METHODS, SYSTEMS, AND KITS FOR TREATMENT OF INFLAMMATORY DISEASES TARGETING TL1A

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Application No. 63/113,657, filed November 13, 2020, U.S. Provisional Application No. 63/136,153, filed January 11, 2021, U.S. Provisional Application No. 63/147,165, filed February 8, 2021, U.S. Provisional Application No. 63/181,074, filed April 28, 2021, U.S. Provisional Application No. 63/226,032, filed July 27, 2021, each of which is incorporated by reference in its entirety.

SEQUENCE LISTING

[0002] The instant 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 November 10, 2021, is named 56884-782_601_SL.txt and is 14,800,566 bytes in size

BACKGROUND

[0003] Inflammatory disease, fibrostenotic disease, and fibrotic disease pose a significant health burden worldwide due to the vast number of individuals affected and heterogeneous disease pathogenesis and varied clinical manifestations. One such disease is inflammatory bowel disease (IBD), which has two common forms, Crohn's disease (CD) and ulcerative colitis (UC). IBD is the chronic, relapsing inflammatory disorders of the gastrointestinal tract. Incidences of IBD are prevalent, affecting nearly three million individuals in the United States alone.

[0004] Few treatment options are available to patients that suffer from inflammatory disease, fibrostenotic disease, and fibrotic disease. Existing anti-inflammatory therapy such as steroids and tumor necrosis factor (TNF) inhibitors are typically used as a first line treatment for treating IBD. Unfortunately, a significant number of patients experience a lack of response or a loss of response to existing anti-inflammatory therapies, especially TNF inhibitors. While the patient is treated with an anti-inflammatory therapy that is ineffective, the disease worsens. Surgery, in the form of structureplasty (reshaping of the intestine) or resection (removal of the intestine), is the only treatment option for patients that do not respond to first line therapies. Surgical treatments for IBD are invasive, causing post-

operative risks for an estimated third of patients undergoing surgery, such as anastomotic leak, infection, and bleeding.

[0005] The pathogenesis of inflammatory disease, fibrostenotic disease, and fibrotic disease, like IBD, is thought to involve an uncontrolled immune response that may be triggered by certain environmental factors in a genetically susceptible individual. The heterogeneity of disease pathogenesis and clinical course, combined with the variable response to treatment and its associated side effects, suggests a personalized medicine approach to treating these diseases is the best treatment strategy. Yet there are very few personalized therapies available to patients. Accordingly, there is a need to identify targeted therapeutic approaches f or the treatment of inflammatory disease, fibrostenotic disease, and fibrotic disease and subclinical phenotypes thereof, and an even greater need to develop reliable methodology to identifying patients who, based on their genotype, may respond to any given therapeutic approach. The needed methodologies would also identify subjects not yet diagnosed who are at risk of developing the disease, for which preventative interventions could be prescribed to reduce the growing health burden.

SUMMARY

[0006] The genotypes described herein are associated with an increase in a level of *TNFSF15* (TL1A) protein expression in a sample obtained from a subject or patient, as compared to a reference level of *TNFSF15* (TL1A) protein expression (*e.g.,* derived from a normal individual). The genotypes disclosed herein are located at gene or genetic loci that are involved either directly or indirectly with TL1A-mediated or T-cell dependent inflammatory pathways. In addition, some of the genotypes provided herein are also significantly associated with inflammatory bowel disease (IBD), such as Crohn's disease (CD). The genotypes are useful for selecting a patient or a subject for treatment with an inhibitor of TL1A activity or expression. The patient may be diagnosed with IBD, CD, or both. The subject may be suspected of having IBD, CD, or both.

[0007] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and

wherein the inhibitor of TL1A activity or expression is an antibody or antigen binding fragment thereof that competes for binding to human TL1A with a reference antibody comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15. In some embodiments, the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0008] Disclosed herein, in some aspects, is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558,

rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression is an antibody or antigen binding fragment thereof that competes for binding to human TL1A with a reference antibody comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0009] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or

a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15. In some embodiments, the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0010] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558,

rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0011] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or

a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 101-135, or 310-302, and a light chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 201-206 or 303. In some embodiments, the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 101-135, or 310-302. In some embodiments, the light chain variable domain comprises an amino acid sequence at least about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 201-206 or 303. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0012] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor

necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 101-135, or 310-302, and a light chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 201-206 or 303. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0013] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment

thereof that binds to TL1A that comprises: (a) a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework; and (b) a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than about 14 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework. In some embodiments, the at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0014] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509,

rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A that comprises: (a) a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework; and (b) a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than about 14 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework. In some embodiments, an amino acid modification of the less than 14 amino acid modifications comprises: (a) the amino acid modification is at position 47 in the heavy chain variable region, and the amino acid at position 47 is R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (b) the amino acid modification is at position 45 in the heavy chain variable region, and the amino acid at position 45 is A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (c) the amino acid modification is at position 55 in the heavy chain variable region, and the amino acid at position 55 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; (d) the amino acid modification is at position 78 in the heavy chain variable region, and the amino acid at position 78 is A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y; (e) the amino acid modification is at position 80 in the heavy chain variable region, and the amino acid at position 80 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; (f) the amino acid modification is at position 82 in the heavy chain variable region, and the amino acid at position 82 is A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (g) the amino acid modification is at position 89 in the heavy chain variable region, and the amino acid at position 89 is A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y; or (h) the amino acid modification is at position 91 in the heavy chain variable region, and the amino acid at position 91 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; or a combination of two or more modifications selected from (a) to (h). In some embodiments, an amino acid modification of the less than 14 amino acid modifications comprises: A47R, R45K, M55I, V78A, M80I, R82T, V89A, M91L in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, an amino acid modification of the less than 14 amino acid modifications comprises: (a) a modification at amino acid position 54 in the light chain

variable region; and/or (b) a modification at amino acid position 55 in the light chain variable region; per Aho or Kabat numbering. In some embodiments, an amino acid modification of the less than 14 amino acid modifications comprises: (a) the amino acid modification is at position 54 of the light chain variable region, and the amino acid at position 54 is A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V; and/or (b) the amino acid modification is at position 55 of the light chain variable region, and the amino acid at position 55 is A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V. In some embodiments, an amino acid modification of the less than 14 amino acid modifications comprises L54P and/or L55W in the light chain variable region, per Aho or Kabat numbering. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0015] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises: a heavy chain variable region comprising SEQ ID NO: 301
X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS, and a light chain variable region comprising SEQ ID NO: 303

EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0016] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises: a heavy chain variable region comprising SEQ ID NO: 302
X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2] RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS, and a light chain variable region comprising SEQ ID NO: 303
EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V. In some embodiments, the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976,

rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0017] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises: a heavy chain variable region comprising SEQ ID NO: 301 X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2] RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS, and a

light chain variable region comprising SEQ ID NO: 303 EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0018] Disclosed herein, in some aspects is a method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises: a heavy chain variable region comprising SEQ ID NO: 302 X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2] RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS, and a light chain variable region comprising SEQ ID NO: 303

EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V In some embodiments,: (A) X1 is Q or E; (B) X2 is R or K (C) X3 is A or R; (D) X4 is M or I; (E) X5 is V or A; (F) X6 is M or I; (G) X7 is R or T; (H) X8 is V or A; (I) X9 is M or L (J) X10 is L or P; (K) X11 is L or W; or (L) X1-X11 are any combination of (a) to (k). In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR1 as set forth by SEQ ID NO: 1, a heavy chain CDR2 as set forth by any one of SEQ ID NOS: 2-5, a heavy chain CDR3 as set forth by any one of SEQ ID NOS: 6-9, a light chain CDR1 as set forth by SEQ ID NO: 10, a light chain CDR2 as set forth by SEQ ID NO: 11, and a light chain CDR3 as set forth by any one of SEQ ID NOS: 12-15. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain framework (FR) 1 as set forth by SEQ ID NO: 304, a heavy chain FR2 as set forth by SEQ ID NO: 305 or SEQ ID NO: 313, a heavy chain FR3 as set forth by any one of SEQ ID NOS: 306, 307, 314, or 315, a heavy chain FR4 as set forth by SEQ ID NO: 308, a light chain FR1 as set forth by SEQ ID NO: 309, a light chain FR2 as set forth by SEQ ID NO: 310, a light chain FR3 as set forth by SEQ ID NO: 311, or a light chain FR4 as set forth by SEQ ID NO: 312, or a combination thereof. In some embodiments, the antibody or antigen binding fragment comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1 σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and

L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of two or more selected from (a) – (uu), per Kabat numbering. In some embodiments, the antibody or antigen binding fragment comprises a human IgG4 Fc region. In some embodiments, the antibody or antigen binding fragment comprises a Fc region comprising a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362. In some embodiments, the antibody of antigen binding fragment comprises and a fragment crystallizable (Fc) region comprising reduced antibody-dependent cell-mediated cytotoxicity (ADCC) function as compared to human IgG1 and/or reduced complement-dependent cytotoxicity (CDC) as compared to human IgG1. In some embodiments, the Fc comprises the human IgG1 comprises SEQ ID NO: 320. In some embodiments, the ADCC function of the Fc region comprising reduced ADCC is at least about 50% reduced as compared to human IgG1. In some embodiments, the CDC function of the Fc region comprising reduced CDC is at least about 50% reduced as compared to human IgG1. In some embodiments, the Fc comprises (i) a human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P, (b) S228P and L235E, or (c) S228P, F234A, and L235A, per Kabat numbering. In some embodiments, the Fc comprises a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ). In some embodiments, the Fc comprises a human IgG1 with a substitution selected from 329A, 329G, 329Y, 331S, 236F, 236R, 238A, 238E, 238G, 238H, 238I, 238V, 238W, 238Y, 248A, 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, 254V, 264S, 265H, 265K, 265S, 265Y, 265A, 267G, 267H, 267I, 267K, 434I, 438G, 439E, 439H, 439Q, 440A, 440D, 440E, 440F, 440M, 440T, and 440V, per Kabat numbering. In some embodiments, the Fc comprises a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362. In some embodiments, the Fc comprises any one of SEQ ID NOs: 401-413 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 401-413. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain comprising any one of SEQ ID NOs: 501-513 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 501-513. In some embodiments, the antibody or antigen binding fragment comprises a light chain comprising any one of SEQ ID NO: 514 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%,

