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 3518	rs116854 80	0.04587	A	1421	0.622	10292708 6	upstream	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 6579	rs155862 2	0.04587	A	1421	0.622	10293014 7	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 6812	rs101892 02	0.04587	G	1421	0.622	10293038 0	intronic	NA	NA	NA	NA

FIG. 10000

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
CD	Pyoderma G	imm_2_10229 7089	rs101919 14	0.04587	G	1421	0.622	10293065 7	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10229 8358	rs130207 93	0.04587	A	1421	0.622	10293192 6	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10230 1669	rs111239 18	0.04587	G	1421	0.622	10293523 7	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10230 3914	rs414213 2	0.04587	A	1421	0.622	10293748 2	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10230 5866	rs142008 8	0.04587	G	1421	0.622	10293943 4	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10231 5371	rs124663 80	0.04587	G	1421	0.622	10294893 9	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10238 6351	rs103512 7	0.04595	A	5999	1.175	10301991 9	intergenic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10231 7494	rs127121 40	0.04596	A	1421	0.6221	10295106 2	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10231 8230	rs136235 0	0.04603	C	2321	0.8783	10295179 8	intronic	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	imm_2_10234 5460	rs228703 7	0.04625	A	2252	0.8761	10297902 8	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10231 7505	rs199746 7	0.04646	G	1421	0.6226	10295107 3	intronic	NA	NA	NA	NA
CD	Pyoderma G	imm_2_10231 7899	rs199746 6	0.04646	C	1421	0.6226	10295146 7	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10231 7505	rs199746 7	0.04648	G	5997	0.8668	10295107 3	intronic	NA	NA	NA	NA
CD	Paneth-D4 phenotype	imm_2_10231 9499	rs127121 41	0.0468	G	297	-0.809	10295306 7	intronic	NA	NA	NA	NA

FIG. 1PPPP

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	PDM	imm_2_10237 9106	rs170270 71	0.0471	A	2093	1.171	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
CD	Asca CD vs. Asca Ctrl	imm_2_10234 3969	rs671088 5	0.0471	G	2252	0.85	10297753 7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10237 9864	rs377115 7	0.0473460 52	A	94072	0.062386 56	10301343 2	UTR3	NA	NA	NA	NA
CD	IGG Asca CD vs. IGA Asca Ctrl	rs12998521	rs129985 21	0.04742	A	2252	0.8766	10297441 7	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10234 6655	rs114655 72	0.04745	A	7967	0.891	10298022 3	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 54, 0.071599 0.046140 99122702 84	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960	0, 0, 0, 0
CD	L1 B1 vs non-IBD ctrl	imm_2_10234 0561	rs129993 64	0.04747	A	2906	0.7506	10297412 9	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10234 1768	rs129879 77	0.04747	C	2906	0.7506	10297533 6	intronic	NA	NA	NA	NA
CD	L1 B1 vs non-IBD ctrl	imm_2_10234 5460	rs228703 7	0.04747	A	2906	0.7506	10297902 8	intronic	NA	NA	NA	NA

FIG. 1QQQQ

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
CD	L2 colonic	imm_2_10233 1293	rs559272 92	0.04771	A	2162	1.193	10296486 1	intronic	IL1RL1	0.069982 32	0.030542 666	IL1RL1
CD	L1 B1 vs non-IBD ctrl	rs12998521	rs129985 21	0.04782	A	2904	0.7509	10297441 7	intronic	NA	NA	NA	NA
CD	Asca CD vs. Asca Ctrl	imm_2_10237 7761	rs561510 44	0.04792	A	2252	0.8318	10301132 9	intronic	TMEM18 2	0.214216 334	0.038091 085	0
CD	L1 B2a+B2b vs B1	imm_2_10231 7899	rs199746 6	0.04806	C	6002	0.8677	10295146 7	intronic	NA	NA	NA	NA
CD	CD vs. Ctrl	imm_2_10233 6345	rs116885 59	0.0481680 38	A	94036	0.020832 828	10296991 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
CD	CD vs. non-IBD Controls	imm_2_10229 9246	rs791443 24	0.04822	A	7967	0.8967	10293281 4	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
CD	L1 B2a+B2b vs B1	imm_2_10239 9579	rs180778 2	0.04823	G	6002	1.174	10303314 7	intergenic	NA	NA	NA	NA
CD	L2 colonic	imm_2_10233 1764	rs170270 06	0.0484	C	2162	1.193	10296533 2	intronic	IL1RL1	0.066330 072	0.040946 538	IL1RL1
CD	L1 B2a+B2b vs B1	imm_2_10239 1245	rs485100 7	0.0484	A	6001	1.173	10302481 3	intergenic	NA	NA	NA	NA
CD	Smoking_S tatus	imm_2_10233 2499	rs192162 2	0.04853	A	603	1.405	10296606 7	intronic	MAP4K4	0.049614 781	0.016696 387	0
CD	L2 colonic	imm_2_10237 9106	rs170270 71	0.04859	A	2162	1.193	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1RRRR

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	L1 B2a+B2b vs B1	imm_2_10231 7494	rs127121 40	0.04873	A	6002	0.8683	10295106 2	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10235 6166	rs204174 0	0.04889	A	2321	1.138	10298973 4	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10235 9107	rs227029 7	0.04889	A	2321	1.138	10299267 5	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10235 9593	rs675371 7	0.04889	A	2321	1.138	10299316 1	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10236 0488	rs101905 55	0.04889	A	2321	1.138	10299405 6	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10236 1146	rs675002 0	0.04889	G	2321	1.138	10299471 4	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10236 8827	rs375527 4	0.04889	A	2321	1.138	10300239 5	intronic	NA	NA	NA	NA
CD	Cbir CD vs. Cbir Ctrl	imm_2_10236 9475	rs224111 7	0.04889	A	2321	1.138	10300304 3	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10238 6571	rs211066 2	0.04898	A	1051	0.8426	10302013 9	intergenic	IL1RL1	0.060162 739	0.014743 734	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237 1390	rs377115 9	0.04898	G	1051	0.8426	10300495 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237 1762	rs119039 46	0.04898	G	1051	0.8426	10300533 0	intronic	IL1RL1	0.059172 591	0.017080 69	0

FIG. 1SSSS

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237 2880	rs674901 4	0.04898	A	1051	0.8426	10300644 8	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237 5146	rs127121 46	0.04898	A	1051	0.8426	10300871 4	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237 5969	rs485100 4	0.04898	A	1051	0.8426	10300953 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237 6094	rs673213 8	0.04898	A	1051	0.8426	10300966 2	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10237 7669	rs228703 3	0.04898	G	1051	0.8426	10301123 7	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10238 2119	rs142009 4	0.04898	A	1051	0.8426	10301568 7	downstrea m	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10238 4484	rs373212 4	0.04898	A	1051	0.8426	10301805 2	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10238 5432	rs485157 1	0.04898	A	1051	0.8426	10301900 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10238 6217	rs103512 9	0.04898	G	1051	0.8426	10301978 5	intergenic	IL1RL1	0.059172 591	0.017080 69	0

FIG. 1TTTT

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10239 1092	rs758914 2	0.04898	G	1051	0.8426	10302466 0	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10239 4083	rs102009 52	0.04898	C	1051	0.8426	10302765 1	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10239 8001	rs159245 9	0.04898	G	1051	0.8426	10303156 9	intergenic	IL1RL1	0.059172 591	0.017080 69	0
CD	CD vs. non-IBD Controls	imm_2_10237 3483	rs170270 56	0.0493	A	7967	0.8423	10300705 1	intronic	NA	NA	NA	NA
CD	L3 B2a+B2b vs non-IBD ctrl	imm_2_10236 0765	rs204173 9	0.04934	A	1051	0.8428	10299433 3	intronic	IL1RL1	0.059172 591	0.017080 69	0
CD	CD vs. Ctrl	imm_2_10231 7899	rs199746 6	0.0497181 32	G	94091	0.020015 126	10295146 7	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10235 9107	rs227029 7	0.04974	A	6002	1.172	10299267 5	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10235 9593	rs675371 7	0.04974	A	6002	1.172	10299316 1	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10236 0488	rs101905 55	0.04974	A	6002	1.172	10299405 6	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10236 1146	rs675002 0	0.04974	G	6002	1.172	10299471 4	intronic	NA	NA	NA	NA

FIG. 1UUUU

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl_beta	eqtl_p	priority
CD	L1 B2a+B2b vs B1	imm_2_10236 8827	rs3755274	0.04974	A	6002	1.172	103002395	intronic	NA	NA	NA	NA
CD	L1 B2a+B2b vs B1	imm_2_10236 9475	rs2241117	0.04974	A	6002	1.172	103003043	intronic	NA	NA	NA	NA
CD	Paneth-D1 phenotype	imm_2_10234 3118	rs76022452	0.04983	A	297	1.97	102976686	intronic	NA	NA	NA	NA
CD	Paneth-D1 phenotype	imm_2_10239 2402	rs115715837	0.04983	A	297	1.97	103025970	intergenic	NA	NA	NA	NA
CD	Paneth-D1 phenotype	imm_2_10229 7959	rs114275869	0.04983	G	297	1.97	102931527	intronic	NA	NA	NA	NA
CD	Paneth-D1 phenotype	imm_2_10230 1640	rs78535598	0.04983	A	297	1.97	102935208	intronic	NA	NA	NA	NA
CD	Paneth-D1 phenotype	imm_2_10232 0927	rs78841971	0.04983	G	297	1.97	102954495	intronic	NA	NA	NA	NA
CD	B3	imm_2_10233 7597	rs56386507	0.04984	A	2170	0.8435	102971165	intronic	IL1RL1	0.067510094	0.037554638	IL1RL1
CD	Asca CD vs. Asca Ctrl	imm_2_10234 1196	rs10170583	0.04984	A	2252	1.137	102974764	intronic	NA	NA	NA	NA
CD	CD vs. non-IBD Controls	imm_2_10238 2648	rs55664618	0.05256	A	7967	0.9294	103016216	downstream	IL1RL1	0.055883857	0.041785706	0
CD	CD vs. non-IBD Controls	imm_2_10232 8361	rs1946131	0.05452	A	7966	0.8939	102961929	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.0841962068519057, 0.0522514054377319,	0.0202861227094196, 0.0335291660561106,	0, 0, 0, 0

FIG. 1VVVV

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.182483 69615647 6, 0.071599 60571287 88	0.044536 41274960 54, 0.046140 99122702 84	
											0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	
CD	CD vs. non-IBD Controls	imm_2_10232 2694	rs130227 99	0.06155	G	7967	0.8922	10295626 2	intronic	RPL31, TMEM18 2			0, 0
											0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	
CD	CD vs. non-IBD Controls	imm_2_10232 5512	rs130167 71	0.06155	A	7967	0.8922	10295908 0	intronic	RPL31, TMEM18 2			0, 0
											0.183805 83508376 3, 0.072846 56664620 62, 0.137933 54023836 9, 0.044269 31647866 52, 0.063773 12169075 73	0.025156 57045410 81, 0.026697 12994903 49, 0.038090 48430715 86, 0.046927 56736444 61, 0.049859 99527230 28	
CD	CD vs. non-IBD Controls	imm_2_10235 3645	rs114655 97	0.06547	G	7967	0.9001	10298721 3	intronic	RPL31, MAP4K4, CNOT11, TMEM18 2, RPL31			0, 0, 0, 0, 0

FIG. 1W

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. non-IBD Controls	imm_2_10234 7450	rs105159 21	0.06602	C	7967	0.905	10298101 8	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 98393204 15	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	0, 0, 0
CD	CD vs. non-IBD Controls	imm_2_10230 3976	rs101891 54	0.06705	A	7966	1.098	10293754 4	intronic	IL18R1	- 0.041927 743	0.040233 926	0
CD	CD vs. non-IBD Controls	imm_2_10230 1406	rs101794 58	0.06787	A	7967	1.098	10293497 4	intronic	IL18R1	- 0.041927 743	0.040233 926	0
CD	CD vs. non-IBD Controls	imm_2_10229 8044	rs728236 35	0.06946	G	7967	1.097	10293161 2	intronic	IL18R1	- 0.041927 743	0.040233 926	0
CD	CD vs. non-IBD Controls	imm_2_10229 8944	rs950881	0.07084	A	7964	1.097	10293251 2	intronic	IL18R1	- 0.041927 743	0.040233 926	0
CD	CD vs. non-IBD Controls	imm_2_10234 9061	rs114655 84	0.07403	A	7967	0.9075	10298262 9	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 98393204 15	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	0, 0, 0

FIG. 1XXXX

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. non-IBD Controls	imm_2_10234 8465	rs728236 69	0.08181	A	7967	1.093	10298203 3	intronic	IL18R1	0.041927 743	0.040233 926	IL18R1
CD	CD vs. non-IBD Controls	imm_2_10232 0049	rs377118 0	0.08233	A	7967	1.093	10295361 7	intronic	IL18R1	0.041927 743	0.040233 926	0
CD	CD vs. non-IBD Controls	imm_2_10233 0381	rs130289 93	0.09159	G	7966	0.9066	10296394 9	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
CD	CD vs. non-IBD Controls	imm_2_10234 0760	rs561790 05	0.0948	A	7967	1.089	10297432 8	intronic	IL18R1	0.041927 743	0.040233 926	IL18R1
CD	CD vs. non-IBD Controls	imm_2_10235 3793	rs757973 7	0.0949	G	7967	0.9359	10298736 1	intronic	IL1RL1, IL1R1	0.062593 42627782 42, 0.033745 39374329 71	0.020438 98041109 64, 0.037319 11651842 61	0, 0
CD	CD vs. non-IBD Controls	imm_2_10232 7798	rs130140 44	0.09642	G	7967	0.908	10296136 6	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0