96%, 97%, 98%, or 99% identical to any one of SEQ ID NO: 514. In some embodiments, the at least three polymorphisms are predictive of the positive therapeutic response with the positive predictive value and a specificity of at least about 51%. In some embodiments, the positive predictive value is greater than or equal about 60%, 65%, 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%. In some embodiments, the positive predictive value is between about 60% - 100%, 65%-95%, 70%- 90%, 75%-85%, and 70%-80%. In some embodiments, the specificity is greater than or equal to about 60%, 65%, 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%. In some embodiments, the specificity is between about 60% - 100%, 65%-95%, 70%- 90%, 75%-85%, and 70%-80%. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs56124762, and rs1892231. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs56124762, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs1892231, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs56124762, rs1892231, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs2070558, and rs1892231. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs2070558, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs1892231, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs2070558, rs1892231, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs2070561, and rs1892231. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs2070561 , and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs1892231, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs2070561, rs1892231, and rs16901748. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs7935393, and rs1892231. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs7935393, and rs9806914. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs7935393, and rs7278257. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs7935393, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs1892231, and rs9806914. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs1892231, and rs7278257. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs1892231, and rs2070557. In some embodiments, the

at least three polymorphisms comprise: rs6478109, rs9806914, and rs7278257. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs9806914, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs7278257, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs7935393, rs1892231, and rs9806914. In some embodiments, the at least three polymorphisms comprise: rs7935393, rs1892231, and rs7278257. In some embodiments, the at least three polymorphisms comprise: rs7935393, rs1892231, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs7935393, rs9806914, and rs7278257. In some embodiments, the at least three polymorphisms comprise: rs7935393, rs9806914, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs7935393, rs7278257, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs1892231, rs9806914, and rs7278257. In some embodiments, the at least three polymorphisms comprise: rs1892231, rs9806914, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs1892231, rs7278257, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs9806914, rs7278257, and rs2070557. In some embodiments, the at least three polymorphisms comprise: rs6478109, rs56124762, and rs1892231. In some embodiments, the at least three polymorphisms further comprises a fourth polymorphism comprising rs16901748, rs1892231, rs56124762, rs6478109, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R2 of at least 0.85, or a combination thereof. In some embodiments, the at least three polymorphisms are detected in the sample by subjecting the sample to an assay configured to detect a presence of at least three nucleotides corresponding to nucleic acid position 501 within at least three of SEQ ID NOS: 2001-20041, or 20057-20059. In some embodiments, the inflammatory, fibrotic, or fibrostenotic disease or condition comprises inflammatory bowel disease, Crohn's disease, obstructive Crohn's disease, ulcerative colitis, intestinal fibrosis, intestinal fibrostenosis, rheumatoid arthritis, pulmonary fibrosis, scleroderma, or primary sclerosing cholangitis. In some embodiments, the Crohn's disease is ileal, ileocolonic, or colonic Crohn's disease. In some embodiments, the pulmonary fibrosis comprises idiopathic

pulmonary fibrosis. In some embodiments, the subject has, or is at risk for developing, a non-response or loss-of-response to a standard therapy comprising glucocorticosteriods, anti-TNF therapy, anti-a4-b7 therapy, anti-IL12p40 therapy, or a combination thereof. In some embodiments, the method further comprises determining whether the subject with an inflammatory, a fibrotic, or a fibrostenotic disease or condition is suitable for treatment with an inhibitor of TL1A activity or expression based, at least in part, on the at least three polymorphisms detected in the sample. In some embodiments, the method further comprises obtaining, or having obtained, the sample from the subject. In some embodiments, the at least three polymorphisms are detected in utilizing assay comprising a quantitative polymerase chain reaction (qPCR), nucleic acid sequencing reaction, or a genotyping array. In some embodiments, the at least three polymorphisms comprise three polymorphisms selected from Table 1 (3-SNP models). In some embodiments, the at least three polymorphisms comprise four polymorphisms selected from Table 1 (4-SNP models). In some embodiments, the at least three polymorphisms comprise five polymorphisms selected from Table 1 (5-SNP models). In some embodiments, the at least three polymorphisms comprise six polymorphisms selected from Table 1 (6-SNP models). In some embodiments, the at least three polymorphisms comprise seven polymorphisms selected from Table 1 (7-SNP models). In some embodiments, the at least three polymorphisms comprise eight polymorphisms from one or more 8-SNP models provided in Table 25. In some embodiments, the at least three polymorphisms comprise nine polymorphisms selected from Table 1 (9-SNP models). In some embodiments, the at least three polymorphisms comprise ten polymorphisms selected from Table 1 (10-SNP models).

[0019] In further embodiments, at least three polymorphisms is at least eight polymorphisms. In some embodiments, the at least eight polymorphisms are provided in an 8-SNP model in Table 25.

[0020] Additional aspects and advantages of the present disclosure will become readily apparent to those skilled in this art from the following detailed description, wherein only illustrative embodiments of the present disclosure are shown and described. As will be realized, the present disclosure is capable of other and different embodiments, and its several details are capable of modifications in various obvious respects, all without departing from the disclosure. Accordingly, the drawings and description are to be regarded as illustrative in nature, and not as restrictive.

INCORPORATION BY REFERENCE

[0021] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference. To the extent publications and patents or patent applications incorporated by reference contradict the disclosure contained in the specification, the specification is intended to supersede and/or take precedence over any such contradictory material.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] The novel features of the inventive concepts set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings (also "Figure" and "FIG." herein), of which:

[0023] **FIG. 1** shows a workflow according to an embodiment of the present disclosure for processing a biological sample obtained from a subject to inform the selection of a therapeutic agent to treat a disease or a condition of the subject.

[0024] **FIG. 2** shows a computer-implemented workflow according to an embodiment of the present disclosure for generating an electronic report to a user, such as a physician, comprising a TNFSF15 profile of a subject based on an analysis of genotype data from the subject.

[0025] **FIG. 3** shows a computer system that is programmed or otherwise configured to implement methods provided herein.

[0026] **FIG. 4** shows a computer-implemented workflow according to an embodiment of the present disclosure for producing a TNFSF15 profile.

[0027] **FIG. 5A-5C** shows a clustering analysis within our the TL1A companion diagnostic (CDx) dataset according to some embodiments herein. **FIG. 5A** shows cluster 1, **FIG. 5B** shows cluster 2, and **FIG. 5C** shows cluster 3, from the TL1A CDx dataset.

[0028] **FIG. 6** shows that the 3 clusters from FIG. 5A-5C were collapsed into 2 clusters (high TL1A expression clusters shown on the left) and (low TL1A expression clusters on the right).

[0029] **FIGS. 7A-7C** show chromatograms for analytical size exclusion chromatography of anti-TL1A antibodies. **FIG. 7A** shows chromatograms for analytical size exclusion chromatography of antibodies A193, A194, and A195. **FIG. 7B** shows chromatograms for

analytical size exclusion chromatography of antibodies A196, A197, and A198. **FIG. 7C** shows chromatograms for analytical size exclusion chromatography of antibodies A199, A200, and A201.

[0030] **FIG. 8A-8B** depict inhibition of interferon gamma in human blood with anti-TL1A antibodies. **FIG. 8A** depicts inhibition of interferon gamma in human blood with anti-TL1A antibodies A219 and A213. **FIG. 8B** depicts inhibition of interferon gamma in human blood with anti-TL1A antibody A212.

[0031] **FIG. 9A-9C** depicts a PLS model demonstrating effect of pH and protein concentration on viscosity. **FIG. 9A** shows a PLS graph, **FIG. 9B** shows a model of the predicted viscosity versus anti-TL1A antibody concentration in mg/mL, and **FIG. 9C** shows a model of the estimated viscosity versus actual viscosity. Viscosity units are in mPa-s.

[0032] **FIG. 10** illustrates, according to some embodiments, the TL1A CDx performance statustics against TL1A ex vivo production assay.

[0033] **FIGS. 11A-11B** show exemplary clinical trial studies of the anti-TL1A antibodies disclosed herein. **FIG. 11A** depicts the study schema for induction period for the phase 2 clinical trial for A219 in UC in accordance with some embodiments herein. **FIG. 11B** depicts the study schema for open-label extension period for the phase 2 clinical trial for A219 in UC in accordance with some embodiments herein.

DETAILED DESCRIPTION

[0034] Provided herein are methods, systems, and kits for treating a subject who may be suitable for treatment with an inhibitor of Tumor Necrosis Factor (Ligand) Superfamily, Member 15 (TL1A) activity or expression, provided the subject is a carrier of a genotype. The subject may be a patient, who may be diagnosed with an inflammatory disease, a fibrostenotic disease, or a fibrotic disease, such as inflammatory bowel disease (IBD) or Crohn's disease (CD). The subject may not be a patient, but may be suspected of having the inflammatory disease, the fibrostenotic disease, or the fibrotic disease. The genotype may, in some cases, be useful for treating the inflammatory fibrostenotic, or fibrotic disease or condition, as mediated by TL1A. The subject, in some embodiments, is treated by administering the inhibitor of TL1A activity or expression (*e.g.*, anti-TL1A antibody) to the subject, provided the genotype is detected. In some cases, identifying the subject as being suitable for treatment with the inhibitor of activity or expression is required in order to administer the inhibitor to the subject.

[0035] Referring to **FIG. 1**, the methods, systems and kits of the present disclosure involve, in some embodiments, the steps of providing a buccal swab sample from a subject 101, optionally purifying DNA from the sample by processing the sample 102, assaying the optionally processed sample to detect genotypes of at least three genetic loci in the sample 103, processing the genotypes to produce a TNFSF15 profile 104, and treating the subject with an anti-TL1A antibody or antibody fragment as disclosed herein to treat a disease or disorder of the subject based on the TNFSF15 profile 105.

[0036] The genotypes described herein are detected using suitable genotyping devices (*e.g.*, array, sequencing). In some instances, a sample is obtained from the subject or patient indirectly or directly. In some instances, the sample may be obtained by the subject. In other instances, the sample may be obtained by a healthcare professional, such as a nurse or physician. The sample may be derived from virtually any biological fluid or tissue containing genetic information, such as blood.

[0037] The subject disclosed herein can be a mammal, such as for example a mouse, rat, guinea pig, rabbit, non-human primate, or farm animal. In some instances, the subject is human. 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).

[0038] 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). The subject may experience, or is suspected of experiencing, non-response or loss-of-response to a standard treatment (e.g., anti-TNF alpha therapy, anti-a4-b7 therapy (vedolizumab), anti-IL12p40 therapy (ustekinumab), Thalidomide, or Cytoxin).

[0039] The disease or condition disclosed herein may be an inflammatory disease, a fibrostenotic disease, or a fibrotic disease. In some instances, the disease or the condition is a TL1A-mediated disease or condition. The term, "TL1A-mediated disease or condition" refers to a disease or a condition pathology or pathogenesis that is driven, at least in part, by TL1A signaling. In some instances, the disease or the condition is immune-mediated disease or condition, such as those mediated by TL1A.

[0040] In some embodiments the disease or the condition is an inflammatory disease or disorder that is mediated, at least in part, by TL1A signaling. Non-limiting examples of inflammatory disease include, allergy, ankylosing spondylitis, asthma, atopic dermatitis, autoimmune diseases or disorders, cancer, celiac disease, chronic obstructive pulmonary disease (COPD), chronic peptic ulcer, cystic fibrosis, diabetes (e.g., type 1 diabetes and type

2 diabetes), glomerulonephritis, gout, hepatitis (e.g., active hepatitis), an immune-mediated disease or disorder, inflammatory bowel disease (IBD) such as Crohn's disease and ulcerative colitis, myositis, osteoarthritis, pelvic inflammatory disease (PID), multiple sclerosis, neurodegenerative diseases of aging, periodontal disease (e.g., periodontitis), preperfusion injury transplant rejection, psoriasis, pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis), rheumatic disease, scleroderma, sinusitis, tuberculosis.

[0041] In some embodiments, the disease or the condition is an autoimmune disease that is mediated, at least in part, by TL1A signaling. Non-limiting examples of autoimmune disease or disorder include Achalasia, Addison's disease, Adult Still's disease, Agammaglobulinemia, Alopecia areata, Amyloidosis, Ankylosing spondylitis, Anti-GBM/Anti-TBM nephritis, Antiphospholipid syndrome, Autoimmune angioedema, Autoimmune dysautonomia, Autoimmune encephalomyelitis, Autoimmune hepatitis, Autoimmune inner ear disease (AIED), Autoimmune myocarditis, Autoimmune oophoritis, Autoimmune orchitis, Autoimmune pancreatitis, Autoimmune retinopathy, Autoimmune urticaria, Axonal & neuronal neuropathy (AMAN), Baló disease, Behcet's disease, Benign mucosal pemphigoid, Bullous pemphigoid, Castleman disease (CD), Celiac disease, Chagas disease, Chronic inflammatory demyelinating polyneuropathy (CIDP), Chronic recurrent multifocal osteomyelitis (CRMO), Churg-Strauss Syndrome (CSS) or Eosinophilic Granulomatosis (EGPA), Cicatricial pemphigoid, Cogan's syndrome, Cold agglutinin disease, Congenital heart block, Coxsackie myocarditis, CREST syndrome, Crohn's disease, Dermatitis herpetiformis, Dermatomyositis, Devic's disease (neuromyelitis optica), Discoid lupus, Dressler's syndrome, Endometriosis, Eosinophilic esophagitis (EoE), Eosinophilic fasciitis, Erythema nodosum, Essential mixed cryoglobulinemia, Evans syndrome, Fibromyalgia, Fibrosing alveolitis, Giant cell arteritis (temporal arteritis), Giant cell myocarditis, Glomerulonephritis, Goodpasture's syndrome, Granulomatosis with Polyangiitis, Graves' disease, Guillain-Barre syndrome, Hashimoto's thyroiditis, Hemolytic anemia, Henoch-Schonlein purpura (HSP), Herpes gestationis or pemphigoid gestationis (PG), Hidradenitis Suppurativa (HS) (Acne Inversa), Hypogammalglobulinemia, IgA Nephropathy, IgG4-related sclerosing disease, Immune thrombocytopenic purpura (ITP), Inclusion body myositis (IBM), Interstitial cystitis (IC), Juvenile arthritis, Juvenile diabetes (Type 1 diabetes), Juvenile myositis (JM), Kawasaki disease, Lambert-Eaton syndrome, Leukocytoclastic vasculitis, Lichen planus, Lichen sclerosus, Ligneous conjunctivitis, Linear IgA disease (LAD), Lupus, Lyme disease chronic, Meniere's disease, Microscopic polyangiitis (MPA), Mixed connective tissue disease (MCTD), Mooren's ulcer, Mucha-

Habermann disease, Multifocal Motor Neuropathy (MMN) or MMNCB, Multiple sclerosis, Myasthenia gravis, Myositis, Narcolepsy, Neonatal Lupus, Neuromyelitis optica, Neutropenia, Ocular cicatricial pemphigoid, Optic neuritis, Palindromic rheumatism (PR), PANDAS, Paraneoplastic cerebellar degeneration (PCD), Paroxysmal nocturnal hemoglobinuria (PNH), Parry Romberg syndrome, Pars planitis (peripheral uveitis), Parsonage-Turner syndrome, Pemphigus, Peripheral neuropathy, Perivenous encephalomyelitis, Pernicious anemia (PA), POEMS syndrome, Polyarteritis nodosa, Polyglandular syndromes type I, II, III, Polymyalgia rheumatica, Polymyositis, Postmyocardial infarction syndrome, Postpericardiotomy syndrome, Primary biliary cirrhosis, Primary sclerosing cholangitis, Progesterone dermatitis, Psoriasis, Psoriatic arthritis, Pure red cell aplasia (PRCA), Pyoderma gangrenosum, Raynaud's phenomenon, Reactive Arthritis, Reflex sympathetic dystrophy, Relapsing polychondritis, Restless legs syndrome (RLS), Retroperitoneal fibrosis, Rheumatic fever, Rheumatoid arthritis, Sarcoidosis, Schmidt syndrome, Scleritis, Scleroderma, Sjögren's syndrome, Sperm & testicular autoimmunity, Stiff person syndrome (SPS), Subacute bacterial endocarditis (SBE), Susac's syndrome, Sympathetic ophthalmia (SO), Takayasu's arteritis, Temporal arteritis/Giant cell arteritis, Thrombocytopenic purpura (TTP), Tolosa-Hunt syndrome (THS), Transverse myelitis, Type 1 diabetes, Ulcerative colitis (UC), Undifferentiated connective tissue disease (UCTD), Uveitis, Vasculitis, Vitiligo, and Vogt-Koyanagi-Harada Disease.

[0042] In some embodiments, the disease or the condition is a cancer that is mediated, at least in part, by TL1A signaling. Non-limiting examples of cancers include Adenoid Cystic Carcinoma, Adrenal Gland Cancer, Amyloidosis, Anal Cancer, Ataxia-Telangiectasia, Atypical Mole Syndrome, Basal Cell Carcinoma, Bile Duct Cancer, Birt Hogg Dube Syndrome, Bladder Cancer, Bone Cancer, Brain Tumor, Breast Cancer, Breast Cancer in Men, Carcinoid Tumor, Cervical Cancer, Colorectal Cancer, Ductal Carcinoma, Endometrial Cancer, Esophageal Cancer, Gastric Cancer, Gastrointestinal Stromal Tumor (GIST), HER2-Positive Breast Cancer, Islet Cell Tumor, Juvenile Polyposis Syndrome, Kidney Cancer, Laryngeal Cancer, Leukemia - Acute Lymphoblastic Leukemia, Leukemia - Acute Lymphocytic (ALL), Leukemia - Acute Myeloid AML, Leukemia - Adult, Leukemia - Childhood, Leukemia - Chronic Lymphocytic (CLL), Leukemia - Chronic Myeloid (CML), Liver Cancer, Lobular Carcinoma, Lung Cancer, Lung Cancer - Small Cell (SCLC), Lung Cancer - Non-small Cell (NSCLC), Lymphoma - Hodgkin's, Lymphoma - Non-Hodgkin's, Malignant Glioma, Melanoma, Meningioma, Multiple Myeloma, Myelodysplastic Syndrome (MDS), Nasopharyngeal Cancer, Neuroendocrine Tumor, Oral Cancer, Osteosarcoma,

Ovarian Cancer, Pancreatic Cancer, Pancreatic Neuroendocrine Tumors, Parathyroid Cancer, Penile Cancer, Peritoneal Cancer, Peutz-Jeghers Syndrome, Pituitary Gland Tumor, Polycythemia Vera, Prostate Cancer, Renal Cell Carcinoma, Retinoblastoma, Salivary Gland Cancer, Sarcoma, Sarcoma - Kaposi, Skin Cancer, Small Intestine Cancer, Stomach Cancer, Testicular Cancer, Thymoma, Thyroid Cancer, Uterine (Endometrial) Cancer, Vaginal Cancer, and Wilms' Tumor.

[0043] In some embodiments, the disease or the condition is an inflammatory bowel disease, such as Crohn's disease (CD) or ulcerative colitis (UC). A subject may suffer from fibrosis, fibrostenosis, or a fibrotic disease, either isolated or in combination with an inflammatory disease. In some cases, the CD is severe CD. The severe CD may result from inflammation that has led to the formation of scar tissue in the intestinal wall (fibrostenosis) and/or swelling. In some cases, the severe CD is characterized by the presence of fibrotic and/or inflammatory strictures. The strictures may be determined by computed tomography enterography (CTE), and magnetic resonance imaging enterography (MRE). The disease or condition may be characterized as refractory, which in some cases, means the disease is resistant to a standard treatment (*e.g.*, anti-TNFα therapy). Non-limiting examples of standard treatment include glucocorticosteriods, anti-TNF therapy, anti-a4-b7 therapy (vedolizumab), anti-IL12p40 therapy (ustekinumab), Thalidomide, and Cytoxin.

Genotypes

[0044] Disclosed herein are genotypes that may be detected in a sample obtained from a subject by analyzing the genetic material in the sample. In some instances, the subject may be human. In some embodiments, the genetic material is obtained from a subject having a disease or condition disclosed herein. In some cases, the genetic material is obtained from blood, serum, plasma, sweat, hair, tears, urine, and other techniques known by one of skill in the art. In some cases, the genetic material is obtained from a biopsy, e.g., from the intestinal track of the subject.

[0045] The genotypes of the present disclosure comprise genetic material that is deoxyribonucleic acid (DNA). In some instances, the genotype comprises a denatured DNA molecule or fragment thereof. In some instances, the genotype 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.

[0046] The genotypes disclosed herein comprise at least one polymorphism at a gene or genetic locus described herein. In some instances, the gene or genetic locus is selected from the group consisting of Tumor Necrosis Factor (Ligand) Superfamily, Member 15 (TNFSF15), THADA Armadillo Repeat Containing (THADA), Pleckstrin Homology, MyTH4 And FERM Domain Containing H2 (PLEKHH2), XK Related 6 (XKR6), Myotubularin Related Protein 9 (MTMR9), ETS Proto-Oncogene 1, Transcription Factor (ETS1), C-Type Lectin Domain Containing 16A (CLEC16A), Suppressor Of Cytokine Signaling 1 (SOCS1), Protein Tyrosine Phosphatase Non-Receptor Type 2 (PTPN2), Inducible T Cell Costimulator Ligand (ICOSLG), Janus Kinase 2 (JAK2), Catenin Delta 2 (CTNND2), Regulator Of G Protein Signaling 7 (RGS7), RNA Binding Fox-1 Homolog 1 (RBFOX1), RNA Binding Motif Protein 17 (RBM17), 6-Phosphofructo-2-Kinase/Fructose-2,6-Biphosphatase 3 (PFKFB3), Ecto-NOX Disulfide-Thiol Exchanger 1 (ENOX1), Coiled-Coil Domain Containing 122 (CCDC122), Regulator Of Telomere Elongation Helicase 1 (RTEL1), TNF Receptor Superfamily Member 6b (TNFRSF6B), GLIS Family Zinc Finger 3 (GLIS3), Solute Carrier Family 1 Member 1 (SLC1A1), IKAROS Family Zinc Finger 2 (IKZF2), Fatty Acyl-CoA Reductase 1 (FAR1), Spondin 1(SPON1), Plexin A2 (PLXNA2), MIR205 Host Gene (MIR205HG), C-Type Lectin Domain Containing 16A (CLEC16A), PR/SET Domain 14 (PRDM), Autophagy Related 5 (ATG5), and Prostaglandin E Receptor 4 (PTGER4). In some instances, the gene or genetic locus comprises a gene or genetic locus provided in **Table 1**. The genotypes disclosed herein are, in some cases, a haplotype. In some instances, the genotype comprises a particular polymorphism, a polymorphism in linkage disequilibrium (LD) therewith, or a combination thereof. In some cases, LD is defined by an r^2 of at least or about 0.70, 0.75, 0.80, 0.85, 0.90, or 1.0. The genotypes disclosed herein can comprise at least or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more polymorphisms. In preferred embodiments, the genotypes disclosed herein comprise a combination of 3 polymorphisms, such as those provided in **Table 1**.

[0047] The polymorphisms described herein can be a single nucleotide polymorphism, or an indel (insertion/deletion). In some instances, the polymorphism is an insertion or a deletion of at least one nucleobase (*e.g.*, an indel). In some instances, the genotype may comprise a copy number variation (CNV), which is a variation in a number of a nucleic acid sequence between individuals in a given population. In some instances, the CNV comprises at least or about two, three, four, five, six, seven, eight, nine, ten, twenty, thirty, forty or fifty

nucleic acid molecules. In some instances, the genotype is heterozygous. In some instances, the genotype is homozygous.