FIG. 1YYYY

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
CD	CD vs. non-IBD Controls	imm_2_10232 9171	rs129891 97	0.09642	A	7967	0.908	10296273 9	intronic	RPL31, RPL31, TMEM18 2	0.086163	0.013815	0, 0, 0
											09453828	65927969	
											11, 0.196351 87035986	0.026913 52129718	
CD	CD vs. non-IBD Controls	imm_2_10233 0060	rs129960 97	0.09642	A	7967	0.908	10296362 8	intronic	RPL31, RPL31, TMEM18 2	0.086163	0.013815	0, 0, 0
											09453828	65927969	
											11, 0.196351 87035986	0.026913 52129718	
CD	CD vs. non-IBD Controls	imm_2_10233 1824	rs129995 42	0.09642	C	7967	0.908	10296539 2	intronic	RPL31, RPL31, TMEM18 2	0.086163	0.013815	0, 0, 0
											09453828	65927969	
											11, 0.196351 87035986	0.026913 52129718	
IBD	IBD vs. Ctrl	imm_2_10230 5468	rs130013 25	3.67E-30	A	128356	0.098880 788	10293903 6	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10232 4148	rs142010 1	4.12E-30	A	128415	0.098806 47	10295771 6	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 5593	rs124792 10	7.96E-30	A	128424	0.098296 035	10294916 1	intronic	NA	NA	NA	NA

FIG. 1ZZZZ

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10234 1768	rs129879 77	3.00E-29	C	128443	0.096278 493	10297533 6	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 8258	rs130205 53	3.31E-29	G	128429	0.097206 781	10293182 6	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 8994	rs950880				0.097170 905	10293256 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234 0561	rs129993 64	3.64E-29	A	128422	0.096133 294	10297412 9	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234 5460	rs228703 7	4.75E-29	A	123133	0.098525 881	10297902 8	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	rs12998521	rs129985 21	6.84E-28	A	126705	0.094620 715	10297441 7	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 7254	rs130190 81	1.19E-27	C	124874	0.096173 343	10295082 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10232 3964	rs373212 9	4.23E-27	G	128430	0.101647 477	10295753 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10232 2292	rs377117 7	4.33E-27	A	128438	0.101628 97	10295586 0	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10232 2115	rs873022	4.42E-27	A	128438	0.101610 659	10295568 3	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 8792	rs170269 74	8.74E-27	A	128409	0.100686 347	10295236 0	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 5251	rs142010 2	2.10E-26	G	128385	0.088328 518	10294881 9	intronic	NA	NA	NA	NA

FIG. 1A AAAA

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10233 1174	rs130174 55	2.69E-26	A	125514	0.092932 136	10296474 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 9499	rs127121 41	2.77E-26	A	128443	0.088078 914	10295306 7	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10230 5866	rs142008 8	4.16E-26	A	128434	0.087762 381	10293943 4	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 7982	rs155861 9	4.44E-26	C	128433	0.087709 429	10293155 0	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 5371	rs124663 80	4.96E-26	A	128438	0.087625 645	10294893 9	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 7505	rs199746 7	5.39E-26	A	128423	0.087562 386	10295107 3	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10230 2563	rs116904 43	8.81E-26	T	128429	0.087174 567	10293613 1	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10230 3914	rs414213 2	1.05E-25	G	128437	0.087043 518	10293748 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233 4276	rs111239 23	1.13E-25	A	128409	0.090002 416	10296784 4	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 7380	rs127121 35	1.20E-25	A	128436	0.086938 94	10293094 8	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 8230	rs136235 0	1.24E-25	G	127309	0.087621 728	10295179 8	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10230 3413	rs974389	1.70E-25	G	128439	0.086660 895	10293698 1	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 8234	rs129965 05	2.09E-25	A	128438	0.086817 134	10293180 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 3518	rs116854 80	2.48E-25	G	128411	0.086358 4	10292708 6	upstream	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 3413	rs116854 24	2.54E-25	G	128439	0.086339 944	10292698 1	upstream	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10230 6844	rs670684 4	2.55E-25	A	128412	0.086377 784	10294041 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 8679	rs101833 88	2.74E-25	G	128439	0.086284 126	10293224 7	intronic	NA	NA	NA	NA

FIG. 1BBBBB

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Chr2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
IBD	IBD vs. Ctrl	imm_2_10229_8358	rs13020793	2.78E-25	G	128421	0.086267249	102931926	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229_7313	rs10189711	2.99E-25	A	128434	0.086245847	102930881	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229_6579	rs1558622	4.36E-25	G	128397	0.085945027	102930147	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229_5444	rs6733174	4.58E-25	A	128441	0.086187567	102929012	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229_6812	rs10189202	6.13E-25	A	128443	0.085638919	102930380	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229_7089	rs10191914	6.13E-25	A	128440	0.085638919	102930657	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10232_0622	rs59247511	7.00E-25	A	122976	0.087564876	102954190	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10230_1669	rs11123918	7.91E-25	A	127911	0.085663138	102935237	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235_0711	rs1420098	1.03E-24	G	120004	0.09062335	102984279	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233_1764	rs17027006	1.30E-24	C	128437	0.09667698	102965332	intronic	IL1RL1	0.066330072	0.040946538	IL1RL1
IBD	IBD vs. Ctrl	imm_2_10234_3969	rs6710885	1.30E-24	G	121235	0.09024457	102977537	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233_2499	rs1921622	1.66E-24	G	128426	0.085291013	102966067	intronic	MAP4K4	0.049614781	0.016696387	0
IBD	IBD vs. Ctrl	imm_2_10233_2303	rs12469506	3.08E-24	A	128441	0.095882552	102965871	intronic	IL1RL1	0.065931376	0.047728888	IL1RL1
IBD	IBD vs. Ctrl	imm_2_10236_1452	rs2080289	4.24E-24	A	128393	0.095580947	102995020	intronic	IL1RL1	0.067250733	0.043692753	0
IBD	IBD vs. Ctrl	imm_2_10237_2819	rs4851570	4.82E-24	G	128424	0.095462395	103006387	intronic	IL1RL1	0.067250733	0.043692753	0

FIG. 1CCCCC

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10235 2382	rs377117 1	4.91E-24	G	127351	0.096005 088	10298595 0	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235 2244	rs377117 2	5.03E-24	A	128434	0.095391 676	10298581 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10238 2350	rs170270 87	6.61E-24	A	128442	0.095171 195	10301591 8	downstrea m	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10235 2586	rs216020 2	7.05E-24	A	127368	0.095669 087	10298615 4	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10239 1170	rs485100 6	7.18E-24	A	127366	0.095682 243	10302473 8	intergenic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233 1293	rs559272 92	7.63E-24	A	128397	0.095003 584	10296486 1	intronic	IL1RL1	0.069982 32	0.030542 666	IL1RL1
IBD	IBD vs. Ctrl	imm_2_10229 7827	rs155862 0	7.75E-24	A	124132	0.084775 307	10293139 5	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10237 7020	rs228703 4	7.94E-24	A	128430	0.094999 873	10301058 8	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10236 3304	rs382120 3	8.17E-24	A	128369	0.094972 916	10299687 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10237 3999	rs170270 60	8.34E-24	G	128438	0.094953 622	10300756 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10236 5744	rs562584 75	8.42E-24	G	128385	0.094944 895	10299931 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10236 1316	rs170270 37	8.51E-24	G	128418	0.094935 542	10299488 4	intronic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1DDDDDD

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10235 8511	rs227029 8	1.04E-23	G	128440	0.094745 625	10299207 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10238 4509	rs373212 3	1.12E-23	G	128437	0.094677 857	10301807 7	intergenic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10237 9106	rs170270 71	1.57E-23	A	128442	0.094325 862	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10236 3237	rs116837 00	1.70E-23	A	128441	0.094292 346	10299680 5	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10236 4165	rs114656 33	4.50E-23	A	127248	0.093989 209	10299773 3	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10231 8404	rs136234 9	7.15E-23	G	121312	0.084155 425	10295197 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 9984	rs196817 1	1.11E-22	NA	NA	0.084401 483	10293355 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10238 0394	rs373212 6	1.41E-22	C	124130	0.093747 072	10301396 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10238 0734	rs113535 4	1.57E-22	C	128411	0.092014 287	10301430 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10239 0763	rs558831 25	1.97E-21	A	124115	0.090889 909	10302433 1	intergenic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10233 6239	rs677237 47	4.51E-21	NA	NA	0.092135 645	10296980 7	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10236 0488	rs101905 55	1.68E-20	A	127048	0.090406 892	10299405 6	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10236 7834	rs103513 0	5.72E-20	A	121324	0.088430 571	10300140 2	exonic	NA	NA	NA	NA

FIG. 1E-EEEE

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
IBD	IBD vs. Ctrl	imm_2_10238_6351	rs1035127	6.61E-20	A	128385	0.088476633	103019919	intergenic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10237_5142	rs12712145	1.78E-19	A	128424	0.087436993	103008710	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10236_9475	rs2241117	3.85E-19	A	128442	0.086578323	103003043	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10236_8827	rs3755274	4.37E-19	A	128437	0.086442672	103002395	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10238_1128	rs1568681	4.73E-19	G	128410	0.086395644	103014696	UTR3	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235_9107	rs2270297	4.75E-19	A	128426	0.086352238	102992675	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10237_4055	rs3860444	5.24E-19	A	128415	0.086253947	103007623	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235_1856	rs2058622	5.25E-19	A	128439	0.086277322	102985424	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10236_1146	rs6750020	5.87E-19	G	128434	0.086125054	102994714	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10239_1245	rs4851007	6.34E-19	A	128428	0.086074298	103024813	intergenic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235_9593	rs6753717	7.11E-19	A	128424	0.085949895	102993161	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10239_9579	rs1807782	9.01E-19	G	128384	0.085603395	103033147	intergenic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10239_1635	rs4851575	1.70E-18	G	127285	0.085681257	103025203	intergenic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235_1116	rs1558627	2.40E-18	G	126175	0.085574863	102984684	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10238_2648	rs55664618	2.61E-18	A	128443	0.072955858	103016216	downstream	IL1RL1	0.055883857	0.041785706	0
IBD	IBD vs. Ctrl	imm_2_10233_8297	rs13015714	2.98E-18	C	128429	0.084386105	102971865	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235_6166	rs2041740	8.03E-17	A	124067	0.081799982	102989734	intronic	NA	NA	NA	NA

FIG. 1FFFFF

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Chr2	snp location	cis_eGE	eqtl beta	eqtl p	priority
IBD	IBD vs. Ctrl	imm_2_10231_5064	rs1420103	3.30E-15	A	128436	0.075416 507	102948632	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229_4158	rs6543116	1.18E-14	A	128409	0.073868 574	102927726	upstream	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10237_7984	rs4851005	8.43E-12	A	128361	0.059963 6	103011552	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10233_2499	rs1921622	8.43E-09	G	9366	1.203	1029666067	intronic	MAP4K4	0.049614781	0.016696387	0
IBD	IBD vs. non-IBD Controls	imm_2_10232_4148	rs1420101	7.37E-07	A	9365	0.846	102957716	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10234_0561	rs12999364	9.29E-07	A	9366	0.848	102974129	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10234_1768	rs12987977	9.36E-07	C	9366	0.8481	102975336	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10230_5468	rs13001325	9.53E-07	A	9366	0.8475	102939036	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10231_5593	rs12479210	9.95E-07	A	9366	0.8477	102949161	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10234_5460	rs2287037	1.12E-06	A	9364	0.849	102979028	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10233_4276	rs11123923	1.13E-06	A	9366	0.8491	102967844	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_8258	rs13020553	1.15E-06	G	9365	0.8486	102931826	intronic	NA	NA	NA	NA

FIG. 1GGGGG

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. non-IBD Controls	imm_2_10229 8994	rs950880	1.19E-06	A	9366	0.8487	10293256 2	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	rs12998521	rs129985 21	1.19E-06	A	9364	0.8494	10297441 7	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10232 6078	rs621526 61	1.69E-05	G	128435	0.059277 456	10295964 6	intronic	IL1R2, IL1RL2	0.231497 33812603 4, 0.122966 17855485 1	0.040373 08383166 27, 0.045654 18745379 71	0, 0
IBD	IBD vs. Ctrl	imm_2_10230 4821	rs142008 9	1.71E-05	G	128433	0.059176 026	10293838 9	intronic	IL1R2, IL1RL2	0.231497 33812603 4, 0.122966 17855485 1	0.040373 08383166 27, 0.045654 18745379 71	0, 0
IBD	IBD vs. Ctrl	imm_2_10233 1585	rs176963 76	2.17E-05	A	128437	0.058757 136	10296515 3	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
IBD	IBD vs. Ctrl	imm_2_10234 0654	rs121058 08	2.26E-05	T	128437	0.058763 565	10297422 2	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0

FIG. 1HHHHHH

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. non-IBD Controls	imm_2_10235 1116	rs155862 7	3.23E-05	G	9355	1.169	10298468 4	intronic	NA	NA	NA	NA
	IBD vs. non-IBD Controls	imm_2_10235 2412	rs377117 0	3.41E-05	A	9365	1.168	10298598 0	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10237 9334	rs142009 5	3.44E-05	G	128411	0.062511 542	10301290 2	intronic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	0, 0, 0, 0, 0, 0, 0
	IBD vs. non-IBD Controls	imm_2_10235 1856	rs205862 2	3.49E-05	A	9366	1.168	10298542 4	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10236 9466	rs560300 66	3.90E-05	C	128443	0.062309 423	10300303 4	intronic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, -	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87,	0, 0, 0, 0, 0, 0, 0

FIG. 1IIII

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.263402 64500044 6	0.033428 43922870 19	
IBD	IBD vs. non-IBD Controls	imm_2_10233 8297	rs130157 14	4.67E-05	C	9363	1.165	10297186 5	intronic	NA	NA	NA	NA
											0.049683 04632082 74, 85, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	
IBD	IBD vs. Ctrl	imm_2_10233 5102	rs782486 80	5.94E-05	G	128435	0.055949 959	10296867 0	intronic	IL1R1, IL1R2, IL1RL2			0, 0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10238 2476	rs111239 26	6.24E-05	C	9366	1.161	10301604 4	downstrea m	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10235 9107	rs227029 7	6.63E-05	A	9366	1.16	10299267 5	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10235 9593	rs675371 7	6.63E-05	A	9366	1.16	10299316 1	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10236 0488	rs101905 55	6.63E-05	A	9366	1.16	10299405 6	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10236 1146	rs675002 0	6.63E-05	G	9366	1.16	10299471 4	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10236 8827	rs375527 4	6.63E-05	A	9366	1.16	10300239 5	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10236 9475	rs224111 7	6.63E-05	A	9366	1.16	10300304 3	intronic	NA	NA	NA	NA

FIG. 1JJJJ

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. non-IBD Controls	imm_2_10231 8792	rs170269 74	6.77E-05	A	9366	0.8605	10295236 0	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10237 5142	rs127121 45	6.84E-05	A	9364	1.16	10300871 0	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10237 4055	rs386044 4	6.93E-05	A	9366	1.16	10300762 3	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10238 1128	rs156868 1	7.03E-05	G	9366	1.16	10301469 6	UTR3	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10232 8773	rs621526 62	7.88E-05	A	127038	0.055099 604	10296234 1	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 0.046936 06576706 77	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10239 1245	rs485100 7	7.91E-05	A	9364	1.158	10302481 3	intergenic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10239 9579	rs180778 2	8.18E-05	G	9366	1.158	10303314 7	intergenic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10232 2292	rs377117 7	8.37E-05	A	9364	0.8621	10295586 0	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10232 2115	rs873022	8.44E-05	A	9366	0.8622	10295568 3	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10232 3964	rs373212 9	8.44E-05	G	9366	0.8622	10295753 2	intronic	NA	NA	NA	NA

FIG. 1L L L L L

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. non-IBD Controls	imm_2_10236 1452	rs208028 9	0.0002976	A	9364	0.8722	10299502 0	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10235 2244	rs377117 2	0.0003058	A	9366	0.8724	10298581 2	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10235 8511	rs227029 8	0.0003167	G	9366	0.8727	10299207 9	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10236 3304	rs382120 3	0.0003167	A	9366	0.8727	10299687 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10236 5744	rs562584 75	0.0003167	G	9366	0.8727	10299931 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10237 2819	rs485157 0	0.0003167	G	9366	0.8727	10300638 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10237 3999	rs170270 60	0.0003167	G	9366	0.8727	10300756 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10238 4509	rs373212 3	0.0003169	G	9366	0.8727	10301807 7	intergenic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10233 1764	rs170270 06	0.0003329	C	9366	0.8729	10296533 2	intronic	IL1RL1	0.066330 072	0.040946 538	IL1RL1
IBD	IBD vs. non-IBD Controls	imm_2_10231 9499	rs127121 41	0.0003265	A	9366	1.124	10295306 7	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10237 7020	rs228703 4	0.0003369	A	9365	0.8732	10301058 8	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10236 1316	rs170270 37	0.0003456	G	9366	0.8735	10299488 4	intronic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1MMMMM

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. non-IBD Controls	imm_2_10238 0734	rs113535 4	0.0003517	C	9362	0.8737	10301430 2	UTR3	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. non-IBD Controls	imm_2_10233 2303	rs124695 06	0.0003542	A	9366	0.8737	10296587 1	intronic	IL1RL1	0.065931 376	0.047728 888	IL1RL1
IBD	IBD vs. non-IBD Controls	imm_2_10236 3237	rs116837 00	0.0003827	A	9366	0.8743	10299680 5	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10233 4360	rs498895 5	0.0004037 49	G	128413	0.030203 133	10296792 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
IBD	IBD vs. Ctrl	imm_2_10233 8096	rs980796 2	0.0004151 53	G	127307	0.030388 214	10297166 4	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233 7738	rs980845 3	0.0004226 42	A	128328	0.030100 368	10297130 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
IBD	IBD vs. Ctrl	imm_2_10233 3668	rs134240 06	0.0004262 65	G	128431	0.030067 988	10296723 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
IBD	IBD vs. Ctrl	imm_2_10233 6537	rs116956 27	0.0004956 56	G	127909	0.029821 196	10297010 5	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
IBD	IBD vs. non-IBD Controls	imm_2_10233 1293	rs559272 92	0.0005418	A	9365	0.8776	10296486 1	intronic	IL1RL1	0.069982 32	0.030542 666	IL1RL1
IBD	IBD vs. non-IBD Controls	imm_2_10237 9106	rs170270 71	0.0005512	A	9366	0.8777	10301267 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
IBD	IBD vs. Ctrl	imm_2_10235 2654	rs377116 6	0.0005569 75	A	128393	0.029481 767	10298622 2	intronic	IL1RL1	0.053336 426	0.042506 604	0
IBD	IBD vs. Ctrl	imm_2_10234 1482	rs101731 93	0.0006049 99	A	128395	0.029290 608	10297505 0	intronic	IL1RL1	0.053336 426	0.042506 604	0
IBD	IBD vs. Ctrl	imm_2_10234 7408	rs114655 75	0.0006494 64	G	127363	0.094773 504	10298097 6	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233 9231	rs485156 6	0.0006686 35	C	126710	0.029265 738	10297279 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
IBD	IBD vs. Ctrl	imm_2_10234 6056	rs930885 7	0.0006729 59	A	128434	0.029043 412	10297962 4	intronic	IL1RL1	0.053336 426	0.042506 604	0

FIG. 1NNNNN

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
IBD	IBD vs. Ctrl	imm_2_10235_2807	rs1974675	0.000783694	A	128436	0.028685275	10298637	intronic	IL1RL1	0.053336426	0.042506604	0
IBD	IBD vs. non-IBD Controls	imm_2_10231_7505	rs1997467	0.0008366	A	9361	1.115	10295107	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233_3845	rs6751967	0.000873963	G	128440	0.028404096	10296741	intronic	IL1RL1	0.053336426	0.042506604	IL1RL1
IBD	IBD vs. non-IBD Controls	imm_2_10231_7899	rs1997466	0.0009135	G	9365	1.114	10295146	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10231_7494	rs12712140	0.0009707	C	9366	1.113	10295106	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10230_3914	rs4142132	0.00101	G	9364	1.113	10293748	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10231_5371	rs12466380	0.00105	A	9365	1.112	10294893	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10230_5866	rs1420088	0.001051	A	9366	1.112	10293943	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10231_5251	rs1420102	0.001067	G	9366	1.112	10294881	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_3518	rs11685480	0.001087	G	9366	1.112	10292708	upstream	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_6579	rs1558622	0.001087	G	9366	1.112	10293014	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_6812	rs10189202	0.001087	A	9366	1.112	10293038	intronic	NA	NA	NA	NA

FIG. 1000000

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
IBD	IBD vs. non-IBD Controls	imm_2_10229_8358	rs13020793	0.001088	G	9365	1.112	102931926	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_7089	rs10191914	0.001123	A	9366	1.111	102930657	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_7982	rs1558619	0.001143	C	9366	1.111	102931550	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10230_1669	rs11123918	0.001147	A	9365	1.111	102935237	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10230_2563	rs11690443	0.001151	T	9357	1.111	102936131	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234_3628	rs6543123	0.0012648	A	117767	0.028792478	102977196	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234_6655	rs11465572	0.001281995	A	128427	0.043279714	102980223	intronic	MAP4K4, TMEM182, RPL31, RPL31	0.0841962068519057, 0.0522514054377319, 0.182483696156476, 0.07159900461409912270284	0.0202861227094196, 0.0335291660561106, 0.0445364127496054, 0.0461409912270284	0, 0, 0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10229_8679	rs10183388	0.001332	G	9365	1.11	102932247	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_8234	rs12996505	0.001334	A	9366	1.11	102931802	intronic	NA	NA	NA	NA

FIG. 1PPPPP

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10233 7913	rs485156 5	0.0014609 98	A	115855	0.028572 905	10297148 1	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235 1056	rs136234 8	0.0015445 19	G	123086	0.027649 527	10298462 4	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233 6345	rs116885 59	0.0015965 62	A	128358	0.027045 71	10296991 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
											0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, MAP4K4, TMEM18 0.071599 60571287 88	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140 99122702 84	0, 0, 0, 0
IBD	IBD vs. Ctrl	imm_2_10232 8361	rs194613 1	0.0016430 53	A	128332	0.042451 676	10296192 9	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.053336 426	0.042506 604	IL1RL1
IBD	IBD vs. Ctrl	imm_2_10233 4290	rs675248 2	0.0017306 11	G	128407	0.026936 07	10296785 8	intronic	IL1RL1	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229 3413	rs116854 24	0.001776	G	9366	1.107	10292698 1	upstream	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229 5444	rs673317 4	0.001776	A	9366	1.107	10292901 2	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229 7313	rs101897 11	0.001776	A	9366	1.107	10293088 1	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10230 3413	rs974389	0.001871	G	9366	1.106	10293698 1	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10237 7761	rs561510 44	0.0019175 2	A	128404	0.045508 346	10301132 9	intronic	TMEM18 2	0.214216 334	0.038091 085	0

FIG. 1QQQQQ

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
IBD	IBD vs. non-IBD Controls	imm_2_10230_6844	rs6706844	0.001935	A	9366	1.106	102940412	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234_1343	rs76721133	0.001962243	C	128441	0.131283383	102974911	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10235_3891	rs6543124	0.001995255	A	128345	0.026477762	102987459	intronic	IL1RL1	0.053489519	0.039961127	0
IBD	IBD vs. Ctrl	imm_2_10232_9171	rs12989197	0.00209727	A	128408	0.041392393	102962739	intronic	RPL31, RPL31, TMEM182	0.0861630945382811, 0.196351870359868, 0.0475017877204885	0.0138156592796922, 0.026913521297184, 0.0485345852467778	0, 0, 0
IBD	IBD vs. Ctrl	imm_2_10239_0028	rs78178597	0.00210633	A	122067	0.031810852	103023596	intergenic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234_4162	rs10204837	0.002324195	A	116243	0.027560765	102977730	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10229_7380	rs12712135	0.002429	A	9366	1.103	102930948	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234_4891	rs3755276	0.002433043	A	124136	0.026240744	102978459	intronic	IL1RL1	0.053336426	0.042506604	0
IBD	IBD vs. Ctrl	imm_2_10236_8082	rs17651485	0.002513254	A	128423	0.04427545	103001650	intronic	TMEM182	0.214216334	0.038091085	0
IBD	IBD vs. Ctrl	imm_2_10232_7798	rs13014044	0.002599135	G	128415	0.040433125	102961366	intronic	RPL31, RPL31, TMEM182	0.0861630945382811, 0.196351870359868, 0.0475017877204885	0.0138156592796922, 0.026913521297184, 0.0485345852467778	0, 0, 0

FIG. 1RRRRR

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											78772048 85	58524677 78	
IBD	IBD vs. Ctrl	imm_2_10237 9864	rs377115 7	0.0026994 78	A	128403	0.076596 306	10301343 2	UTR3	NA	NA	NA	NA
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
IBD	IBD vs. Ctrl	imm_2_10233 0381	rs130289 93	0.0029678 23	G	128439	0.039880 482	10296394 9	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
IBD	IBD vs. Ctrl	imm_2_10233 0060	rs129960 97	0.0031650 86	A	128413	0.039603 477	10296362 8	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0
IBD	IBD vs. Ctrl	imm_2_10232 8782	rs105409 6	0.0032523 5	G	128200	0.039505 477	10296235 0	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10234 1196	rs101705 83	0.0034702 49	A	121317	0.025597 9	10297476 4	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 7754	rs754520 14	0.0035614 93	A	128377	0.118676 494	10293132 2	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10237 7984	rs485100 5	0.003743	A	9366	0.9032	10301155 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10233 1824	rs129995 42	0.0038109 92	C	128442	0.038807 104	10296539 2	intronic	RPL31, RPL31,	0.086163 09453828 11,	0.013815 65927969 22,	0, 0, 0

FIG. 1SSSSS

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10233 3863	rs670456 5	0.0039400 98	A	128350	0.024850 796	10296743 1	intronic	TMEM18 2	0.196351 87035986 8, 0.047501 78772048 85	0.026913 52129718 4, 0.048534 58524677 78	
IBD	anti-TNF time to loss of response	imm_2_10231 7909	rs763626 90	0.0042448 1	G	344	-2.85937	10295147 7	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
IBD	IBD vs. Ctrl	imm_2_10233 7795	rs130146 44	0.0056335 A		118867	0.038728 363	10297136 3	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.084196 20685190 57, 0.052251 40543773 19, 0.182483 0.044536 69615647 6, 0.071599 60571287 88	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140 99122702 84	0, 0, 0, 0
IBD	anti-TNF time to loss of response	imm_2_10229 9246	rs791443 24	0.0059022 3	A	344	-2.75316	10293281 4	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
IBD	anti-TNF time to loss of response	imm_2_10231 7614	rs118918 27	0.0059022 3	G	344	-2.75316	10295118 2	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 0.035378	0.003507 22414540 951, 0.016098	IL1RL1 , 0

FIG. 1TTTTT

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											8545241 76	12306193 59	
											0.089477 14269207 61, 0.060198 0.018871	0.018208 05166194 05, 0.018871	
IBD	IBD vs. Ctrl	imm_2_10230 4398	rs129877 82	0.0063640 62	A	128433	0.039192 889	10293796 6	intronic	MAP4K4, TMEM18 2	97220702 9	92869050 61	0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10236 9697	rs224111 6	0.006672 A	A	9366	0.8937	10300326 5	intronic	NA	NA	NA	NA
											0.089477 14269207 61, 0.060198 0.018871	0.018208 05166194 05, 0.018871	
IBD	IBD vs. Ctrl	imm_2_10231 4613	rs176956 48	0.0078752 31	G	128442	0.038243 144	10294818 1	intronic	MAP4K4, TMEM18 2	97220702 9	92869050 61	0, 0
											0.089477 14269207 61, 0.060198 0.018871	0.018208 05166194 05, 0.018871	
IBD	IBD vs. Ctrl	imm_2_10231 8649	rs375527 8	0.0079334 77	G	128435	0.038127 87	10295221 7	intronic	MAP4K4, TMEM18 2	97220702 9	92869050 61	0, 0
											0.089477 14269207 61, 0.060198 0.018871	0.018208 05166194 05, 0.018871	
IBD	IBD vs. non-IBD Controls	imm_2_10231 8649	rs375527 8	0.008664 G	G	9366	0.8683	10295221 7	intronic	MAP4K4, TMEM18 2	97220702 9	92869050 61	0, 0
											0.154006 31456082 4, 0.052797 13115951 81,-	0.006657 33914116 06, 0.010799 75270327 78,	IL1RL1 , 0, 0, 0, 0
IBD	IBD vs. Ctrl	imm_2_10231 3976	rs771271 14	0.0092706 51	A	128409	0.053748 117	10294754 4	intronic	IL1RL1, MAP4K4, IL18RAP, CNOT11, MAP4K4	0.135420	0.023225	