[0048] Disclosed herein, in the following embodiments, are genotypes disclosed herein:

1. A genotype comprising at least one polymorphism at a gene or genetic locus.
2. The genotype of embodiment 1 comprising a polymorphism provided in **Table 1**.
3. The genotype of embodiments 1-2 that is heterozygous.
4. The genotype of embodiments 1-2 that is homozygous.
5. The genotype of embodiments 1-4, wherein the genotype comprises at least two polymorphisms.
6. The genotype of embodiments 1-4, wherein the genotype comprises at least three polymorphisms.
7. The genotype of embodiments 1-4, wherein the genotype comprises at least four polymorphisms.
8. The genotype of embodiments 1-4, wherein the genotype comprises at least five polymorphisms.
9. The genotype of embodiments 1-4, wherein the genotype comprises at least six polymorphisms.
10. The genotype of embodiments 1-4, wherein the genotype comprises at least seven polymorphisms.
11. The genotype of embodiments 1-4, wherein the genotype comprises at least eight polymorphisms.
12. The genotype of embodiment 1, comprising a polymorphism in linkage disequilibrium with a polymorphism provided in **Table 1.**
13. The genotype of embodiment 12, wherein LD is defined by (i) a D' value of at least about 0.70, or (ii) a D' value of 0 and an r^2 value of at least about 0.70.
14. The genotype of embodiment 12, wherein LD is defined by (i) a D' value of at least about 0.80, or (ii) a D' value of 0 and an r^2 value of at least about 0.80.
15. The genotype of embodiment 12, wherein LD is defined by (i) a D' value of at least about 0.90, or (ii) a D' value of 0 and an r^2 value of at least about 0.90.
16. The genotype of embodiment 12, wherein LD is defined by (i) a D' value of at least about 0.95, or (ii) a D' value of 0 and an r^2 value of at least about 0.95.
17. The genotype of embodiments 1-16, wherein the gene or genetic locus is selected from the group consisting of Tumor Necrosis Factor (Ligand) Superfamily, Member 15 (TNFSF15), THADA Armadillo Repeat Containing (THADA), Pleckstrin

Homology, MyTH4 And FERM Domain Containing H2 (PLEKHH2), XK Related 6 (XKR6), Myotubularin Related Protein 9 (MTMR9), ETS Proto-Oncogene 1, Transcription Factor (ETS1), C-Type Lectin Domain Containing 16A (CLEC16A), Suppressor Of Cytokine Signaling 1 (SOCS1), Protein Tyrosine Phosphatase Non-Receptor Type 2 (PTPN2), Inducible T Cell Costimulator Ligand (ICOSLG), Janus Kinase 2 (JAK2), Catenin Delta 2 (CTNND2), Regulator Of G Protein Signaling 7 (RGS7), RNA Binding Fox-1 Homolog 1 (RBFOX1), RNA Binding Motif Protein 17 (RBM17), 6-Phosphofructo-2-Kinase/Fructose-2,6-Biphosphatase 3 (PFKFB3), Ecto-NOX Disulfide-Thiol Exchanger 1 (ENOX1), Coiled-Coil Domain Containing 122 (CCDC122), Regulator Of Telomere Elongation Helicase 1 (RTEL1), TNF Receptor Superfamily Member 6b (TNFRSF6B), GLIS Family Zinc Finger 3 (GLIS3), Solute Carrier Family 1 Member 1 (SLC1A1), IKAROS Family Zinc Finger 2 (IKZF2), Fatty Acyl-CoA Reductase 1 (FAR1), Spondin 1(SPON1), Plexin A2 (PLXNA2), MIR205 Host Gene (MIR205HG), C-Type Lectin Domain Containing 16A (CLEC16A), PR/SET Domain 14 (PRDM), Autophagy Related 5 (ATG5), and Prostaglandin E Receptor 4 (PTGER4).

18. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from:

(1) rs16901748, rs7759385, rs4246905;
(2) rs16901748, rs7759385, rs7935393;
(3) rs16901748, rs7759385, rs1892231;
(4) rs16901748, rs7759385, rs12934476;
(5) rs16901748, rs7759385, rs9806914;
(6) rs16901748, rs7759385, rs2297437;
(7) rs16901748, rs7759385, rs2070557;
(8) rs16901748, rs7759385, rs7278257;
(9) rs16901748, rs7759385, rs11221332;
(10) rs16901748, rs7759385, rs41309367;
(11) rs16901748, rs7759385, rs6478109;
(12) rs16901748, rs4246905, rs7935393;
(13) rs16901748, rs4246905, rs1892231;
(14) rs16901748, rs4246905, rs12934476;
(15) rs16901748, rs4246905, rs9806914;
(16) rs16901748, rs4246905, rs2297437;

(17) rs16901748, rs4246905, rs2070557;

(18) rs16901748, rs4246905, rs7278257;

(19) rs16901748, rs4246905, rs11221332;

(20) rs16901748, rs4246905, rs41309367;

(21) rs16901748, rs4246905, rs6478109;

(22) rs16901748, rs7935393, rs1892231;

(23) rs16901748, rs7935393, rs12934476;

(24) rs16901748, rs7935393, rs9806914;

(25) rs16901748, rs7935393, rs2297437;

(26) rs16901748, rs7935393, rs2070557;

(27) rs16901748, rs7935393, rs7278257;

(28) rs16901748, rs7935393, rs11221332;

(29) rs16901748, rs7935393, rs41309367;

(30) rs16901748, rs7935393, rs6478109;

(31) rs16901748, rs1892231, rs12934476;

(32) rs16901748, rs1892231, rs9806914;

(33) rs16901748, rs1892231, rs2297437;

(34) rs16901748, rs1892231, rs2070557;

(35) rs16901748, rs1892231, rs7278257;

(36) rs16901748, rs1892231, rs11221332;

(37) rs16901748, rs1892231, rs41309367;

(38) rs16901748, rs1892231, rs6478109;

(39) rs16901748, rs12934476, rs9806914;

(40) rs16901748, rs12934476, rs2297437;

(41) rs16901748, rs12934476, rs2070557;

(42) rs16901748, rs12934476, rs7278257;

(43) rs16901748, rs12934476, rs11221332;

(44) rs16901748, rs12934476, rs41309367;

(45) rs16901748, rs12934476, rs6478109;

(46) rs16901748, rs9806914, rs2297437;

(47) rs16901748, rs9806914, rs2070557;

(48) rs16901748, rs9806914, rs7278257;

(49) rs16901748, rs9806914, rs11221332;

(50) rs16901748, rs9806914, rs41309367;

(51) rs16901748, rs9806914, rs6478109;
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(53) rs16901748, rs2297437, rs7278257;
(54) rs16901748, rs2297437, rs11221332;
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(56) rs16901748, rs2297437, rs6478109;
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(68) rs7759385, rs4246905, rs1892231;
(69) rs7759385, rs4246905, rs12934476;
(70) rs7759385, rs4246905, rs9806914;
(71) rs7759385, rs4246905, rs2297437;
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(168) rs7935393, rs1892231, rs9806914;
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(180) rs7935393, rs12934476, rs41309367;
(181) rs7935393, rs12934476, rs6478109;
(182) rs7935393, rs9806914, rs2297437;
(183) rs7935393, rs9806914, rs2070557;
(184) rs7935393, rs9806914, rs7278257;
(185) rs7935393, rs9806914, rs11221332;
(186) rs7935393, rs9806914, rs41309367;

(187) rs7935393, rs9806914, rs6478109;

(188) rs7935393, rs2297437, rs2070557;

(189) rs7935393, rs2297437, rs7278257;

(190) rs7935393, rs2297437, rs11221332;

(191) rs7935393, rs2297437, rs41309367;

(192) rs7935393, rs2297437, rs6478109;

(193) rs7935393, rs2070557, rs7278257;

(194) rs7935393, rs2070557, rs11221332;

(195) rs7935393, rs2070557, rs41309367;

(196) rs7935393, rs2070557, rs6478109;

(197) rs7935393, rs7278257, rs11221332;

(198) rs7935393, rs7278257, rs41309367;

(199) rs7935393, rs7278257, rs6478109;

(200) rs7935393, rs11221332, rs4130936;7

(201) rs7935393, rs11221332, rs6478109;

(202) rs7935393, rs41309367, rs6478109;

(203) rs1892231, rs12934476, rs9806914;

(204) rs1892231, rs12934476, rs2297437;

(205) rs1892231, rs12934476, rs2070557;

(206) rs1892231, rs12934476, rs7278257;

(207) rs1892231, rs12934476, rs11221332;

(208) rs1892231, rs12934476, rs41309367;

(209) rs1892231, rs12934476, rs6478109;

(210) rs1892231, rs9806914, rs2297437;

(211) rs1892231, rs9806914, rs2070557;

(212) rs1892231, rs9806914, rs7278257;

(213) rs1892231, rs9806914, rs11221332;

(214) rs1892231, rs9806914, rs41309367;

(215) rs1892231, rs9806914, rs6478109;

(216) rs1892231, rs2297437, rs2070557;

(217) rs1892231, rs2297437, rs7278257;

(218) rs1892231, rs2297437, rs11221332;

(219) rs1892231, rs2297437, rs41309367;

(220) rs1892231, rs2297437, rs6478109;

(221) rs1892231, rs2070557, rs7278257;
(222) rs1892231, rs2070557, rs11221332;
(223) rs1892231, rs2070557, rs41309367;
(224) rs1892231, rs2070557, rs6478109;
(225) rs1892231, rs7278257, rs11221332;
(226) rs1892231, rs7278257, rs41309367;
(227) rs1892231, rs7278257, rs6478109;
(228) rs1892231, rs11221332, rs41309367;
(229) rs1892231, rs11221332, rs6478109;
(230) rs1892231, rs41309367, rs6478109;
(231) rs12934476, rs9806914, rs2297437;
(232) rs12934476, rs9806914, rs2070557;
(233) rs12934476, rs9806914, rs7278257;
(234) rs12934476, rs9806914, rs11221332;
(235) rs12934476, rs9806914, rs41309367;
(236) rs12934476, rs9806914, rs6478109;
(237) rs12934476, rs2297437, rs2070557;
(238) rs12934476, rs2297437, rs7278257;
(239) rs12934476, rs2297437, rs11221332;
(240) rs12934476, rs2297437, rs41309367;
(241) rs12934476, rs2297437, rs6478109;
(242) rs12934476, rs2070557, rs7278257;
(243) rs12934476, rs2070557, rs11221332;
(244) rs12934476, rs2070557, rs41309367;
(245) rs12934476, rs2070557, rs6478109;
(246) rs12934476, rs7278257, rs11221332;
(247) rs12934476, rs7278257, rs41309367;
(248) rs12934476, rs7278257, rs6478109;
(249) rs12934476, rs11221332, rs41309367;
(250) rs12934476, rs11221332, rs6478109;
(251) rs12934476, rs41309367, rs6478109;
(252) rs9806914, rs2297437, rs2070557;
(253) rs9806914, rs2297437, rs7278257;
(254) rs9806914, rs2297437, rs11221332;

(255) rs9806914, rs2297437, rs41309367;

(256) rs9806914, rs2297437, rs6478109;

(257) rs9806914, rs2070557, rs7278257;

(258) rs9806914, rs2070557, rs11221332;

(259) rs9806914, rs2070557, rs41309367;

(260) rs9806914, rs2070557, rs6478109;

(261) rs9806914, rs7278257, rs11221332;

(262) rs9806914, rs7278257, rs41309367;

(263) rs9806914, rs7278257, rs6478109;

(264) rs9806914, rs11221332, rs41309367;

(265) rs9806914, rs11221332, rs6478109;

(266) rs9806914, rs41309367, rs6478109;

(267) rs2297437, rs2070557, rs7278257;

(268) rs2297437, rs2070557, rs11221332;

(269) rs2297437, rs2070557, rs41309367;

(270) rs2297437, rs2070557, rs6478109;

(271) rs2297437, rs7278257, rs11221332;

(272) rs2297437, rs7278257, rs41309367;

(273) rs2297437, rs7278257, rs6478109;

(274) rs2297437, rs11221332, rs41309367;

(275) rs2297437, rs11221332, rs6478109;

(276) rs2297437, rs41309367, rs6478109;

(277) rs2070557, rs7278257, rs11221332;

(278) rs2070557, rs7278257, rs41309367;

(279) rs2070557, rs7278257, rs6478109;

(280) rs2070557, rs11221332, rs41309367;

(281) rs2070557, rs11221332, rs6478109;

(282) rs2070557, rs41309367, rs6478109;

(283) rs7278257, rs11221332, rs41309367;

(284) rs7278257, rs11221332, rs6478109;

(285) rs7278257, rs41309367, rs6478109; or

(286) rs11221332, rs41309367, rs6478109.

19. The genotype of embodiment 18, wherein the rs7278257 is replaced with rs56124762.

20. The genotype of embodiment 18, wherein the rs7278257 is replaced with rs2070558.
21. The genotype of embodiment 18, wherein the rs7278257 is replaced with rs2070561.
22. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, imm_11_127948309, and rs1892231.
23. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, imm_11_127948309, and rs9806914.
24. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, imm_11_127948309, and imm_21_44478192.
25. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, imm_11_127948309, and imm_21_44479552.
26. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, rs1892231, and rs9806914.
27. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, rs1892231, and imm_21_44478192.
28. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, rs1892231, and imm_21_44479552.
29. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, rs9806914, and imm_21_44478192.
30. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, rs9806914, and imm_21_44479552.
31. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_9_116608587, imm_21_44478192, andimm_21_44479552.
32. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_11_127948309, rs1892231, and rs9806914.

33. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_11_127948309, rs1892231, and imm_21_44478192.
34. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_11_127948309, rs1892231, and imm_21_44479552.
35. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_11_127948309, rs9806914, and imm_21_44478192.
36. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_11_127948309, rs9806914, and imm_21_44479552.
37. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from imm_11_127948309, imm_21_44478192, and imm_21_44479552.
38. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs1892231, rs9806914, and imm_21_44478192.
39. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs1892231, rs9806914, and imm_21_44479552.
40. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs1892231, imm_21_44478192, and imm_21_44479552.
41. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs9806914, imm_21_44478192, and imm_21_44479552.
42. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs56124762, and rs1892231.
43. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs56124762, and rs16901748.
44. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs1892231, and rs16901748.
45. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs56124762, rs1892231, and rs16901748.

46. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs2070558, and rs1892231.
47. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs2070558, and rs16901748.
48. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs1892231, and rs16901748.
49. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs2070558, rs1892231, and rs16901748.
50. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs2070561, and rs1892231.
51. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs2070561 , and rs16901748.
52. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs6478109, rs1892231, and rs16901748.
53. The genotype of embodiments 5-6, wherein the genotype comprises at least two polymorphisms selected from rs2070561, rs1892231, and rs16901748.
54. The genotype of embodiment 11 , wherein the genotype comprises eight polymorphisms selected from:
    (1) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs2297437
    (2) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs1326860
    (3) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs12457255
    (4) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs2815844
    (5) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs10974900
    (6) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs2409750
    (7) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs1541020
    (8) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs4942248

(9) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs7759385

(10) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs1326860

(11) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs12457255

(12) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs2815844

(13) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs10974900

(14) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs2409750

(15) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs1541020

(16) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs4942248

(17) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs7759385

(18) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs12457255

(19) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs2815844

(20) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs10974900

(21) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs2409750

(22) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs1541020

(23) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs4942248

(24) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs7759385

(25) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs12457255,rs2815844

(26) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs12457255,rs10974900

(27) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs12457255,rs2409750

(28) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs12457255,rs1541020

(29) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs12457255,rs4942248

(30) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs12457255,rs7759385

(31) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2815844,rs10974900

(32) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2815844,rs2409750

(33) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2815844,rs1541020

(34) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2815844,rs4942248

(35) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2815844,rs7759385

(36) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs10974900,rs2409750

(37) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs10974900,rs1541020

(38) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs10974900,rs4942248

(39) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs10974900,rs7759385

(40) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2409750,rs1541020

(41) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2409750,rs4942248

(42) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs2409750,rs7759385

(43) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs1541020,rs4942248

(44) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs1541020,rs7759385

(45) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393, rs4942248,rs7759385

(46) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs1326860

(47) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs12457255

(48) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs2815844

(49) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs10974900

(50) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs2409750

(51) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs1541020

(52) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs4942248

(53) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2297437,rs7759385

(54) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1326860,rs12457255

(55) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1326860,rs2815844

(56) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1326860,rs10974900

(57) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1326860,rs2409750

(58) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1326860,rs1541020

(59) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1326860,rs4942248

(60) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1326860,rs7759385

(61) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs12457255,rs2815844

(62) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs12457255,rs10974900

(63) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs12457255,rs2409750

(64) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs12457255,rs1541020

(65) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs12457255,rs4942248

(66) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs12457255,rs7759385

(67) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2815844,rs10974900

(68) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2815844,rs2409750

(69) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2815844,rs1541020

(70) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2815844,rs4942248

(71) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2815844,rs7759385

(72) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs10974900,rs2409750

(73) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs10974900,rs1541020

(74) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs10974900,rs4942248

(75) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs10974900,rs7759385

(76) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2409750,rs1541020

(77) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2409750,rs4942248

(78) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs2409750,rs7759385

(79) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1541020,rs4942248

(80) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs1541020,rs7759385

(81) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914, rs4942248,rs7759385

(82) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs1326860,rs12457255

(83) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs1326860,rs2815844

(84) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs1326860,rs10974900

(85) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs1326860,rs2409750

(86) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs1326860,rs1541020

(87) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs1326860,rs4942248

(88) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs1326860,rs7759385

(89) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs12457255,rs2815844

(90) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs12457255,rs10974900

(91) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs12457255,rs2409750

(92) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs12457255,rs1541020

(93) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs12457255,rs4942248

(94) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs12457255,rs7759385

(95) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs2815844,rs10974900

(96) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs2815844,rs2409750

(97) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs2815844,rs1541020

(98) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs2815844,rs4942248

(99) rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs2297437, rs2815844,rs7759385

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(458) rs6478109,rs56124762,rs1892231,rs16901748,rs1326860,rs2409750,rs 1541020,rs7759385

(459) rs6478109,rs56124762,rs1892231,rs16901748,rs1326860,rs2409750,rs 4942248,rs7759385

(460) rs6478109,rs56124762,rs1892231,rs16901748,rs1326860,rs1541020,rs 4942248,rs7759385

(461) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs10974900,rs2409750

(462) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs10974900,rs1541020

(463) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs10974900,rs4942248

(464) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs10974900,rs7759385

(465) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs2409750,rs1541020

(466) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs2409750,rs4942248

(467) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs2409750,rs7759385

(468) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs1541020,rs4942248

(469) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs1541020,rs7759385

(470) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2815844, rs4942248,rs7759385

(471) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs10974900 ,rs2409750,rs1541020

(472) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs10974900 ,rs2409750,rs4942248

(473) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs10974900 ,rs2409750,rs7759385

(474) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs10974900 ,rs1541020,rs4942248

(475) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs10974900 ,rs1541020,rs7759385

(476) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs10974900 ,rs4942248,rs7759385

(477) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2409750, rs1541020,rs4942248

(478) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2409750, rs1541020,rs7759385

(479) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs2409750, rs4942248,rs7759385

(480) rs6478109,rs56124762,rs1892231,rs16901748,rs12457255,rs1541020, rs4942248,rs7759385

(481) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs10974900, rs2409750,rs1541020

(482) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs10974900, rs2409750,rs4942248

(483) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs10974900, rs2409750,rs7759385

(484) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs10974900, rs1541020,rs4942248

(485) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs10974900, rs1541020,rs7759385

(486) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs10974900, rs4942248,rs7759385

(487) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs2409750,rs 1541020,rs4942248

(488) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs2409750,rs 1541020,rs7759385

(489) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs2409750,rs 4942248,rs7759385

(490) rs6478109,rs56124762,rs1892231,rs16901748,rs2815844,rs1541020,rs 4942248,rs7759385

(491) rs6478109,rs56124762,rs1892231,rs16901748,rs10974900,rs2409750, rs1541020,rs4942248

(492) rs6478109,rs56124762,rs1892231,rs16901748,rs10974900,rs2409750, rs1541020,rs7759385

(493) rs6478109,rs56124762,rs1892231,rs16901748,rs10974900,rs2409750, rs4942248,rs7759385

(494) rs6478109,rs56124762,rs1892231,rs16901748,rs10974900,rs1541020, rs4942248,rs7759385

(495) rs6478109,rs56124762,rs1892231,rs16901748,rs2409750,rs1541020,rs 4942248,rs7759385

55. The genotype of embodiments 1-53, wherein the genotype comprises a minor allele provided in **Table 1** for at least one polymorphism.

56. The genotype of embodiments 1-53, wherein the genotype comprises a major allele provided in **Table 1** for at least one polymorphism.

57. The genotype of embodiments 1-56, wherein a presence of the genotype is predictive of a positive therapeutic response to a treatment with an inhibitor of TL1A activity of expression at a positive predictive value of at least about 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%.

58. The genotype of embodiments 1-57, wherein a presence of the genotype is predictive of a positive therapeutic response to a treatment with an inhibitor of TL1A activity of expression with a specificity of at least about 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%.

[0049] Aspects disclosed herein provide genotypes that are associated with, and therefore indicative of, a subject having or being susceptible to developing a particular disease or condition, or a subclinical phenotype thereof. In addition, the genotypes disclosed herein are associated with an increase *TNFSF15* (TL1A) expression or activity. Thus, the genotypes are indicative that the subject will have a positive therapeutic response to an inhibitor of TL1A activity or expression. **Table 1** provides exemplary polymorphisms associated with, and therefore predictive of, a positive therapeutic response to an inhibitor of *TNFSF15* (TL1A) expression or activity. The term, "positive therapeutic response" refers to a reduction or an elimination of at least one symptom of the disease or the condition (*e.g.,* Cohn's disease) after induction of a therapy (*e.g.,* anti-TL1A antibody).

Table 1. Exemplary Polymorphisms

rsID	Chip_id	Gene	Minor Allele	Major Allele	SEQ ID NO
rs11897732	1kg_2_43394890	THADA	G	A	2001
rs6740739	1kg_2_43709147	THADA,PLEKHH2	A	G	2002
rs17796285	1kg_8_11161865	XKR6,MTMR9	G	C	2003
rs7935393	imm_11_127948309	ETS1	C	A	2004
rs12934476	imm_16_11239010	CLEC16A,SOCS1	G	A	2005
rs12457255	imm_18_12749976	LOC100996324,PTPN2	A	C	2006
rs2070557	imm_21_44479552	ICOSLG	A	T	2007
rs4246905	imm_9_116593070	TNFSF15	A	G	2008
rs10974900	imm_9_4977958	JAK2	A	G	2009
rs12434976	rs12434976	LINC01550,C14orf177	C	A	20010
rs16901748	rs16901748	CTNND2	A	C	20011
rs2815844	rs2815844	RGS7	A	G	20012
rs889702	rs889702	RBFOX1	G	A	20013
rs2409750	1kg_8_11125104	XKR6,MTMR9	C	A	20014
rs1541020	imm_10_6205036	RBM17,PFKFB3	A	G	20015
rs4942248	imm_13_43304805	ENOX1,CCDC122	T	A	20016
rs12934476	imm_16_11239010	CLEC16A,SOCS1	G	A	20017
rs12457255	imm_18_12749976	LOC100996324,PTPN2	A	C	20018
rs2297437	imm_20_61775718	RTEL1-TNFRSF6B	A	G	20019
rs41309367	imm_20_61779998	RTEL1-TNFRSF6B	G	A	20020
rs10733509	imm_9_4298050	GLIS3,SLC1A1	A	G	20021
rs10750376	rs10750376	LOC101929497,ETS1	G	A	20022
rs10932456	rs10932456	MIR4776-2,IKZF2	G	A	20023
rs1326860	rs1326860	LINC01031,NONE	A	G	20024
rs1528663	rs1528663	FAR1,SPON1	G	A	20025
rs1892231	rs1892231	LINC01550,C14orf177	C	A	20026
rs951279	rs951279	PLXNA2,MIR205HG	G	A	20027
rs9806914	rs9806914	RBFOX1	A	G	20028
rs7935393	imm_11_127948309	ETS1	C	A	20029
rs1690492	imm_16_11226317	CLEC16A,SOCS1	G	C	20030

Table 1. Exemplary Polymorphisms					
rsID	**Chip_id**	**Gene**	**Minor Allele**	**Major Allele**	**SEQ ID NO**
rs420726	imm_21_44483873	ICOSLG	G	A	20031
rs7759385	imm_6_106695463	PRDM1,ATG5	T	A	20032
rs10974900	imm_9_4977958	JAK2	A	G	20033
rs1326860	rs1326860	LINC01031,NONE	A	G	20034
rs2548147	rs2548147	LINC00603,PTGER4	C	G	20035
rs2815844	rs2815844	RGS7	A	G	20036
rs889702	rs889702	RBFOX1	G	A	20037
rs9806914	rs9806914	RBFOX1	A	G	20038
rs6478109	imm_9_116608587	TNFSF15	A	G	20039
rs7278257	imm_21_44478192	ICOSLG	C	G	20040
rs11221332	imm_11_127886184	ETS1	A	G	20041
rs56124762	imm_21_44482902	ICOSLG	A	G	20057
rs2070558	imm_21_44480086	ICOSLG	G	A	20058
rs2070561	rs2070561	ICOSLG	T	C	20059

[0050] The instant disclosure provides models comprising 3 polymorphisms (e.g., "3-SNP Models") that, when detected in a sample obtained from a subject, indicate a positive therapeutic response in the subject to a treatment, such as with an inhibitor of TL1A activity or expression. Non-limiting examples of models described herein include Model A (rs6478109, rs7278257, and rs1892231); Model B (rs6478109, rs2070557, and rs9806914); Model C (rs6478109, rs7935393, and rs1892231); Model D (rs6478109, rs7935393, and rs9806914); Model E (rs6478109, rs9806914, and rs16901748); Model F (rs6478109, rs16901748, and rs2297437); Model G (rs6478109, rs1892231, and rs16901748); Model H (rs6478109, rs2070557, and rs7935393); Model I (rs6478109, rs7278257, and rs7935393); Model J (rs6478109, rs9806914, and rs1892231); and Model K (rs6478109, rs7278257, and rs16901748).