FIG. 1UUUUU

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											47625685 3, 0.203509 01597676 2, 0.097682 68462740 83	60255846 7, 0.037112 34476033 54, 0.043278 92676263 28	
IBD	anti-TNF time to loss of response	imm_2_10237 9359	rs114656 55	0.0098280 3	G	344	2.58182	10301292 7	intronic	NA	NA	NA	NA
IBD	anti-TNF time to loss of response	imm_2_10238 4428	rs673628 7	0.0098280 3	G	344	2.58182	10301799 6	intergenic	NA	NA	NA	NA
IBD	anti-TNF time to loss of response	imm_2_10238 6928	rs118919 65	0.0098280 3	A	344	2.58182	10302049 6	intergenic	NA	NA	NA	NA
											0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	
IBD	IBD vs. non-IBD Controls	imm_2_10229 6297	rs130050 49	0.01103	A	9366	0.8721	10292986 5	intronic	MAP4K4, TMEM18 2			0, 0
IBD	anti-TNF time to loss of response	imm_2_10239 2402	rs115715 837	0.0113392	A	344	2.53207	10302597 0	intergenic	NA	NA	NA	NA
											0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	
IBD	IBD vs. non-IBD Controls	imm_2_10231 4613	rs176956 48	0.01154	G	9366	0.8729	10294818 1	intronic	MAP4K4, TMEM18 2			0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10234 6655	rs114655 72	0.01174	A	9366	0.8793	10298022 3	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.084196 20685190 57, 0.052251	0.020286 12270941 96, 0.033529	0, 0, 0, 0

FIG. 1VVVVV

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											40543773 19, 0.182483 69615647 6, 0.071599 60571287 88	16605611 06, 0.044536 41274960 54, 0.046140 99122702 84	
											0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 0.071599 60571287 88	0.020286 12270941 96, 0.033529 16605611 06, 0.04536 41274960 54, 0.046140 99122702 84	
IBD	IBD vs. non-IBD Controls	imm_2_10232 8361	rs194613 1	0.01223	A	9365	0.8797	10296192 9	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	0, 0, 0, 0, 0, 0, 0
IBD	IBD vs. Ctrl	imm_2_10232 2694	rs130227 99	0.0124537 05	G	128427	0.035749 299	10295626 2	intronic	RPL31, TMEM18 2	0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	0, 0, 0, 0, 0, 0, 0
IBD	IBD vs. Ctrl	imm_2_10232 9504	rs654311 9	0.0134976 A	A	127322	0.021419 196	10296307 2	intronic	NA	NA	NA	NA
IBD	IBD vs. Ctrl	imm_2_10229 6297	rs130050 49	0.0138697 7	A	128442	0.035502 022	10292986 5	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0

FIG. 1 WWWWW

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10232 5512	rs130167 71	0.0139637 9	A	128436	0.035115 477	10295908 0	intronic	RPL31, TMEM18 2	0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10230 4398	rs129877 82	0.01445 A	A	9365	0.8775	10293796 6	intronic	MAP4K4, TMEM18 2	0.089477 14269207 61, 0.060198 97220702 9	0.018208 05166194 05, 0.018871 92869050 61	0, 0
IBD	IBD vs. Ctrl	imm_2_10235 4958	rs342160 45	0.0150829 91	A	128421	0.151414 998	10298852 6	exonic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10232 2694	rs130227 99	0.01693 G	G	9366	0.8798	10295626 2	intronic	RPL31, TMEM18 2	0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10232 5512	rs130167 71	0.01693 A	A	9366	0.8798	10295908 0	intronic	RPL31, TMEM18 2	0.080113 65109899 88, 0.054650 28305726 37	0.028513 38003838 03, 0.029259 85864311 15	0, 0
IBD	anti-TNF time to loss of response	imm_2_10231 9876	rs176392 15	0.0179803 A	A	344	-2.36602	10295344 4	intronic	IL1RL1, MAP4K4 5	0.107679 30429227 7, 0.035460 38514225 5	0.005065 12943857 112, 0.011522 77515793 16	IL1RL1 , 0
IBD	anti-TNF time to loss of response	imm_2_10235 3525	rs114655 96	0.0180663 A	A	344	-2.36426	10298709 3	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6,	0.002283 01835533 339,	0, 0, 0

FIG. 1XXXXXX

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
											0.038448 96044717 03, - 0.096712 98393204 15	0.006014 83658512 599, 0.016548 43859053 64	
											0.086163 09453828 11, 0.196351 87035986 8,	0.013815 65927969 22, 0.026913 52129718 4,	
IBD	IBD vs. non-IBD Controls	imm_2_10233 0381	rs130289 93	0.01969	G	9364	0.8878	10296394 9	intronic	RPL31, RPL31, TMEM18 2	0.047501 78772048 85	0.048534 58524677 78	0, 0, 0
											0.086163 09453828 11, 0.196351 87035986 8,	0.013815 65927969 22, 0.026913 52129718 4,	
IBD	IBD vs. non-IBD Controls	imm_2_10232 7798	rs130140 44	0.02156	G	9366	0.8894	10296136 6	intronic	RPL31, RPL31, TMEM18 2	0.047501 78772048 85	0.048534 58524677 78	0, 0, 0
											0.086163 09453828 11, 0.196351 87035986 8,	0.013815 65927969 22, 0.026913 52129718 4,	
IBD	IBD vs. non-IBD Controls	imm_2_10232 9171	rs129891 97	0.02156	A	9366	0.8894	10296273 9	intronic	RPL31, RPL31, TMEM18 2	0.047501 78772048 85	0.048534 58524677 78	0, 0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10233 1824	rs129995 42	0.02156	C	9366	0.8894	10296539 2	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11,	0.013815 65927969 22,	0, 0, 0

FIG. 1YYYYY

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
										TMEM182	0.196351870359868, 0.0475017877204885	0.026913521297184, 0.0485345852467778	
											0.0861630945382811, 0.196351870359868, 0.0475017877204885	0.0138156592796922, 0.026913521297184, 0.0485345852467778	
IBD	IBD vs. non-IBD Controls	imm_2_102330060	rs12996097	0.022	A	9365	0.8897	102963628	intronic	RPL31, RPL31, TMEM182			0, 0, 0
											0.116814314103196, 0.0384480.0060149604471703,- 0.0967120.01654898393204	0.00228301835533339, 0.00601483658512599, 0.0165484385905364	
IBD	anti-TNF time to loss of response	imm_2_102347450	rs10515921	0.0228109	C	344	-2.27659	102981018	intronic	IL1RL1, MAP4K4, IL18RAP			0, 0, 0
											0.116814314103196, 0.0384480.0060149604471703,- 0.0967120.01654898393204	0.00228301835533339, 0.00601483658512599, 0.0165484385905364	
IBD	anti-TNF time to loss of response	imm_2_102349061	rs11465584	0.0228109	A	344	-2.27659	102982629	intronic	IL1RL1, MAP4K4, IL18RAP			0, 0, 0
IBD	IBD vs. non-IBD Controls	imm_2_102382648	rs55664618	0.02296	A	9366	0.9281	103016216	downstream	IL1RL1	-0.055883857	0.041785706	0

FIG. 1ZZZZL

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. Ctrl	imm_2_10235 3645	rs114655 97	0.0251670 23	G	128439	0.029970 974	10298721 3	intronic	RPL31, MAP4K4, CNOT11, TMEM18 2, RPL31	0.183805 83508376 3, 0.072846 56664620 62, 0.137933 54023836 9, 0.044269 31647866 52, 0.063773 12169075 73	0.025156 57045410 81, 0.026697 12994903 49, 0.038090 48430715 86, 0.046927 56736444 61, 0.049859 99527230 28	
IBD	IBD vs. Ctrl	imm_2_10239 6980	rs116123 489	0.0259131 41	A	128389	0.133845 725	10303054 8	intergenic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10232 8782	rs105409 6	0.0285	G	9352	0.8941	10296235 0	intronic	NA	NA	NA	NA
IBD	anti-TNF time to loss of response	imm_2_10234 3118	rs760224 52	0.0353701	A	344	2.1041	10297668 6	intronic	NA	NA	NA	NA
IBD	anti-TNF time to loss of response	imm_2_10229 7959	rs114275 869	0.0353701	G	344	2.1041	10293152 7	intronic	NA	NA	NA	NA
IBD	anti-TNF time to loss of response	imm_2_10230 1640	rs785355 98	0.0353701	A	344	2.1041	10293520 8	intronic	NA	NA	NA	NA
IBD	anti-TNF time to loss of response	imm_2_10232 0927	rs788419 71	0.0353701	G	344	2.1041	10295449 5	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10235 3645	rs114655 97	0.03645	G	9366	0.9007	10298721 3	intronic	RPL31, MAP4K4, CNOT11,	0.183805 83508376 3,	0.025156 57045410 81,	0, 0, 0, 0, 0, 0, 0, 0

FIG. 1A A A A A A

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
										TMEM18 2, RPL31	0.072846 56664620 62, 0.137933 54023836 9, 0.044269 31647866 52, 0.063773 12169075 73	0.026697 12994903 49, 0.038090 48430715 86, 0.046927 56736444 61, 0.049859 99527230 28	
IBD	anti-TNF time to loss of response	imm_2_10238 4560	rs129917 37	0.0374639	T	344	2.08067	10301812 8	intergenic	IL18R1	- 0.040366 43	0.035376 172	IL18R1
IBD	anti-TNF time to loss of response	imm_2_10239 1706	rs101817 85	0.0374639	A	344	2.08067	10302527 4	intergenic	IL18R1	- 0.040366 43	0.035376 172	IL18R1
IBD	anti-TNF time to loss of response	imm_2_10239 2170	rs116877 68	0.0374639	G	344	2.08067	10302573 8	intergenic	IL18R1	- 0.040366 43	0.035376 172	IL18R1
IBD	anti-TNF time to loss of response	imm_2_10239 4498	rs758698 3	0.0374639	A	344	2.08067	10302806 6	intergenic	IL18R1	- 0.040366 43	0.035376 172	IL18R1
IBD	anti-TNF time to loss of response	imm_2_10233 2499	rs192162 2	0.0397877	A	344	-2.05595	10296606 7	intronic	MAP4K4	0.049614 781	0.016696 387	0
IBD vs. non-IBD Controls		imm_2_10230 3976	rs101891 54	0.04235	A	9364	1.095	10293754 4	intronic	IL18R1	0.041927 743	0.040233 926	0
IBD	anti-TNF time to loss of response	imm_2_10235 7080	rs170270 29	0.0428184	G	344	2.02548	10299064 8	intronic	IL18R1	- 0.040366 43	0.035376 172	IL18R1
IBD	anti-TNF time to loss of response	imm_2_10236 4316	rs321373 3	0.0428184	A	344	2.02548	10299788 4	intronic	IL18R1	- 0.040366 43	0.035376 172	IL18R1

FIG. 1BBBBBB

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
IBD	anti-TNF time to loss of response	imm_2_10237_0393	rs3771161	0.0428184	A	344	2.02548	10300396	intronic	IL18R1	0.04036643	0.035376172	IL18R1
IBD	anti-TNF time to loss of response	imm_2_10237_6326	rs3771158	0.0428184	G	344	2.02548	10300989	intronic	IL18R1	0.04036643	0.035376172	IL18R1
IBD	anti-TNF time to loss of response	imm_2_10238_0182	rs3732127	0.0428184	C	344	2.02548	10301375	UTR3	IL18R1	0.04036643	0.035376172	IL18R1
IBD	IBD vs. non-IBD Controls	imm_2_10229_8944	rs950881	0.04469	A	9363	1.094	10293251	intronic	IL18R1	0.041927743	0.040233926	0
IBD	anti-TNF time to loss of response	imm_2_10232_0808	rs985523	0.0448952	A	344	-2.00563	10295437	intronic	IL1RL1, MAP4K4	0.0971334683625956, 0.0304620603987191	0.00992307563826999, 0.0269535983184194	IL1RL1, 0
IBD	anti-TNF time to loss of response	imm_2_10232_4668	rs6719130	0.0448952	A	344	-2.00563	10295823	intronic	IL1RL1, MAP4K4	0.0971334683625956, 0.0304620603987191	0.00992307563826999, 0.0269535983184194	IL1RL1, 0
IBD	IBD vs. non-IBD Controls	imm_2_10230_1406	rs10179458	0.04538	A	9366	1.094	10293497	intronic	IL18R1	0.041927743	0.040233926	0
IBD	IBD vs. non-IBD Controls	imm_2_10229_8044	rs72823635	0.04674	G	9366	1.093	10293161	intronic	IL18R1	0.041927743	0.040233926	0
IBD	IBD vs. non-IBD Controls	imm_2_10232_0049	rs3771180	0.05053	A	9366	1.092	10295361	intronic	IL18R1	0.041927743	0.040233926	0
IBD	IBD vs. non-IBD Controls	imm_2_10234_8465	rs72823669	0.06029	A	9366	1.088	10298203	intronic	IL18R1	0.041927743	0.040233926	IL18R1

FIG. 1CCCCCCC

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
IBD	IBD vs. non-IBD Controls	imm_2_10237 3483	rs170270 56	0.06823	A	9366	0.8735	10300705 1	intronic	NA	NA	NA	NA
IBD	IBD vs. non-IBD Controls	imm_2_10234 0760	rs561790 05	0.0689	A	9366	1.085	10297432 8	intronic	IL18R1	0.041927 743	0.040233 926	IL18R1
IBD	IBD vs. non-IBD Controls	imm_2_10235 3793	rs757973 7	0.07095	G	9366	0.9396	10298736 1	intronic	IL1RL1, IL1R1	0.062593 42627782 42, 0.033745 39374329 71	0.020438 98041109 64, 0.037319 11651842 61	0, 0
IBD	IBD vs. non-IBD Controls	imm_2_10231 7614	rs118918 27	0.08512	G	9364	0.9213	10295118 2	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
IBD	IBD vs. non-IBD Controls	imm_2_10237 5844	rs116791 46	0.0886	G	9366	1.079	10300941 2	intronic	IL18R1	0.046361 422	0.019212 446	IL18R1
IBD	IBD vs. non-IBD Controls	imm_2_10229 9246	rs791443 24	0.09265	A	9366	0.9231	10293281 4	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
IBD	IBD vs. non-IBD Controls	imm_2_10237 7761	rs561510 44	0.09277	A	9366	0.9146	10301132 9	intronic	TMEM18 2	0.214216 334	0.038091 085	0
IBD	IBD vs. non-IBD Controls	imm_2_10234 7450	rs105159 21	0.0941	C	9366	0.9246	10298101 8	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,-	0.002283 01835533 339, 0.006014 83658512 599,	0, 0, 0

FIG. 1DDDDDD

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.096712 98393204 15	0.016548 43859053 64	
IBD	IBD vs. non-IBD Controls	imm_2_10236 8082	rs176514 85	0.09547	A	9363	0.915	10300165 0	intronic	TMEM18 2	0.214216 334	0.038091 085	0
IBD	IBD vs. non-IBD Controls	imm_2_10231 7909	rs763626 90	0.09736	G	9366	0.9241	10295147 7	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
											0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 0.016548	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	
IBD	IBD vs. non-IBD Controls	imm_2_10235 3525	rs114655 96	0.09863	A	9366	0.925	10298709 3	intronic	IL1RL1, MAP4K4, IL18RAP	0.046361 422	0.019212 446	IL18R1
IBD	IBD vs. non-IBD Controls	imm_2_10236 3483	rs728236 77	0.09929	A	9366	1.076	10299705 1	intronic	IL18R1			
UC	UC vs. Ctrl	imm_2_10234 1768	rs129879 77	2.10E-12	C	95393	0.077317 704	10297533 6	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10234 0561	rs129993 64	2.98E-12	A	95381	0.076780 488	10297412 9	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10234 5460	rs228703 7	4.77E-12	A	92068	0.078588 212	10297902 8	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	rs129985 21		5.07E-12	A	94754	0.076365 864	10297441 7	intronic	NA	NA	NA	NA

FIG. 1EEEEEE

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. Ctrl	imm_2_10233 4276	rs111239 23	6.06E-11	A	95379	0.071911 072	10296784 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235 0711	rs142009 8	7.92E-11	G	88812	0.073044 062	10298427 9	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233 1174	rs130174 55	9.15E-11	A	93635	0.072426 102	10296474 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10234 3969	rs671088 5	9.49E-11	G	89377	0.072630 773	10297753 7	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10230 5468	rs130013 25	1.34E-10	A	95338	0.071321 907	10293903 6	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10231 5593	rs124792 10	1.47E-10	A	95383	0.070963 943	10294916 1	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232 4148	rs142010 1	1.99E-10	A	95374	0.070622 444	10295771 6	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229 8258	rs130205 53	2.38E-10	G	95381	0.070337 165	10293182 6	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229 8994	rs950880	2.45E-10	A	95388	0.070291 323	10293256 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232 3964	rs373212 9	4.60E-10	G	95381	0.075329 08	10295753 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232 2292	rs377117 7	4.76E-10	A	95389	0.075242 175	10295586 0	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232 2115	rs873022	5.10E-10	A	95390	0.075110 686	10295568 3	intronic	NA	NA	NA	NA

FIG. 1FFFFF

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. Ctrl	imm_2_10231 7254	rs130190 81	6.78E-10	C	93843	0.069239 504	10295082 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235 2382	rs377117 1	7.49E-10	G	94548	0.074752 717	10298595 0	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10231 8792	rs170269 74	9.05E-10	A	95369	0.073841 694	10295236 0	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233 1764	rs170270 06	9.64E-10	C	95391	0.074027 249	10296533 2	intronic	IL1RL1	0.066330 072	0.040946 538	IL1RL1
UC	UC vs. Ctrl	imm_2_10235 2586	rs216020 2	1.01E-09	A	94558	0.074183 758	10298615 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235 2244	rs377117 2	1.02E-09	A	95387	0.073872 256	10298581 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233 2303	rs124695 06	1.12E-09	A	95392	0.073734 885	10296587 1	intronic	IL1RL1	0.065931 376	0.047728 888	IL1RL1
UC	UC vs. Ctrl	imm_2_10231 5251	rs142010 2	1.67E-09	G	95356	0.064251 649	10294881 9	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233 1293	rs559272 92	1.85E-09	A	95358	0.072734 101	10296486 1	intronic	IL1RL1	0.069982 32	0.030542 666	IL1RL1
UC	UC vs. Ctrl	imm_2_10229 7380	rs127121 35	2.22E-09	A	95390	0.063758 794	10293094 8	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10230 5866	rs142008 8	2.23E-09	A	95388	0.063730 235	10293943 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229 8234	rs129965 05	2.55E-09	A	95390	0.063503 038	10293180 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229 7982	rs155861 9	2.57E-09	C	95387	0.063503 553	10293155 0	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10231 7505	rs199746 7	2.67E-09	A	95378	0.063437 792	10295107 3	intronic	NA	NA	NA	NA

FIG. 1GGGGG

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. Ctrl	imm_2_10230 3914	rs414213 2	3.02E-09	G	95388	0.063205 386	10293748 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10231 5371	rs124663 80	3.18E-09	A	95390	0.063131 928	10294893 9	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10236 1452	rs208028 9	3.30E-09	A	95372	0.071569 814	10299502 0	intronic	IL1RL1	0.067250 733	0.043692 753	0
UC	UC vs. Ctrl	imm_2_10229 8679	rs101833 88	3.49E-09	G	95390	0.062950 063	10293224 7	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10230 2563	rs116904 43	3.49E-09	T	95389	0.062948 031	10293613 1	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10236 1316	rs170270 37	3.59E-09	G	95375	0.071427 609	10299488 4	intronic	IL1RL1	0.067250 733	0.043692 753	0
UC	UC vs. Ctrl	imm_2_10237 2819	rs485157 0	3.73E-09	G	95382	0.071326 588	10300638 7	intronic	IL1RL1	0.067250 733	0.043692 753	0
UC	UC vs. Ctrl	imm_2_10230 6844	rs670684 4	3.77E-09	A	95369	0.062833 448	10294041 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229 3518	rs116854 80	3.84E-09	G	95373	0.062803 834	10292708 6	upstream	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233 6239	rs677237 47	3.98E-09	NA	NA	0.073029 042	10296980 7	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10230 3413	rs974389	4.08E-09	G	95390	0.062695 598	10293698 1	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10231 9499	rs127121 41	4.08E-09	A	95393	0.062693 252	10295306 7	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10230 1669	rs111239 18	4.35E-09	A	95145	0.062751 235	10293523 7	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10236 5744	rs562584 75	4.35E-09	G	95358	0.071041 876	10299931 2	intronic	IL1RL1	0.067250 733	0.043692 753	0
UC	UC vs. Ctrl	imm_2_10232 0622	rs592475 11	4.48E-09	A	90228	0.063402 036	10295419 0	intronic	NA	NA	NA	NA

FIG. 1HHHHHH

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp_location	cis_eGENE	eqtl_beta	eqtl_p	priority
UC	UC vs. Ctrl	imm_2_102363304	rs3821203	4.53E-09	A	95344	0.070959146	102996872	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102391170	rs4851006	4.63E-09	A	94559	0.071162921	103024738	intergenic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_102379106	rs17027071	4.74E-09	A	95393	0.070823548	103012674	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102295444	rs6733174	4.79E-09	A	95392	0.062408187	102929012	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_102377020	rs2287034	4.82E-09	A	95383	0.0708366	103010588	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102358511	rs2270298	5.01E-09	G	95390	0.070757221	102992079	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102382350	rs17027087	5.07E-09	A	95392	0.070715568	103015918	downstream	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102298358	rs13020793	5.54E-09	G	95378	0.062151514	102931926	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_102380394	rs3732126	5.67E-09	C	91115	0.071185176	103013962	UTR3	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102318230	rs1362350	5.81E-09	G	94516	0.062381063	102951798	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_102296812	rs10189202	5.84E-09	A	95393	0.062059298	102930380	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_102373999	rs17027060	5.87E-09	G	95390	0.070417357	103007567	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102363237	rs11683700	5.93E-09	A	95391	0.07041779	102996805	intronic	IL1RL1	0.067250733	0.043692753	0

FIG. 1IIIII

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
UC	UC vs. Ctrl	imm_2_10229_7089	rs10191914	6.15E-09	A	95392	0.061967617	102930657	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229_3413	rs11685424	6.35E-09	G	95391	0.062089463	102926981	upstream	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229_7313	rs10189711	6.44E-09	A	95387	0.061902181	102930881	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229_6579	rs1558622	6.48E-09	G	95364	0.061874867	102930147	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10238_4509	rs3732123	7.12E-09	G	95389	0.070026417	103018077	intergenic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_10236_4165	rs11465633	7.50E-09	A	94483	0.070226238	102997733	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10238_0734	rs1135354	1.66E-08	C	95377	0.068198704	103014302	UTR3	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_10229_7827	rs1558620	2.22E-08	A	91113	0.060018097	102931395	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233_2499	rs1921622	2.35E-08	G	95383	0.059888432	102966067	intronic	MAP4K4	0.049614781	0.016696387	0
UC	UC vs. Ctrl	imm_2_10231_8404	rs1362349	2.59E-08	G	89644	0.060360739	102951972	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10239_0763	rs55883125	3.36E-08	A	91103	0.067134358	103024331	intergenic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_10236_7834	rs1035130	6.76E-08	A	90081	0.066228276	103001402	exonic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10238_2648	rs55664618	7.13E-08	A	95393	0.057768253	103016216	downstream	IL1RL1	0.055883857	0.041785706	0
UC	UC vs. Ctrl	imm_2_10229_9984	rs1968171	3.85E-07	NA	NA	0.055733746	102933552	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10236_0488	rs10190555	2.60E-06	A	94433	0.058969297	102994056	intronic	NA	NA	NA	NA

FIG. 1JJJJJ

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
UC	UC vs. Ctrl	imm_2_10238_6351	rs1035127	1.35E-05	A	95362	0.054227 693	10301991 9	intergenic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10237_5142	rs12712145	1.48E-05	A	95381	0.053961 101	10300871 0	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10238_1128	rs1568681	2.01E-05	G	95371	0.053145 495	10301469 6	UTR3	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235_1856	rs2058622	2.05E-05	A	95389	0.053080 682	10298542 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10236_8827	rs3755274	2.18E-05	A	95390	0.052886 325	10300239 5	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10236_1146	rs6750020	2.21E-05	G	95385	0.052840 503	10299471 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10236_9475	rs2241117	2.21E-05	A	95392	0.052840 503	10300304 3	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235_9593	rs6753717	2.25E-05	A	95379	0.052794 681	10299316 1	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235_9107	rs2270297	2.33E-05	A	95381	0.052695 443	10299267 5	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10237_4055	rs3860444	2.35E-05	A	95375	0.052688 398	10300762 3	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235_1116	rs1558627	2.67E-05	G	94316	0.052682 96	10298468 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10239_9579	rs1807782	2.69E-05	G	95356	0.052265 262	10303314 7	intergenic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10239_1245	rs4851007	3.39E-05	A	95381	0.051645 409	10302481 3	intergenic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233_8297	rs13015714	3.98E-05	C	95382	0.051183 799	10297186 5	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10239_1635	rs4851575	5.95E-05	G	94510	0.050325 805	10302520 3	intergenic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235_6166	rs2041740	7.62E-05	A	91089	0.049607 193	10298973 4	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10233_2499	rs1921622	9.29E-05	G	6864	1.194	10296606 7	intronic	MAP4K4	0.049614 781	0.016696 387	0

FIG. 1KKKKKK

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
UC	UC vs. non-IBD Controls	imm_2_10233_4276	rs111239_23	0.000207	A	6864	0.8381	10296784_4	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10234_0561	rs129993_64	0.0002372	A	6864	0.8396	10297412_9	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10234_1768	rs129879_77	0.0002444	C	6864	0.8399	10297533_6	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	rs12998521	rs129985_21	0.0002558	A	6863	0.8403	10297441_7	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10237_7984	rs485100_5	0.0002698_88	A	95340	0.040891_269	10301155_2	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10234_5460	rs228703_7	0.0002701	A	6862	0.8408	10297902_8	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10230_5468	rs130013_25	0.0002995	A	6864	0.8415	10293903_6	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10231_5593	rs124792_10	0.0003053	A	6864	0.8417	10294916_1	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10229_8258	rs130205_53	0.0003541	G	6864	0.8433	10293182_6	intronic	NA	NA	NA	NA

FIG. 1LLLLLL

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. non-IBD Controls	imm_2_10229 8994	rs950880	0.0003541	A	6864	0.8433	10293256 2	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10232 4148	rs142010 1	0.0003861	A	6863	0.8442	10295771 6	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233 8096	rs980796 2	0.0005320 26	G	94529	0.037976 298	10297166 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10234 1482	rs101731 93	0.0006561 24	A	95368	0.037156 248	10297505 0	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	UC vs. Ctrl	imm_2_10233 4360	rs498895 5	0.0006677 77	G	95373	0.037091 549	10296792 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. Ctrl	imm_2_10234 6056	rs930885 7	0.0006782 73	A	95388	0.037057 932	10297962 4	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	UC vs. Ctrl	imm_2_10233 7738	rs980845 3	0.0006861 64	A	95325	0.037022 802	10297130 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. Ctrl	imm_2_10233 9231	rs485156 6	0.0006989 63	C	94760	0.037156 221	10297279 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	UC vs. Ctrl	imm_2_10233 3668	rs134240 06	0.0007098 85	G	95385	0.036908 697	10296723 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. Ctrl	imm_2_10235 2654	rs377116 6	0.0007188 18	A	95357	0.036895 661	10298622 2	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	UC vs. Ctrl	imm_2_10229 4158	rs654311 6	0.0008279 65	A	95366	0.041114 856	10292772 6	upstream	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10235 1056	rs136234 8	0.0008335 26	G	90305	0.036911 959	10298462 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10231 5064	rs142010 3	0.0008389 75	A	95390	0.041082 765	10294863 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10233 3845	rs675196 7	0.0009618 17	G	95391	0.036092 331	10296741 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. Ctrl	imm_2_10235 2807	rs197467 5	0.0010561 82	A	95389	0.035714 957	10298637 5	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	UC vs. Ctrl	imm_2_10233 6537	rs116956 27	0.0010872 27	G	95129	0.035729 824	10297010 5	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1