Methods of Treatment

[0051] Disclosed herein are methods of treating a disease or condition, or a symptom of the disease or condition, in a subject, comprising administrating 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. In some embodiments, the therapeutic

agent comprises an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression.

[0052] Various embodiments provide for methods of treating inflammatory bowel disease (IBD), comprising administering an anti-TL1A antibody described herein to a subject in need thereof. In some embodiments, the subject comprises one or more risk genotypes. In some embodiments, the IBD is a severe form of IBD.

[0053] In various embodiments, provided herein is a method of treating inflammatory bowel disease (IBD) in a subject in need thereof, comprising: administering to the subject a therapeutically effective amount of an antibody or an antigen-binding fragment that specifically binds TL1A. In some embodiments, the anti-TL1A antibody comprises antibody A. In some embodiments, the anti-TL1A antibody comprises antibody B. In some embodiments, the anti-TL1A antibody comprises antibody C. In some embodiments, the anti-TL1A antibody comprises antibody D. In some embodiments, the anti-TL1A antibody comprises antibody E. In some embodiments, the anti-TL1A antibody comprises antibody F. In some embodiments, the anti-TL1A antibody comprises antibody G. In some embodiments, the anti-TL1A antibody comprises antibody I. In some embodiments, the anti-TL1A antibody comprises antibody H. In some embodiments, the anti-TL1A antibody comprises antibody A2. In some embodiments, the anti-TL1A antibody comprises antibody B2. In some embodiments, the anti-TL1A antibody comprises antibody C2. In some embodiments, the anti-TL1A antibody comprises antibody D2. In some embodiments, the anti-TL1A antibody comprises antibody E2. In some embodiments, the anti-TL1A antibody comprises antibody F2. In some embodiments, the anti-TL1A antibody comprises antibody G2. In some embodiments, the anti-TL1A antibody comprises antibody I2. In some embodiments, the anti-TL1A antibody comprises antibody H2. In certain embodiments, the anti-TL1A antibody comprises any one of the antibodies of **Table 10**. In some embodiments, the anti-TL1A antibody comprises antibody A217. In some embodiments, the anti-TL1A antibody comprises antibody A220. In some embodiments, the anti-TL1A antibody comprises antibody A223. In some embodiments, the anti-TL1A antibody comprises antibody A219. In some embodiments, the anti-TL1A antibody comprises antibody A221. In some embodiments, the anti-TL1A antibody comprises antibody A200. In some embodiments, the anti-TL1A antibody comprises antibody A213. In some embodiments, the anti-TL1A antibody comprises antibody A212. In some embodiments, the anti-TL1A antibody comprises antibody A107. In some embodiments, the anti-TL1A antibody comprises antibody A205. In some embodiments, the anti-TL1A antibody comprises antibody A211. In

some embodiments, the anti-TL1A antibody comprises antibody A199. In some embodiments, the anti-TL1A antibody comprises antibody A15. In some embodiments, the anti-TL1A antibody comprises antibody A30. In some embodiments, the anti-TL1A antibody comprises antibody A100. In some embodiments, the anti-TL1A antibody comprises antibody A181. In some embodiments, the anti-TL1A antibody comprises antibody A129. In some embodiments, the anti-TL1A antibody comprises antibody A214. In some embodiments, the anti-TL1A antibody comprises antibody A216. In some embodiments, the anti-TL1A antibody comprises antibody A122. In some embodiments, the anti-TL1A antibody comprises antibody A222. In some embodiments, the anti-TL1A antibody comprises antibody A188. In some embodiments, the anti-TL1A antibody comprises antibody A203. In some embodiments, the anti-TL1A antibody comprises antibody A147. In some embodiments, the anti-TL1A antibody comprises antibody A127. In some embodiments, the anti-TL1A antibody comprises antibody A126. In some embodiments, the anti-TL1A antibody comprises antibody A160. In some embodiments, the anti-TL1A antibody comprises antibody A157. In some embodiments, the anti-TL1A antibody comprises antibody A159. In some embodiments, the anti-TL1A antibody comprises antibody A218. In some embodiments, the anti-TL1A antibody comprises antibody A158. In some embodiments, the anti-TL1A antibody comprises antibody A125. In some embodiments, the anti-TL1A antibody comprises antibody A103. In some embodiments, the anti-TL1A antibody comprises antibody A64. In some embodiments, the anti-TL1A antibody comprises antibody A67. In some embodiments, the anti-TL1A antibody comprises antibody A138. In some embodiments, the anti-TL1A antibody comprises antibody A68. In some embodiments, the anti-TL1A antibody comprises antibody A94. In some embodiments, the anti-TL1A antibody comprises antibody A110. In some embodiments, the anti-TL1A antibody comprises antibody A197. In some embodiments, the anti-TL1A antibody comprises antibody A112. In some embodiments, the anti-TL1A antibody comprises antibody A169. In some embodiments, the anti-TL1A antibody comprises antibody A173. In some embodiments, the anti-TL1A antibody comprises antibody A179. In some embodiments, the anti-TL1A antibody comprises antibody A148. In some embodiments, the anti-TL1A antibody comprises antibody A115. In some embodiments, the anti-TL1A antibody comprises antibody A149. In some embodiments, the anti-TL1A antibody comprises antibody A134. In some embodiments, the anti-TL1A antibody comprises antibody A113. In some embodiments, the anti-TL1A antibody comprises antibody A151. In some embodiments, the anti-TL1A antibody comprises antibody A96. In some embodiments,

the anti-TL1A antibody comprises antibody A132. In some embodiments, the anti-TL1A antibody comprises antibody A196. In some embodiments, the anti-TL1A antibody comprises antibody A172. In some embodiments, the anti-TL1A antibody comprises antibody A75. In some embodiments, the anti-TL1A antibody comprises antibody A174. In some embodiments, the anti-TL1A antibody comprises antibody A109. In some embodiments, the anti-TL1A antibody comprises antibody A198. In some embodiments, the anti-TL1A antibody comprises antibody A170. In certain embodiments, the anti-TL1A antibody comprises any one of the antibodies of **Tables 20-21**. In some embodiments, the anti-TL1A antibody comprises antibody clone 34. In some embodiments, the anti-TL1A antibody comprises antibody 5C3D11. In some embodiments, the anti-TL1A antibody comprises antibody 9E12E5. In some embodiments, the anti-TL1A antibody comprises antibody AS12824. In some embodiments, the anti-TL1A antibody comprises antibody AS12823. In some embodiments, the anti-TL1A antibody comprises antibody AS12819. In some embodiments, the anti-TL1A antibody comprises antibody AS12816. In some embodiments, the anti-TL1A antibody comprises antibody AS12825. In some embodiments, the anti-TL1A antibody comprises antibody 12835. In some embodiments, the anti-TL1A antibody comprises antibody 18-7 S93E. In some embodiments, the anti-TL1A antibody comprises antibody 18-7. In some embodiments, the anti-TL1A antibody comprises antibody 18-7 S92D. In some embodiments, the anti-TL1A antibody comprises antibody 18-7 S92H. In some embodiments, the anti-TL1A antibody comprises antibody 18-7 S92N. In some embodiments, the anti-TL1A antibody comprises antibody 18-7 S92Q. In some embodiments, the anti-TL1A antibody comprises antibody 18-7 CDRv. In some embodiments, the anti-TL1A antibody comprises antibody 21-3. In some embodiments, the anti-TL1A antibody comprises antibody 21-3 V102K. In some embodiments, the anti-TL1A antibody comprises antibody 21-3 V102M. In some embodiments, the anti-TL1A antibody comprises antibody 21-3 V102Q. In some embodiments, the anti-TL1A antibody comprises antibody 21-3 V102W. In some embodiments, the anti-TL1A antibody comprises antibody 21-3 CDRv. In some embodiments, the anti-TL1A antibody comprises antibody 21-3 CDRv. In some embodiments, the anti-TL1A antibody comprises antibody clone 2. In some embodiments, the anti-TL1A antibody comprises antibody clone 52. In some embodiments, the anti-TL1A antibody comprises antibody clone 46. In some embodiments, the anti-TL1A antibody comprises antibody clone 47. In some embodiments, the anti-TL1A antibody comprises antibody clone 14. In some embodiments, the anti-TL1A antibody comprises antibody clone 16L. In some embodiments, the anti-TL1A antibody comprises antibody clone

17L. In some embodiments, the anti-TL1A antibody comprises antibody clone 17L-1. In some embodiments, the anti-TL1A antibody comprises antibody clone 23. In some embodiments, the anti-TL1A antibody comprises antibody clone 53. In some embodiments, the anti-TL1A antibody comprises antibody clone E1. In some embodiments, the anti-TL1A antibody comprises antibody clone 3-17L V-A. In some embodiments, the anti-TL1A antibody comprises antibody clone 3-17L. In some embodiments, the anti-TL1A antibody comprises antibody clone L8mod. In some embodiments, the anti-TL1A antibody comprises antibody clone X-V. In some embodiments, the anti-TL1A antibody comprises antibody clone X. In some embodiments, the anti-TL1A antibody comprises antibody clone XL3-6. In some embodiments, the anti-TL1A antibody comprises antibody clone XL3-10. In some embodiments, the anti-TL1A antibody comprises antibody clone XL3-15. In some embodiments, the anti-TL1A antibody comprises antibody clone L3-13. In some embodiments, the anti-TL1A antibody comprises antibody clone H3-1. In some embodiments, the anti-TL1A antibody comprises antibody clone H2-2. In some embodiments, the anti-TL1A antibody comprises antibody clone H2-5. In some embodiments, the anti-TL1A antibody comprises antibody M1. In some embodiments, the anti-TL1A antibody comprises antibody M2. In some embodiments, the anti-TL1A antibody comprises antibody M3. In some embodiments, the anti-TL1A antibody comprises antibody M4. In some embodiments, the anti-TL1A antibody comprises antibody M5. In some embodiments, the anti-TL1A antibody comprises antibody M6. In some embodiments, the anti-TL1A antibody comprises antibody M7. In some embodiments, the anti-TL1A antibody comprises antibody M8. In some embodiments, the anti-TL1A antibody comprises antibody M9. In some embodiments, the anti-TL1A antibody comprises antibody M10. In some embodiments, the anti-TL1A antibody comprises antibody M11. In some embodiments, the anti-TL1A antibody comprises antibody M12.