FIG. 1MMMMMM

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. Ctrl	imm_2_10234 1196	rs101705 83	0.0011048 44	A	89638	0.036039 145	10297476 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10234 0654	rs121058 08	0.0012278 62	T	95393	0.057431 463	10297422 2	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
UC	UC vs. Ctrl	imm_2_10233 1585	rs176963 76	0.0012923 65	A	95391	0.057053 32	10296515 3	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
UC	UC vs. Ctrl	imm_2_10233 6345	rs116885 59	0.0013258 33	A	95340	0.035206 249	10296991 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. Ctrl	imm_2_10234 4891	rs375527 6	0.0014192 05	A	91110	0.035004 921	10297845 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	UC vs. Ctrl	imm_2_10233 7913	rs485156 5	0.0015222 07	A	86444	0.036360 453	10297148 1	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10234 3628	rs654312 3	0.0016049 8	A	87399	0.035969 183	10297719 6	intronic	NA	NA	NA	NA
UC	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10237 6926	rs114656 53	0.001826 A		1147	8.548	10301049 4	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232 6078	rs621526 61	0.0019947 64	G	95390	0.054613 603	10295964 6	intronic	IL1R2, IL1RL2	0.231497 33812603 4, 0.122966	0.040373 08383166 27, 0.045654	0, 0

FIG. 1NNNNNN

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
											178554851	1874537971	
UC	UC vs. Ctrl	imm_2_102334290	rs6752482	0.002024314	G	95368	0.034024157	102967858	intronic	IL1RL1	0.053336426	0.042506604	IL1RL1
UC	UC vs. Ctrl	imm_2_102344162	rs10204837	0.002068675	A	86210	0.035523602	102977730	intronic	NA	NA	NA	NA
	UC vs. non-IBD Controls	imm_2_102322292	rs3771177					102955860	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102322115	rs73022	0.002196	A	6864	0.8469	102955683	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102323964	rs3732129	0.002196	G	6864	0.8469	102957532	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102318792	rs17026974	0.002354	A	6864	0.8479	102952360	intronic	NA	NA	NA	NA
											0.231497338126034,	0.0403730838316627,	
UC	UC vs. Ctrl	imm_2_102304821	rs1420089	0.002370065	G	95385	0.053638026	102938389	intronic	IL1R2, IL1RL2	0.122966178554851	0.0456541874537971	0, 0
											0.0496830463208274,	0.0406804596047685,	
UC	UC vs. Ctrl	imm_2_102335102	rs78248680	0.002594251	G	95387	0.053819029	102968670	intronic	IL1R1, IL1R2, IL1RL2	0.2373440.043046378396056,	0.0430463438168161,	0, 0, 0

FIG. 10000000

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											25442693 9	06576706 77	
											0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	
UC	UC vs. Ctrl	imm_2_10232 8773	rs621526 62	0.0029355 06	A	94431	0.053382 896	10296234 1	intronic	IL1R1, IL1R2, IL1RL2			0, 0, 0
											0.083853 43352003 65, 0.118117 25329138 , 0.231864 78857383 6, 0.170724 36416156 9,- 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	
UC	UC vs. Ctrl	imm_2_10237 9334	rs142009 5	0.0029440 99	G	95373	0.057465 324	10301290 2	intronic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31			0, 0, 0, 0, 0
											0.083853 43352003 65, 0.118117 25329138 , 0.231864 78857383 6, 0.170724 36416156	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180	
UC	UC vs. Ctrl	imm_2_10236 9466	rs560300 66	0.0031055 5	C	95393	0.057346 054	10300303 4	intronic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31			0, 0, 0, 0, 0

FIG. 1PPPPPP

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											9, - 0.263402 64500044 6	87, 0.033428 43922870 19	
UC	UC vs. Ctrl	imm_2_10233 3863	rs670456 5	0.0034571 26	A	95339	0.032305 622	10296743 1	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. Ctrl	imm_2_10235 3891	rs654312 4	0.0037018 33	A	95328	0.031750 776	10298745 9	intronic	IL1RL1	0.053489 519	0.039961 127	0
	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10232 4163	rs781971 97					10295773 1	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10238 2350	rs170270 87	0.005117 A		6864	0.8589	10301591 8	downstrea m	IL1RL1	0.067250 733	0.043692 753	0
											0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	0, IL18R AP, 0, 0, 0
UC	UC vs. Ctrl	imm_2_10239 9158	rs621527 14	0.0052049 79	G	95391	0.052643 792	10303272 6	intergenic	IL1RL1, IL18RAP, RPL31, IL1RL2, RPL31			
UC	UC vs. non-IBD Controls	imm_2_10238 4509	rs373212 3	0.005641 G		6864	0.8604	10301807 7	intergenic	IL1RL1	0.067250 733	0.043692 753	0

FIG. 1QQQQQQ

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Chr	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
UC	UC vs. non-IBD Controls	imm_2_102337597	rs56386507	0.005712	A	6864	0.8606	102971165	intronic	IL1RL1	0.06751094	0.037554638	IL1RL1
											0.154006314560824, 0.0527971311595181, -0.135420476256853, 0.203509015976762, 0.0371123447603354, 0.0432780976826846274083	0.0066573391411606, 0.0107997527032778, 0.023225602558467, 0.0371123447603354, 0.0432780976826846274083	
UC	UC vs. Ctrl	imm_2_102313976	rs77127114	0.00571536	A	95378	0.073140641	102947544	intronic	IL1RL1, MAP4K4, IL18RAP, CNOT11, MAP4K4			IL1RL1, 0, 0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_102363606	rs3771162	0.006074	A	6862	0.8622	102997174	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. Ctrl	imm_2_102390028	rs78178597	0.006447036	A	91238	0.036332125	103023596	intergenic	NA	NA	NA	NA
	IGG Asca UC vs. IGA Asca Ctrl	imm_2_102332499	rs1921622	0.006523	A	1147	1.862	102966067	intronic	MAP4K4	0.049614781	0.016696387	0
UC	UC vs. non-IBD Controls	imm_2_102380734	rs1135354	0.006529	C	6861	0.8627	103014302	UTR3	IL1RL1	0.067250733	0.043692753	0

FIG. 1RRRRRR

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
UC	UC vs. non-IBD Controls	imm_2_10233 1764	rs17027006	0.006589	C	6864	0.8628	102965332	intronic	IL1RL1	0.066330072	0.040946538	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10235 2244	rs3771172	0.006614	A	6864	0.8629	102985812	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10237 9864	rs3771157	0.006679188	A	95366	0.088921732	103013432	UTR3	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10236 1452	rs2080289	0.006826	A	6863	0.8635	102995020	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. non-IBD Controls	imm_2_10235 8511	rs2270298	0.007026	G	6864	0.8639	102992079	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. non-IBD Controls	imm_2_10236 3304	rs3821203	0.007026	A	6864	0.8639	102996872	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. non-IBD Controls	imm_2_10236 5744	rs56258475	0.007026	G	6864	0.8639	102999312	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. non-IBD Controls	imm_2_10237 2819	rs4851570	0.007026	G	6864	0.8639	103006387	intronic	IL1RL1	0.067250733	0.043692753	0
UC	UC vs. non-IBD Controls	imm_2_10237 3999	rs17027060	0.007026	G	6864	0.8639	103007567	intronic	IL1RL1	0.067250733	0.043692753	0

FIG. 1SSSSSS

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10235 3793	rs757973 7	0.00706	G	1147	1.824	10298736 1	intronic	IL1RL1, IL1RL1	0.062593 42627782 42, 0.033745 39374329 71	0.020438 98041109 64, 0.037319 11651842 61	0, 0
UC	UC vs. non-IBD Controls	imm_2_10233 2303	rs124695 06	0.007262	A	6864	0.8644	10296587 1	intronic	IL1RL1	- 0.065931 376	0.047728 888	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10236 1316	rs170270 37	0.007344	G	6864	0.8646	10299488 4	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
UC	UC vs. non-IBD Controls	imm_2_10237 7020	rs228703 4	0.007369	A	6863	0.8647	10301058 8	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
UC	UC vs. non-IBD Controls	imm_2_10233 1293	rs559272 92	0.007849	A	6863	0.8658	10296486 1	intronic	IL1RL1	- 0.069982 32	0.030542 666	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10236 3237	rs116837 00	0.008247	A	6864	0.8665	10299680 5	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
UC	Asca UC vs. Asca Ctrl	imm_2_10232 0324	rs377117 9	0.008958	C	1147	1.639	10295389 2	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10237 9106	rs170270 71	0.009699	A	6864	0.8692	10301267 4	intronic	IL1RL1	- 0.067250 733	0.043692 753	0
UC	Smokinghx	imm_2_10231 8792	rs170269 74	0.009989	A	1243	0.7493	10295236 0	intronic	NA	NA	NA	NA

FIG. 1TTTTTTT

Populatio n	PHENOT YPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	Smokinghx	imm_2_10232 2115	rs873022	0.009989	A	1243	0.7493	10295568 3	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10232 2292	rs377117	0.009989	A	1243	0.7493	10295586 0	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10232 3964	rs373212 9	0.009989	G	1243	0.7493	10295753 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10234 7408	rs114655 75	0.0105811 25	G	94556	0.090519 391	10298097 6	intronic	NA	NA	NA	NA
	UC vs. non-IBD Controls	imm_2_10231 9499	rs127121 41	0.01135	A	6864	1.122	10295306 7	intronic	NA	NA	NA	NA
UC	MRUC vs non- MRUC	rs115532730	NA	0.01136	A	11022	0.6893	10299453 1	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10229 8679	rs101833 88	0.01212	G	6863	1.121	10293224 7	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10229 8234	rs129965 05	0.01214	A	6864	1.121	10293180 2	intronic	NA	NA	NA	NA
UC	Smokinghx A_Spondyl itis	imm_2_10232 4148	rs142010 1	0.01236	A	1243	0.7913	10295771 6	intronic	NA	NA	NA	NA
UC	A_Spondyl itis	imm_2_10234 1482	rs101731 93	0.0127	A	352	1.691	10297505 0	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	A_Spondyl itis	imm_2_10234 4891	rs375527 6	0.0127	A	352	1.691	10297845 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	A_Spondyl itis	imm_2_10234 6056	rs930885 7	0.0127	A	352	1.691	10297962 4	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	A_Spondyl itis	imm_2_10235 2654	rs377116 6	0.0127	A	352	1.691	10298622 2	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	A_Spondyl itis	imm_2_10235 2807	rs197467 5	0.0127	A	352	1.691	10298637 5	intronic	IL1RL1	0.053336 426	0.042506 604	0

FIG. 1UUUUUU

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Chr2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
UC	Asca UC vs. Asca Ctrl	imm_2_10234 4832	rs114655 67	0.01361	G	1147	1.577	10297840	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10236 9697	rs224111 6	0.01381	A	6864	0.863	10300326	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10231 7899	rs199746 6	0.01386	G	6863	1.118	10295146	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10231 7505	rs199746 7	0.01415	A	6859	1.118	10295107	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10230 3914	rs414213 2	0.01424	G	6862	1.118	10293748	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10231 7494	rs127121 40	0.01475	C	6864	1.117	10295106	intronic	NA	NA	NA	NA
UC	A_Spondylitis	imm_2_10233 6345	rs116885 59	0.01517	A	352	1.666	10296991	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	A_Spondylitis	imm_2_10233 6537	rs116956 27	0.01517	G	352	1.666	10297010	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	A_Spondylitis	imm_2_10233 7738	rs980845 3	0.01517	A	352	1.666	10297130	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	A_Spondylitis	imm_2_10233 3668	rs134240 06	0.01517	G	352	1.666	10296723	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	A_Spondylitis	imm_2_10233 3845	rs675196 7	0.01517	G	352	1.666	10296741	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	A_Spondylitis	imm_2_10233 3863	rs670456 5	0.01517	A	352	1.666	10296743	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1

FIG. 1VVVVVV

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Chr2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
UC	A. Spondylitis	imm_2_102334290	rs6752482	0.01517	G	352	1.666	102967858	intronic	IL1RL1	0.053336426	0.042506604	IL1RL1
UC	A. Spondylitis	imm_2_102334360	rs4988955	0.01517	G	352	1.666	102967928	intronic	IL1RL1	0.053336426	0.042506604	IL1RL1
UC	Smokinghx	imm_2_102319499	rs12712141	0.01525	G	1243	0.8085	102953067	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102293518	rs11685480	0.01539	G	6864	1.116	102927086	upstream	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102296579	rs1558622	0.01539	G	6864	1.116	102930147	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102296812	rs10189202	0.01539	A	6864	1.116	102930380	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102298358	rs13020793	0.01541	G	6863	1.116	102931926	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102305866	rs1420088	0.01553	A	6864	1.116	102939434	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102315371	rs12466380	0.01553	A	6863	1.116	102948939	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102297089	rs10191914	0.01567	A	6864	1.116	102930657	intronic	NA	NA	NA	NA

FIG. 1W

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
UC	UC vs. non-IBD Controls	imm_2_10231_5251	rs1420102	0.01572	G	6864	1.116	102948819	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10230_1669	rs11123918	0.0158	A	6863	1.116	102935237	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229_8258	rs13020553	0.0159	G	1243	0.7986	102931826	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229_8994	rs950880	0.0159	A	1243	0.7986	102932562	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10230_2563	rs11690443	0.01605	T	6859	1.116	102936131	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10233_4276	rs11123923	0.01629	A	1243	0.8	102967844	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10229_7380	rs12712135	0.01673	A	6864	1.115	102930948	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10229_7982	rs1558619	0.01702	C	6864	1.115	102931550	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229_7982	rs1558619	0.01731	C	1243	1.232	102931550	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229_7827	rs1558620	0.01745	A	1242	1.231	102931395	intronic	NA	NA	NA	NA
UC	A Spondylitis	imm_2_10233_9231	rs4851566	0.01788	C	352	1.649	102972799	intronic	IL1RL1	0.053336426	0.042506604	0
UC	Smokinghx	imm_2_10230_5468	rs13001325	0.01835	A	1243	0.8024	102939036	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10231_5593	rs12479210	0.01835	A	1243	0.8024	102949161	intronic	NA	NA	NA	NA

FIG. 1XXXXXX

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	MRUC vs non- MRUC	rs1420103	rs1420103	0.0185	A	11022	-0.1008	10294863	intronic; i ntronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10231 7494	rs127121 40	0.01863	C	1243	1.228	10295106	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 3518	rs116854 80	0.01867	G	1243	1.228	10292708	upstream	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 6579	rs155862 2	0.01867	G	1243	1.228	10293014	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 6812	rs101892 02	0.01867	A	1243	1.228	10293038	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 7089	rs101919 14	0.01867	A	1243	1.228	10293065	intronic	NA	NA	NA	NA
UC	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10232 0324	rs377117 9	0.01924	C	1147	2.346	10295389	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10230 3413	rs974389	0.01947	G	6864	1.112	10293698	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10234 0561	rs129993 64	0.01956	A	1243	0.8054	10297412	intronic	NA	NA	NA	NA
UC	Smokinghx	rs12998521	rs129985 21	0.01956	A	1243	0.8054	10297441	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10230 6844	rs670684 4	0.01979	A	6864	1.112	10294041	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 8358	rs130207 93	0.01987	A	1242	0.8157	10293192	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10230 1669	rs111239 18	0.01987	G	1243	0.8156	10293523	intronic	NA	NA	NA	NA

FIG. 1YYYYYY

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. non-IBD Controls	imm_2_10229 3413	rs116854 24	0.01987	G	6864	1.112	10292698 1	upstream	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10229 5444	rs673317 4	0.01987	A	6864	1.112	10292901 2	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10229 7313	rs101897 11	0.01987	A	6864	1.112	10293088 1	intronic	NA	NA	NA	NA
UC	MRUC vs non- MRUC	rs6543116	NA	0.02015	A	11022	-0.0994	10292772 6	upstream	NA	NA	NA	NA
UC	Smokinghx	imm_2_10230 2563	rs116904 43	0.02104	A	1239	0.8169	10293613 1	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10230 5866	rs142008 8	0.02118	G	1243	0.8172	10293943 4	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10231 5251	rs142010 2	0.02118	A	1243	0.8172	10294881 9	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10231 5371	rs124663 80	0.02118	G	1243	0.8172	10294893 9	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10231 7505	rs199746 7	0.02118	G	1243	0.8172	10295107 3	intronic	NA	NA	NA	NA
UC	A_Spondyl itis	imm_2_10235 3891	rs654312 4	0.02149	A	352	1.637	10298745 9	intronic	IL1RL1	0.053489 519	0.039961 127	0
UC	Cbir UC vs. Cbir Ctrl	imm_2_10233 7109	rs769438 77	0.02156	G	1116	1.609	10297067 7	intronic	NA	NA	NA	NA
UC	A_Spondyl itis	imm_2_10235 3525	rs114655 96	0.02182	A	352	1.845	10298709 3	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03,-	0.002283 01835533 339, 0.006014 83658512 599,	0, 0, 0

FIG. 1ZZZZZZ

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.096712 98393204 15	0.016548 43859053 64	
UC	Smokinghx	imm_2_10231 7899	rs199746 6	0.02257	C	1242	0.8189	10295146 7	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10230 3914	rs414213 2	0.02265	A	1242	0.819	10293748 2	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 3413	rs116854 24	0.02285	G	1243	1.22	10292698 1	upstream	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 5444	rs673317 4	0.02285	A	1243	1.22	10292901 2	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 7313	rs101897 11	0.02285	A	1243	1.22	10293088 1	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10234 1768	rs129879 77	0.02311	C	1243	0.8102	10297533 6	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10234 5460	rs228703 7	0.02311	A	1243	0.8102	10297902 8	intronic	NA	NA	NA	NA
	MRUC vs non- MRUC	rs1558627	NA		A	11022	0.0982	10298468 4	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10238 2476	rs111239 26	0.02553	C	6864	1.124	10301604 4	downstrea m	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 8234	rs129965 05	0.02553	A	1243	1.215	10293180 2	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229 8679	rs101833 88	0.02553	G	1243	1.215	10293224 7	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10230 3413	rs974389	0.02583	G	1243	1.215	10293698 1	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10230 6844	rs670684 4	0.02583	A	1243	1.215	10294041 2	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10235 1116	rs155862 7	0.02588	G	6855	1.124	10298468 4	intronic	NA	NA	NA	NA

FIG. 1A A A A A A A A A

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE NE	eqtl_beta	eqtl_p	priority
UC	UC vs. non-IBD Controls	imm_2_10235_2412	rs3771170	0.02596	A	6863	1.124	102985980	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10238_6351	rs1035127	0.02597	A	6861	1.123	103019919	intergenic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10233_1764	rs17027006	0.02603	C	1243	0.782	102965332	intronic	IL1RL1	0.066330072	0.040946538	IL1RL1
UC	Smokinghx	imm_2_10233_2303	rs12469506	0.02603	A	1243	0.782	102965871	intronic	IL1RL1	0.065931376	0.047728888	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10235_1856	rs2058622	0.02622	A	6864	1.124	102985424	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10229_8085	rs115426178	0.026861235	A	95387	0.115560527	102931653	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10229_7380	rs12712135	0.02717	A	1243	1.212	102930948	intronic	NA	NA	NA	NA
UC	MRUC vs non-MRUC	rs2041740	rs2041740	0.02738	A	11022	-0.0955	102989734	intronic;intronic	NA	NA	NA	NA
UC	MRUC vs non-MRUC	rs6753717	NA	0.02758	A	11022	-0.0953	102993161	intronic	NA	NA	NA	NA
UC													
UC		imm_2_10234_6655	rs11465572	0.02762485	A	95385	0.038035379	102980223	intronic	MAP4K4, TMEM182, RPL31, RPL31	0.0841962068519057, 0.0522514054377319, 0.18248306, 0.0453641274960	0.0202861227094196, 0.0335291660561106, 0.0453641274960	0, 0, 0, 0

FIG. 1BBBBBBB

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											6, 0.071599 60571287 88	54, 0.046140 99122702 84	
UC	MRUC vs non- MRUC	rs4851007	NA	0.02765	A	11022	-0.0954	10302481 3	intergenic	NA	NA	NA	NA
UC	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10236 2032	rs127121 44	0.02811	C	1147	0.3769	10299560 0	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10239 9579	rs180778 2	0.02845	G	6864	1.121	10303314 7	intergenic	NA	NA	NA	NA
UC	Cbir UC vs. Cbir Ctrl	imm_2_10234 0654	rs121058 08	0.02847	T	1116	0.571	10297422 2	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, 0, 0
UC	MRUC vs non- MRUC	rs1035127	NA	0.02866	A	11022	-0.0947	10301991 9	intergenic	NA	NA	NA	NA
UC	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10234 4832	rs114655 67	0.02867	G	1147	2.202	10297840 0	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10239 1245	rs485100 7	0.02868	A	6863	1.121	10302481 3	intergenic	NA	NA	NA	NA

FIG. 1CCCCCCC

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z_B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
UC	MRUC vs non-MRUC	rs6750020	NA	0.02914	A	11022	0.0944	102994714	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_102328361	rs1946131	0.029146275	A	95312	0.037784924	102961929	intronic	MAP4K4, TMEM182, RPL31, RPL31	0.0841962068519057, 0.0522514054377319, 0.182483696156476, 0.0715996057128788	0.0202861227094196, 0.0335291660561106, 0.0445364127496054, 0.0461409912270284	0, 0, 0, 0
UC	MRUC vs non-MRUC	rs2241117	NA	0.02938	A	11022	-0.0942	103003043	intronic	NA	NA	NA	NA
UC	MRUC vs non-MRUC	rs2058622	NA	0.0294	A	11022	-0.0944	102985424	intronic	NA	NA	NA	NA
UC	MRUC vs non-MRUC	rs3771170	NA	0.0295	A	11022	-0.0944	102985980	intronic	NA	NA	NA	NA
UC	MRUC vs non-MRUC	rs12712145	NA	0.02968	A	11022	-0.094	103008710	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102338297	rs13015714	0.03017	C	6862	1.121	102971865	intronic	NA	NA	NA	NA
UC	Smokinghx	imm_2_102337597	rs56386507	0.03021	A	1243	0.7872	102971165	intronic	IL1RL1	0.067510094	0.037554638	IL1RL1

FIG. 1DDDDDDDD

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair	snp_location	cis_eGE	eqtl_beta	eqtl_p	priority
UC	MRUC vs non-MRUC	rs3755274	NA	0.03033	A	11022	-0.0937	10300239	intronic	NA	NA	NA	NA
UC	MRUC vs non-MRUC	rs1807782	NA	0.03033	A	11022	0.0936	10303314	intergenic	NA	NA	NA	NA
UC	Smokinghx	imm_2_10236_9697	rs2241116	0.03064	A	1243	0.7664	10300326	intronic	NA	NA	NA	NA
UC	MRUC vs non-MRUC	rs2270297	NA	0.03065	A	11022	-0.0935	10299267	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10238_1128	rs1568681	0.03092	G	6864	1.12	10301469	UTR3	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232_9171	rs12989197	0.03092076	A	95376	0.037300071	10296273	intronic	RPL31, RPL31, TMEM182	0.0861630945382811, 0.196351870359868, 0.0475017877204885	0.0138156592796922, 0.026913521297184, 0.0485345852467778	0, 0, 0
UC	MRUC vs non-MRUC	rs3860444	NA	0.03142	A	11022	-0.0931	10300762	intronic	NA	NA	NA	NA
UC	Cbir UC vs. Cbir Ctrl	imm_2_10233_5102	rs78248680	0.03149	G	1116	0.5759	10296867	intronic	IL1R1, IL1R2, IL1RL2	0.0496830463208274, 0.2373440.043046378396056, 0.126970254426939	0.0406804596047685, 0.0430463438168161, 0.0469360657670677	0, 0, 0

FIG. 1EEEEEE

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. non-IBD Controls	imm_2_10237 5142	rs127121 45	0.03165	A	6862	1.119	10300871 0	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10237 4055	rs386044 4	0.03194	A	6864	1.119	10300762 3	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10231 7614	rs118918 27	0.0331557 02	G	95377	0.033523 797	10295118 2	intronic	IL1RL1, MAP4K4	0.117191 67059551 , 0.035378 85455241 76	0.003507 22414540 951, 0.016098 12306193 59	IL1RL1 , 0
UC	MRUC vs non- MRUC	rs4851575	NA	0.03371	A	11022	0.0988	10302520 3	intergenic	NA	NA	NA	NA
UC	MRUC vs non- MRUC	rs13015714	NA	0.03388	A	11022	0.0919	10297186 5	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232 7798	rs130140 44	0.0355082 36	G	95375	0.036267 924	10296136 6	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
UC	MRUC vs non- MRUC	rs1568681	NA	0.03569	A	11022	0.0909	10301469 6	UTR3	NA	NA	NA	NA
UC	Smokinghx	imm_2_10233 1293	rs559272 92	0.03582	A	1243	0.7941	10296486 1	intronic	IL1RL1	0.069982 32	0.030542 666	IL1RL1

FIG. 1FFFFFFFFFF

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
UC	Smokinghx	imm_2_102352244	rs3771172	0.0361	A	1243	0.7934	102985812	intronic	NA	NA	NA	NA
UC	Cbir UC vs. Cbir Ctrl	imm_2_102328773	rs62152662	0.03756	A	1116	0.5867	102962341	intronic	IL1R1, IL1R2, IL1RL2	0.0496830463208274, 0.2373440.043046378396056, 0.126970254426939	0.0406804596047685, 0.0430463438168161, 0.0469360657670677	0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_102359107	rs2270297	0.03802	A	6864	1.115	102992675	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102359593	rs6753717	0.03802	A	6864	1.115	102993161	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102360488	rs10190555	0.03802	A	6864	1.115	102994056	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102361146	rs6750020	0.03802	G	6864	1.115	102994714	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102368827	rs3755274	0.03802	A	6864	1.115	103002395	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_102369475	rs224117	0.03802	A	6864	1.115	103003043	intronic	NA	NA	NA	NA

FIG. 1GGGGGG

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
UC	Smokinghx	imm_2_10233 2499	rs192162 2	0.03803	A	1243	0.8342	10296606 7	intronic	MAP4K4	0.049614 781	0.016696 387	0
UC	UC vs. Ctrl	imm_2_10233 0060	rs129960 97	0.0381497 96	A	95381	0.035741 213	10296362 8	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
UC	IGA Asca UC vs. IGA Asca Ctrl	imm_2_10230 7187	rs777218 37	0.03824	G	1147	5.487	10294075 5	intronic	NA	NA	NA	NA
UC	Cbir UC vs. Cbir Ctrl	imm_2_10235 3525	rs114655 96	0.03882	A	1116	1.432	10298709 3	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814 31410319 6, 0.038448 96044717 03, - 0.096712 98393204 15	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	0, 0, 0
UC	UC vs. Ctrl	imm_2_10233 0381	rs130289 93	0.0391277 44	G	95391	0.035571 27	10296394 9	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
UC	UC vs. Ctrl	imm_2_10231 7909	rs763626 90	0.0393242 74	G	95389	0.032407 315	10295147 7	intronic	IL1RL1, MAP4K4	0.117191 67059551 ,	0.003507 22414540 951, ,	IL1RL1 , 0

FIG. 1HHHHHHHH

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.035378 85455241 76	0.016098 12306193 59	
UC	A_Spondyl itis	imm_2_10234 0760	rs561790 05	0.03934	A	352	1.724	10297432 8	intronic	IL18R1	0.041927 743	0.040233 926	IL18R1
UC	A_Spondyl itis	imm_2_10234 8465	rs728236 69	0.03934	A	352	1.724	10298203 3	intronic	IL18R1	0.041927 743	0.040233 926	IL18R1
UC	UC vs. Ctrl	imm_2_10229 7754	rs754520 14	0.0394314 63	A	95353	0.106518 809	10293132 2	intronic	NA	NA	NA	NA
											0.116814 31410319 6, 0.038448 96044717 03,- 0.096712 0.016548 98393204 43859053 64	0.002283 01835533 339, 0.006014 83658512 599, 0.016548 43859053 64	
UC	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10235 3525	rs114655 96	0.04094	A	1147	1.753	10298709 3	intronic	IL1RL1, MAP4K4, IL18RAP	15		0, 0, 0
												NA	NA
UC	IGG Asca UC vs. IGA Asca Ctrl	imm_2_10229 7754	rs754520 14	0.04101	A	1147	2.978	10293132 2	intronic	NA	NA	NA	NA
UC	UC vs. Ctrl	imm_2_10232 8782	rs105409 6	0.0431362 7	G	95225	0.034880 247	10296235 0	intronic	NA	NA	NA	NA
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
UC	UC vs. Ctrl	imm_2_10233 1824	rs129995 42	0.0438850 22	C	95393	0.034725 938	10296539 2	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0