[0054] Methods disclosed herein provide methods of treating an inflammatory bowel disease (IBD) in a subject by administering an anti-TL1A antibody described herein to the subject. In various embodiments, IBD is Crohn's Disease (CD) or ulcerative colitis (UC). In some embodiments, the IBD is a severe form of IBD. In some embodiments, the IBD is a moderate to severe form of IBD. In some embodiments, the IBD is a moderate form of IBD. In various other embodiments, the subject is determined to have an increased TL1A expression. In some embodiments, the administration of a therapeutically effective amount of an anti-TL1A antibody causes a decrease in TL1A in the subject treated.

Methods Of Detection

[0055] Methods disclosed herein for detecting a genotype in a sample from a subject comprise analyzing the genetic material in the sample to detect at least one of a presence, an absence, and a quantity of a nucleic acid sequence encompassing the genotype of interest and administering an anti-TL1A antibody or antigen binding fragment as disclosed herein. In some embodiments, the sample is assayed to measure a presence, absence or quantity of at least three polymorphisms. In some embodiments, the sample is assayed to measure a presence, absence, or quantity of at least four polymorphisms. In some embodiments, the sample is assayed to measure a presence, absence, or quantity of at least five polymorphisms. In some embodiments, the sample is assayed to measure a presence, absence, or quantity of at least six polymorphisms. In some embodiments, the sample is assayed to measure a presence, absence, or quantity of at least seven polymorphisms. In some embodiments, the sample is assayed to measure a presence, absence, or quantity of at least eight polymorphisms. In some embodiments, at least three genotypes are detected, using the methods described herein. In some embodiments, at least eight genotypes are detected, using the methods described herein.

[0056] In some cases, the nucleic acid sequence comprises 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 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.

[0057] Nucleic acid-based detection techniques that may be useful for the methods herein include quantitative polymerase chain reaction (qPCR), gel electrophoresis,

immunochemistry, in situ hybridization such as fluorescent in situ hybridization (FISH), cytochemistry, and next generation sequencing. In some embodiments, the methods involve TaqMan™ qPCR, which involves a nucleic acid amplification reaction with a specific primer pair, and hybridization of the amplified nucleic acids with a hydrolysable probe specific to a target nucleic acid.

[0058] In some instances, the methods involve hybridization and/or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses, and probe arrays. Non-limiting amplification reactions include, but are not limited to, qPCR, self-sustained sequence replication, transcriptional amplification system, Q-Beta Replicase, rolling circle replication, or any other nucleic acid amplification known in the art. As discussed, reference to qPCR herein includes use of TaqMan™ methods. An additional exemplary hybridization assay includes 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 of a genotype provided herein. A non-limiting method is one employed in Anal Chem. 2013 Feb 5; 85(3):1932-9.

[0059] In some embodiments, detecting the presence or absence of a genotype comprises sequencing genetic material 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, sequencing by binding (e.g., transient binding), 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, sequencing by transient binding, 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.

[0060] 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.

[0061] Exemplary probes comprise a nucleic acid sequence of at least 10 contiguous nucleic acids provided in any one of SEQ ID NOS: 2001-2048, or 2057-2059, including the nucleobase indicated with a non-nucleobase letter (*e.g.*, R, N, S), or a reverse complement thereof. In some instances, the probes may be used to detect the polymorphisms provided in **Table 1**, wherein the probe comprises a nucleic acid sequence of at least 10 contiguous nucleic acids provided in a corresponding SEQ ID NO or reverse complement thereof, the 10 contiguous nucleic acids comprising the "risk allele" also provided in **Table 1** at a nucleoposition indicated with the non-nucleobase letter, or reverse complement thereof. In some embodiments, the probe comprises at least 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity to any one of SEQ ID NOS: 2001-2048, or 2057-2059, or its reverse complement. In some instances, forward and reverse primers are used to amplify the target nucleic acid sequence. Forward and reverse primers may comprise a nucleic acid sequence flanking the risk allele provided in **Table 1** corresponding to the nucleic acid sequence provided in any one of SEQ ID NOS: 2001-2048, or 2057-2059, or a reverse complement thereof.

[0062] Examples of molecules that are utilized as probes include, but are not limited to, RNA and DNA. In some embodiments, the term "probe" with regards to nucleic acids, refers to any 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′-dimethyloxacarbocyanine (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 BODIPYTM dyes. In some cases, the probe comprises FAM as the dye label.

[0063] In some instances, primers and/or probes described herein for detecting a target nucleic acid are used in an amplification reaction. In some instances, the amplification reaction is qPCR. An exemplary qPCR is a method employing a TaqMan™ assay. Non-limiting examples of primer pairs useful for detecting one or more polymorphisms described herein are provided in **Table 2**, below.

Table 2. Exemplary Primer Sequences

rsID	Forward Primer	Reverse Primer	Wt_Probe_Hex	Mut_Probe_FAM
rs6478109	TGCTTCTGGAAGTGAAAGT (SEQ ID NO: 364101)	TGAGGTTCAAAATGACAGAGG (SEQ ID NO: 364111)	TG+C +AG+A +T+TG GGA (SEQ ID NO: 364121)	TG+C +AGG +TTG GGA (SEQ ID NO: 364131)

rs18922 31	GTCATCATCGCT TTCATGTG (SEQ ID NO: 364102)	TTT TCA ATG CAC AGA TTT AAG GA (SEQ ID NO: 364112)	AT +T+TG +G+A+A AGGG+AA (SEQ ID NO: 364122)	ATT TGG +C+A+A GGG AA (SEQ ID NO: 364132)
rs79353 93	CTGGATGCTCAC AGGTTTG (SEQ ID NO: 364103)	CCT AAG GAG ACT TTT AGT TCT AAG (SEQ ID NO: 364113)	AG+A A+T+A +CA+C A+AG GA (SEQ ID NO: 364123)	T+AG +AA+T +C+C+A CAA (SEQ ID NO: 364133)
rs72782 57	AGTCCCTGTTCT GAATCCTCT (SEQ ID NO: 364104)	ATGGGGAACGT TGTGGCAG (SEQ ID NO: 364114)	TC+C +TA+G +C+G+A TA (SEQ ID NO: 364124)	T+C+C TA+G +G+GA TA (SEQ ID NO: 364134)
rs20705 57	CTT TTT GTC TCC TAC CTC AGA GG (SEQ ID NO: 364105)	CGG CAG CCA GAC AGG TAA (SEQ ID NO: 364115)	CGG GC+A +C+AG C+TC (SEQ ID NO: 364125)	TCG GGC +TC+A GC+T C (SEQ ID NO: 364135)
rs98069 14	ATAAGAACCTCT GCTGCACA (SEQ ID NO: 364106)	ACAGAGGCAGT ATAGCACAG (SEQ ID NO: 364116)	A+GT +GAT T+G+A +CT+C AA (SEQ ID NO: 364126)	AGT GAT T+G+G +CTC AA (SEQ ID NO: 364136)
rs16901 748	TTGGGAATCAGA TAGGTGCA (SEQ ID NO: 364107)	ATC AAG TCA CAA CTG CCA GA (SEQ ID NO: 364117)	C+CA TTA A+A+G +T+CA +GA (SEQ ID NO: 364127)	A+C+C ATT AA+A +T+T+C AGA (SEQ ID NO: 364137)
rs56124 762	AAA CAG GAA CAG GCT GGT TC (SEQ ID NO: 364108)	GCTCTGCCTTCA CATTTCTG (SEQ ID NO: 364118)	TAG +T+T+A +A+G+C CCAT (SEQ ID NO: 364128)	TAG T+T+A +G+GC CCA (SEQ ID NO: 364138)
rs20705 58	CCAAGCCAGTCC CAGTAG (SEQ ID NO: 364109)	AAT GAC CAG ATC CAA ATG AGG (SEQ ID NO: 364119)	AGG GAC +C+G+C TGA (SEQ ID NO: 364129)	AGG GAC +C+A+C +TGA (SEQ ID NO: 364139)
rs20705 61	TTG GCA AGG TTT CAG GTT TG (SEQ ID NO: 364110)	GTC CCC TGG TCT CCC TGT C (SEQ ID NO: 364120)	CGG T+G+C +T+TC GTC C (SEQ ID NO: 364130)	CGG TGC +C+TC GTC C (SEQ ID NO: 364140)
rs56124 762	AAACAGGAACA GGCTGGTTC (SEQ ID NO: 364141)	GCTCTGCCTTCA CATTTCTG (SEQ ID NO: 364145)	+T+T+A +A+G+CCCAT' (SEQ ID NO: 364149)	TAG T+T+A +G+GC CCA (SEQ ID NO: 364153)
rs16901 748	GATCTTGGGAAT CAGATAGGT (SEQ ID NO: 364142)	ACAACTGCCAG ACATATTTG (SEQ ID NO: 364146)	CAT +TAA +A+G+T+CAG A+GT (SEQ ID NO: 364150)	CCA +T+TA AA+T T+CA+GA+G T (SEQ ID NO: 364154)
rs12934 476	GAAATCAGGTTA GAAATACACACA TTA (SEQ ID NO: 364143)	CCCACCAGCCCA TGTTATT (SEQ ID NO: 364147)	CAT +TAA +A+G+T+CAG A+GT (SEQ ID NO: 364151)	AT+TTAA+T+G +CTAA+C+GT (SEQ ID NO: 364155)

rs2274037	CACCCCATTTCTGCTTTCTG (SEQ ID NO: 364144)	AGGATGCCGATTCTTCACA (SEQ ID NO: 364148)	ATT C+G+G GT+G TGCTTG (SEQ ID NO: 364152)	ATT C+A+G GT+G TG+CTTG (SEQ ID NO: 364156)

[0064] "Wt_Probe_Hex" and "Mut_Probe_FAM" mean "Wild type_probes_tagged with HEX reporter dye" and "Mut_probe_tagged with FAM reporter dye", respectively. "+" stands for LNA bases (Locked nucleotides), which are analogues that are modified at 2'-O, 4'-C and form a bridge. This bridge results in restricted base pairing giving room to adjust the Tm as needed between the probes. Thus, + A, + T, + C or + G signify A, T, G or C bases are added on the modified backbone.

[0065] In some instances, qPCR comprises using an intercalating dye. Examples of intercalating dyes include SYBR green I, SYBR green II, SYBR gold, ethidium bromide, methylene blue, Pyronin Y, DAPI, acridine orange, Blue View or phycoerythrin. In some instances, the intercalating dye is SYBR.

[0066] In some instances, a number of amplification cycles for detecting a target nucleic acid in an amplification 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.

[0067] In one aspect, the methods provided herein for determining the presence, absence, and/or quantity of a nucleic acid sequence from a particular genotype comprise an amplification reaction such as qPCR. In an exemplary method, genetic material is obtained from a sample of 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.

[0068] In the exemplary qPCR assay, the nucleic acid sample is combined with primers and probes specific for a target nucleic acid that may or may not be present in the sample, and a DNA polymerase. An amplification reaction is performed with a thermal cycler that heats and cools the sample for nucleic acid amplification, and illuminates the sample at a specific wavelength to excite a fluorophore on the probe and detect the emitted fluorescence. 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.

[0069] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2001 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2001. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2001 comprising a “G” or an “A” allele at nucleoposition 501 within SEQ ID NO: 2001. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a “G” or an “A” allele at nucleoposition 501 within SEQ ID NO: 2001 is sufficient to detect the polymorphism at rs11897732.

[0070] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2002 comprising non-reference allele at nucleoposition 501 within SEQ ID NO: 2002. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2002 comprising an “A” or a “G” allele at nucleoposition 501 within SEQ ID NO: 2002. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an “A” or a “G” allele at nucleoposition 501 within SEQ ID NO: 2002 is sufficient to detect the polymorphism at rs6740739.

[0071] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2003 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2003. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2003 comprising a “G” or a “C” allele at nucleoposition 501 within SEQ ID NO: 2003. In some embodiments, detecting the at least 10

contiguous nucleic acid molecules comprising a "G" or a "C" allele at nucleoposition 501 within SEQ ID NO: 2003 is sufficient to detect the polymorphism at rs17796285.