FIG. 1IIIIII

Population	PHENOTYPE	Marker	dbSNP	p value	A1	n miss	OR Z B	base pair Ch2	snp location	cis_eGE NE	eqtl beta	eqtl p	priority
UC	A_Spondylitis	imm_2_102375844	rs11679146	0.04407	G	352	1.704	103009412	intronic	IL18R1	0.046361422	0.019212446	IL18R1
UC	Asca UC vs. Asca Ctrl	imm_2_102322694	rs13022799	0.0441	G	1147	1.362	102956262	intronic	RPL31, TMEM182	0.0801136510989988, 0.0546502830572637	0.0285133800383803, 0.0292598586431115	0, 0
UC	Asca UC vs. Asca Ctrl	imm_2_102325512	rs13016771	0.0441	A	1147	1.362	102959080	intronic	RPL31, TMEM182	0.0801136510989988, 0.0546502830572637	0.0285133800383803, 0.0292598586431115	0, 0
UC	Cbir UC vs. Cbir Ctrl	imm_2_102347450	rs10515921	0.04415	C	1116	1.41	102981018	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814314103196, 0.0384489604471703, -0.0967120.016548	0.00228301835533339, 0.00601483658512599, 0.0165484385905364	0, 0, 0
UC	Cbir UC vs. Cbir Ctrl	imm_2_102349061	rs11465584	0.04415	A	1116	1.41	102982629	intronic	IL1RL1, MAP4K4, IL18RAP	0.116814314103196, 0.0384489604471703, -0.0967120.016548	0.00228301835533339, 0.00601483658512599, 0.0165484385905364	0, 0, 0
UC	A_Spondylitis	imm_2_102353645	rs11465597	0.04666	G	352	0.4671	102987213	intronic	RPL31, MAP4K4, CNOT11,	0.183805835083763, 0.072846	0.0251565704541081, 0.026697	0, 0, 0, 0, 0

FIG. 1JJJJJJ

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
										TMEM18 2, RPL31	56664620 62, 0.137933 54023836 9, 0.044269 31647866 52, 0.063773 12169075 73	12994903 49, 0.038090 48430715 86, 0.046927 56736444 61, 0.049859 99527230 28	
											0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	
UC	Cbir UC vs. Cbir Ctrl	imm_2_10233 1585	rs176963 76	0.04762	A	1116	0.6085	10296515 3	intronic	IL1RL1, IL1RL2, IL1RL2			0, 0, 0
											0.073999 40230378 46, 0.031027 95309229 53	0.003562 19490432 318, 0.043032 61440576 51	
UC	OMPC UC vs. OMPC Ctrl	imm_2_10236 5952	rs611227 64	0.04765	G	1273	0.7431	10299952 0	intronic	IL1RL1, IL1RL1			0, 0
											- 0.067250 733	0.043692 753	0
UC	Smokinghx IGA Asca UC vs. IGA Asca Ctrl	imm_2_10238 2350	rs170270 87	0.04842	A	1243	0.8043	10301591 8	downstrea m	IL1RL1			
											NA	NA	NA
UC	Asca UC vs. Asca Ctrl	imm_2_10234 4832	rs114655 67	0.04853	G	1147	2.064	10297840 0	intronic	NA	NA	NA	NA
										MAP4K4, TMEM18 2	0.089477 14269207 61,	0.018208 05166194 05,	0, 0
UC	Asca UC vs. Asca Ctrl	imm_2_10231 8649	rs375527 8	0.04876	G	1147	1.355	10295221 7	intronic	TMEM18 2			0, 0

FIG. 1KKKKKKK

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											0.060198 97220702 9	0.018871 92869050 61	
											0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 0.071599 60571287 88	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140 99122702 84	
UC	IGA Asca UC vs. IGA Asca Ctrl	imm_2_10232 8361	rs194613 1	0.04891	A	1147	1.776	10296192 9	intronic	MAP4K4, TMEM18 2, RPL31, RPL31			0, 0, 0, 0
											0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 0.071599 60571287 88	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140 99122702 84	
UC	IGA Asca UC vs. IGA Asca Ctrl	imm_2_10233 7795	rs130146 44	0.04929	A	1147	1.773	10297136 3	intronic	MAP4K4, TMEM18 2, RPL31, RPL31			0, 0, 0, 0
UC	A_Spondyl itis	imm_2_10236 3483	rs728236 77	0.04931	A	352	1.682	10299705 1	intronic	IL18R1	0.046361 422	0.019212 446	IL18R1
											0.073999 40230378 46, 0.031027 95309229 53	0.003562 19490432 318, 0.043032 61440576 51	
UC	OMPC UC vs. OMPC Ctrl	imm_2_10238 6413	rs103512 6	0.04956	A	1273	0.7444	10301998 1	intergenic	IL1RL1, IL1R1			0, 0

FIG. 1LLLLLLL

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	A_Spondyl itis	imm_2_10232 0049	rs377118 0	0.05	A	352	1.679	10295361 7	intronic	IL18R1	0.041927 743	0.040233 926	0
UC	A_Spondyl itis	imm_2_10232 0645	rs728236 46	0.05	A	352	1.679	10295421 3	intronic	IL18R1	0.041927 743	0.040233 926	0
UC	A_Spondyl itis	imm_2_10232 3780	rs101730 81	0.05	A	352	1.679	10295734 8	intronic	IL18R1	0.041927 743	0.040233 926	0
UC	UC vs. non-IBD Controls	imm_2_10232 8361	rs194613 1	0.06268	A	6863	0.8763	10296192 9	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 0.071599 0.046140 60571287 88	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140 99122702 84	0, 0, 0, 0
											0.053336 426	0.042506 604	
											0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 0.071599	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140	
											0.071599	0.046140	
UC	UC vs. non-IBD Controls	imm_2_10233 9231	rs485156 6	0.06317	C	6863	1.089	10297279 9	intronic	IL1RL1	0.053336 426	0.042506 604	0
UC	UC vs. non-IBD Controls	imm_2_10234 6655	rs114655 72	0.0691	A	6864	0.8792	10298022 3	intronic	MAP4K4, TMEM18 2, RPL31, RPL31	0.084196 20685190 57, 0.052251 40543773 19, 0.182483 69615647 6, 0.071599	0.020286 12270941 96, 0.033529 16605611 06, 0.044536 41274960 54, 0.046140	0, 0, 0, 0
											0.071599	0.046140	

FIG. 1MMMMMMMM

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											60571287 88	99122702 84	
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
UC	UC vs. non-IBD Controls	imm_2_10233 0381	rs130289 93	0.0706	G	6863	0.8798	10296394 9	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0
											0.231497 33812603 4, 0.122966 17855485 1	0.040373 08383166 27, 0.045654 18745379 71	0, 0
UC	UC vs. non-IBD Controls	imm_2_10230 4821	rs142008 9	0.0747	G	6864	1.142	10293838 9	intronic	IL1R2, IL1RL2			0, 0
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_10232 7798	rs130140 44	0.07636	G	6864	0.8822	10296136 6	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_10232 9171	rs129891 97	0.07636	A	6864	0.8822	10296273 9	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0

FIG. 1NNNNNNN

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base_pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											78772048 85	58524677 78	
											0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	
UC	UC vs. non-IBD Controls	imm_2_10233 1824	rs129995 42	0.07636	C	6864	0.8822	10296539 2	intronic	RPL31, RPL31, TMEM18 2			0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_10233 7738	rs980845 3	0.07646	A	6863	1.085	10297130 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10233 4290	rs675248 2	0.07747	G	6864	1.085	10296785 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10233 4360	rs498895 5	0.07747	G	6864	1.085	10296792 8	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10233 3845	rs675196 7	0.07808	G	6864	1.084	10296741 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10233 6345	rs116885 59	0.07846	A	6862	1.084	10296991 3	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1

FIG. 10000000

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r_Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
UC	UC vs. non-IBD Controls	imm_2_10233 0060	rs129960 97	0.07859	A	6863	0.883	10296362 8	intronic	RPL31, RPL31, TMEM18 2	0.086163 09453828 11, 0.196351 87035986 8, 0.047501 78772048 85	0.013815 65927969 22, 0.026913 52129718 4, 0.048534 58524677 78	0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_10233 3863	rs670456 5	0.07873	A	6862	1.084	10296743 1	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10233 3668	rs134240 06	0.07932	G	6864	1.084	10296723 6	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10233 6537	rs116956 27	0.07961	G	6861	1.084	10297010 5	intronic	IL1RL1	0.053336 426	0.042506 604	IL1RL1
UC	UC vs. non-IBD Controls	imm_2_10232 8782	rs105409 6	0.09117	G	6859	0.8873	10296235 0	intronic	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_10232 6078	rs621526 61	0.09193	G	6864	1.134	10295964 6	intronic	IL1R2, IL1RL2	0.231497 33812603 4, 0.122966 17855485 1	0.040373 08383166 27, 0.045654 18745379 71	0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_10234 0654	rs121058 08	0.09433	T	6864	1.134	10297422 2	intronic	IL1R1, IL1R2, IL1RL2	0.049683 04632082 74, 0.237344 37839605	0.040680 45960476 85, 0.043046 34381681	0, 0, 0

FIG. 1PPPPPPP

Populatio n	PHENOT YPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pai r Ch2	snp_locat ion	cis_eGE NE	eqtl_beta	eqtl_p	priorit y
											6, 0.126970 25442693 9	61, 0.046936 06576706 77	
UC	UC vs. non-IBD Controls	imm_2_10238 2648	rs556646 18	0.09464	A	6864	0.926	10301621 6	downstrea m	IL1RL1	- 0.055883 857	0.041785 706	0
											0.083853 43352003 65, 0.118117 25329138 , - 0.231864 78857383 6, 0.170724 36416156 9, - 0.263402 64500044 6	0.003724 27407991 006, 0.020080 42083512 32, 0.023900 24043710 04, 0.025751 93290180 87, 0.033428 43922870 19	
UC	UC vs. non-IBD Controls	imm_2_10239 9158	rs621527 14	0.09558	G	6864	1.148	10303272 6	intergenic	IL1R1, IL18RAP, RPL31, IL1RL2, RPL31	0.049683 04632082 74, 0.237344 37839605 6, 0.126970 25442693 9	0.040680 45960476 85, 0.043046 34381681 61, 0.046936 06576706 77	0, IL18R AP, 0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_10233 1585	rs176963 76	0.09589	A	6864	1.134	10296515 3	intronic	IL1R1, IL1R2, IL1RL2			0, 0, 0
UC	UC vs. non-IBD Controls	imm_2_10234 6056	rs930885 7	0.09713	A	6863	1.079	10297962 4	intronic	IL1RL1	0.053336 426	0.042506 604	0

FIG. 1QQQQQQQ

Population	PHENOTYPE	Marker	dbSNP	p_value	A1	n_miss	OR_Z_B	base pair Ch2	snp_location	cis_eGE_NE	eqtl_beta	eqtl_p	priority
UC	UC vs. non-IBD Controls	imm_2_4158_10229	rs6543116	0.09726	A	6864	1.09	102927726	upstream	NA	NA	NA	NA
UC	UC vs. non-IBD Controls	imm_2_1482_10234	rs10173193	0.09821	A	6864	1.079	102975050	intronic	IL1RL1	0.053336426	0.042506604	0
UC	UC vs. non-IBD Controls	imm_2_2654_10235	rs3771166	0.09821	A	6864	1.079	102986222	intronic	IL1RL1	0.053336426	0.042506604	0
UC	UC vs. non-IBD Controls	imm_2_2807_10235	rs1974675	0.09821	A	6864	1.079	102986375	intronic	IL1RL1	0.053336426	0.042506604	0
Ulcerative Colitis	anti-TNF time to loss of response	imm_2_9659_10232	rs17696274	0.00171702	G	99	3.13526	102963227	intronic	NA	NA	NA	NA
Ulcerative Colitis	anti-TNF time to loss of response	imm_2_6926_10237	rs11465653	0.00215197	A	99	3.06842	103010494	intronic	NA	NA	NA	NA
Ulcerative Colitis	anti-TNF time to loss of response	imm_2_9359_10237	rs11465655	0.01311151	G	99	2.48063	103012927	intronic	NA	NA	NA	NA
Ulcerative Colitis	anti-TNF time to loss of response	imm_2_4428_10238	rs6736287	0.01311151	G	99	2.48063	103017996	intergenic	NA	NA	NA	NA
Ulcerative Colitis	anti-TNF time to loss of response	imm_2_6928_10238	rs11891965	0.01311151	A	99	2.48063	103020496	intergenic	NA	NA	NA	NA

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2020/017212

Box No. 1 Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

a. ☒ forming part of the international application as filed:

☒ in the form of an Annex C/ST.25 text file.

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☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

SEQ ID NOs: 1-11 were searched.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2020/017212

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A61K 38/00; A61P 1/00; A61P 37/02; C07K 14/715; C12N 15/12; C12Q 1/68 (2020.01)

CPC - A61K 38/00; A61K 38/1793; A61P 1/00; A61P 37/02; C07K 14/00; C12Q 1/6883; C12Q 2600/112; G01N 2800/065 (2020.02)

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC - 424/85.2; 435/6; 435/375; 514/13.2; 530/350; 536/23.5 (keyword delimited)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2002/0098185 A1 (SIMS et al) 25 July 2002 (25.07.2002) entire document	1-9, 18-20
Y	WO 2017/161342 A1 (CEDARS-SINAI MEDICAL CENTER) 21 September 2017 (21.09.2017) entire document	1-9, 18-20
Y	— CLEYNEN et al. "Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study," Lancet, 18 October 2015 (18.10.2015), Vol. 387, Iss. 10014, Pgs. 156-67. entire document	18-20
A	US 2008/0063644 A1 (SEKIYAMA) 13 March 2008 (13.03.2008) entire document	1-20
A	— ZHU et al. "Interleukin 18 receptor 1 gene polymorphisms are associated with asthma," European Journal of Human Genetics, 02 April 2008 (02.04.2008), Vol. 16, Iss. 9, Pgs. 1083-1090. entire document	1-20

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

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