[0072] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2004 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2004. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2004 comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 2004. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 2004 is sufficient to detect the polymorphism at rs7935393.

[0073] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2005 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2005. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2005 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 2005. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" of an "A" allele at nucleoposition 501 within SEQ ID NO: 2005 is sufficient to detect the polymorphism at rs12934476.

[0074] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2006 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2006. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2006 comprising an "A" or a "C" allele at nucleoposition 501 within SEQ ID NO: 2006. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "C" allele at nucleoposition 501 within SEQ ID NO: 2006 is sufficient to detect the polymorphism at rs12457255.

[0075] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2007 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2007. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2007 comprising an "A" or a "T" allele at nucleoposition 501 within SEQ ID NO: 2007. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "T" allele at nucleoposition 501 within SEQ ID NO: 2007 is sufficient to detect the polymorphism at rs2070557.

[0076] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2008 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2008. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2008 comprising an "A" or a "G" allele at

nucleoposition 501 within SEQ ID NO: 2008. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or "G" allele at nucleoposition 501 within SEQ ID NO: 2008 is sufficient to detect the polymorphism at rs4246905.

[0077] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2009 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2009. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2009 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 2009. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 2009 is sufficient to detect the polymorphism at rs10974900.

[0078] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2010 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2010. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 2010 comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 2010. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 2010 is sufficient to detect the polymorphism at rs12434976.

[0079] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20011 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20011. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20011 comprising an "A" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20011. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20011 is sufficient to detect the polymorphism at rs16901748.

[0080] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20012 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20012. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20012 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20012. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20012 is sufficient to detect the polymorphism at rs2815844.

[0081] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20013 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20013. In some embodiments, the target nucleic acid is at least 10

contiguous nucleic acid molecules of SEQ ID NO: 20013 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20013. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 2013 is sufficient to detect the polymorphism at rs889702.

[0082] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20014 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20014. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20014 comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20014. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20014 is sufficient to detect the polymorphism at rs2409750.

[0083] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20015 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20015. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20015 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20015. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or "G" allele at nucleoposition 501 within SEQ ID NO: 2015 is sufficient to detect the polymorphism at rs1541020.

[0084] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20016 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20016. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20016 comprising a "T" or an "A" allele at nucleoposition 501 within SEQ ID NO: 2016. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "T" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20016 is sufficient to detect the polymorphism at rs4942248.

[0085] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20017 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20017. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20017 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20017. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20017 is sufficient to detect the polymorphism at rs12934476.

[0086] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20018 comprising a non-reference allele at nucleoposition 501

within SEQ ID NO: 20018. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20018 comprising an "A" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20018. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20018 is sufficient to detect the polymorphism at rs12457255.

[0087] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20019 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20019. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20019 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20019. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20019 is sufficient to detect the polymorphism at rs2297437.

[0088] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20020 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20020. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20020 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20020. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20020 is sufficient to detect the polymorphism at rs41309367.

[0089] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20021 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20021. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20021 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 2021. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20021 is sufficient to detect the polymorphism at rs10733509.

[0090] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20022 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20022. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20022 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20022. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20022 is sufficient to detect the polymorphism at rs10750376.

[0091] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20023 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20023. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20023 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20023. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20023 is sufficient to detect the polymorphism at rs10932456.

[0092] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20024 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20024. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20024 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20024. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20024 is sufficient to detect the polymorphism at rs1326860.

[0093] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20025 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20025. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20025 is sufficient to detect the polymorphism at rs1528663.

[0094] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20026 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20026. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20026 comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20026. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20026 is sufficient to detect the polymorphism at rs1892231.

[0095] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20027 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20027. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20027 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20027. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20027 is sufficient to detect the polymorphism at rs951279.

[0096] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20028 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20028. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20028 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20028. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20028 is sufficient to detect the polymorphism at rs9806914.

[0097] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20029 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20029. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20029 comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20029. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "C" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20029 is sufficient to detect the polymorphism at rs7935393.

[0098] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20030 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20030. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20030 comprising a "G" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20030. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20030 is sufficient to detect the polymorphism at rs1690492.

[0099] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20031 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20031. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20031 comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20031. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20031 is sufficient to detect the polymorphism at rs420726.

[0100] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20032 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20032. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20032 comprising a "T" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20032. In some embodiments, detecting the at least

10 contiguous nucleic acid molecules comprising a "T" of an "A" allele at nucleoposition 501 within SEQ ID NO: 20032 is sufficient to detect the polymorphism at rs7759385.

[0101] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20033 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20033. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20033 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20033. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20033 is sufficient to detect the polymorphism at rs10974900.

[0102] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20034 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20034. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20034 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20034. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20034 is sufficient to detect the polymorphism at rs1326860.

[0103] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20035 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 2035. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20035 comprising a "C" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20035. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "C" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20035 is sufficient to detect the polymorphism at rs2548147.

[0104] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20036 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20036. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20036 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20036. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" of a "G" allele at nucleoposition 501 within SEQ ID NO: 20036 is sufficient to detect the polymorphism at rs2815844.

[0105] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20037 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20037. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20037 comprising a "G" or an "A" allele

at nucleoposition 501 within SEQ ID NO: 20037. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "G" or an "A" allele at nucleoposition 501 within SEQ ID NO: 20037 is sufficient to detect the polymorphism at rs889702.

[0106] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20038 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20038. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20038 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20038. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20038 is sufficient to detect the polymorphism at rs9806914.

[0107] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20039 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20039. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20039 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20039. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20039 is sufficient to detect the polymorphism at rs6478109.

[0108] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20040 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20040. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20040 comprising a "C" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20040. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising a "C" or a "G" allele at nucleoposition 501 within SEQ ID NO: 2040 is sufficient to detect the polymorphism at rs7278257.

[0109] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20041 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20041. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20041 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20041. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20041 is sufficient to detect the polymorphism at rs11221332.

[0110] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20057 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20057. In some embodiments, the target nucleic acid is at least 10

contiguous nucleic acid molecules of SEQ ID NO: 20057 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20057. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20057 is sufficient to detect the polymorphism at rs56124762.

[0111] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20058 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20058. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20058 comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20058. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "A" or a "G" allele at nucleoposition 501 within SEQ ID NO: 20058 is sufficient to detect the polymorphism at rs2070558.

[0112] In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20059 comprising a non-reference allele at nucleoposition 501 within SEQ ID NO: 20059. In some embodiments, the target nucleic acid is at least 10 contiguous nucleic acid molecules of SEQ ID NO: 20059 comprising an "T" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20059. In some embodiments, detecting the at least 10 contiguous nucleic acid molecules comprising an "T" or a "C" allele at nucleoposition 501 within SEQ ID NO: 20059 is sufficient to detect the polymorphism at rs2070561.

[0113] In some embodiments, one target nucleic acid (e.g., a polymorphism) is detected with the methods disclosed herein. In some embodiments, at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 target nucleic acids are detected. In some embodiments, the at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 target nucleic acids are detected in a single multiplexed assay. In some embodiments, when 4 target nucleic acids are detected in a sample from subject, 4 unique 3-polymorphism combinations are measured. In a non-limiting example, a sample (e.g., blood or plasma) obtained from a subject is contacted by 4 primer pairs, each primer pair individually adapted to amplify rs6487109, rs56124762, rs1892231, and rs16901748, respectively. A positive, negative, or indeterminate TNFSF15 profile may depend, at least in part, on which of the 3-polymorphism combinations is detected in the sample, and/or whether the genotype is heterozygous or homozygous for the polymorphism. In this example, assaying 4 polymorphism means a total of 4 unique 3-polymorphisms may be detected in the patient sample, which are rs6478109, rs56124762, rs1892231; rs6478109, rs56124762, rs16901748;rs6478109, rs1892231, rs16901748; and rs56124762, rs1892231, rs16901748. Each polymorphism detected may be heterozygous or homozygous.

[0114] Disclosed herein, in some aspects are methods of sample preparation, the methods comprising: (a) extracting a plurality of nucleic acids from a sample disclosed herein that has been obtained from a subject; and (b) enriching a target nucleic acid from the plurality of nucleic acids comprising one or more polymorphisms disclosed herein, wherein the enriching is performed by (i) brining a fluid reaction formulation comprising a synthetic oligonucleotide molecule in contact with the sample; (ii) hybridizing the synthetic oligonucleotide molecule and the target nucleic acid molecule; and (iii) amplifying the target nucleic acid molecule, thereby enriching the target nucleic acid molecule in the fluid reaction formulation. In some embodiments, the methods further comprise detecting the target nucleic acid molecule that was enriched in (b). In some embodiments, the target nucleic acid comprises a TNFSF15 gene locus. In some embodiments, the one or more polymorphisms comprises a polymorphism provided in Table 1. In some embodiments, the one or more polymorphisms comprises a combination of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, or more polymorphisms provided in Table 1. In some embodiments, the synthetic oligonucleotide comprises a primer sequence. In some embodiments, the synthetic oligonucleotide comprises a detectable probe.

[0115] To practice the methods and systems provided herein, genetic material may be 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).

[0116] 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. In some embodiments, the target protein is TL1A, or a binding partner of TL1A such as Death Domain Receptor 3 (DcR3). 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.

[0117] In some cases, a target protein may be detected by detecting binding between the target protein and a binding partner of the target protein. Non-limiting examples of binding partners to TL1A include DcR3, and Tumor necrosis factor receptor superfamily member 25 (TNR25). 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.

[0118] Disclosed herein 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), antibody against E.coli outer membrane porin protein C (anti-OmpC), 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.

Therapeutic agents

Antibodies

[0119] In one aspect, provided herein are antibodies and antigen-binding fragments. In some embodiments, an antibody comprises an antigen-binding fragment that refers to a portion of an antibody having antigenic determining variable regions of an antibody. Examples of antigen-binding fragments include, but are not limited to, Fab, Fab', $F(ab')_2$, and Fv fragments, linear antibodies, single chain antibodies, and multispecific antibodies formed from antibody fragments. In some embodiments, an antibody refers to an immunoglobulin molecule that recognizes and specifically binds to a target, such as a protein, polypeptide,

peptide, carbohydrate, polynucleotide, lipid, or combinations of the foregoing through at least one antigen recognition site within the variable region of the immunoglobulin molecule. In some embodiments, an antibody includes intact polyclonal antibodies, intact monoclonal antibodies, antibody fragments (such as Fab, Fab', $F(ab')_2$, and Fv fragments), single chain Fv (scFv) mutants, a CDR-grafted antibody, multispecific antibodies, chimeric antibodies, humanized antibodies, human antibodies, fusion proteins comprising an antigen determination portion of an antibody, and any other modified immunoglobulin molecule comprising an antigen recognition site so long as the antibodies exhibit the desired biological activity. An antibody can be of any the five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, or subclasses (isotypes) thereof (e.g. IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2), based on the identity of their heavy-chain constant domains referred to as alpha, delta, epsilon, gamma, and mu, respectively. The different classes of immunoglobulins have different and well-known subunit structures and three-dimensional configurations. Antibodies can be naked or conjugated to other molecules such as toxins, radioisotopes, etc.

[0120] In some embodiments, a humanized antibody refers to forms of non-human (e.g., murine) antibodies having specific immunoglobulin chains, chimeric immunoglobulins, or fragments thereof that contain minimal non-human (e.g., murine) sequences. In a non-limiting example, a humanized antibody comprises less than about 40% non-human sequence in the variable region. In some cases, a humanized antibody comprises less than about 20% non-human sequence in a full-length antibody sequence. In a further non-limiting example, a humanized antibody comprises less than about 20% non-human sequence in the framework region of each of the heavy chain and light chain variable regions. For instance, the humanized antibody comprises less than about 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% non-human sequence in the framework region of each of the heavy chain and light chain variable regions. As another example, the humanized antibody comprises about or less than about 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 non-human sequences in the framework region of each of the heavy chain and light chain variable regions. In some cases, humanized antibodies are human immunoglobulins in which residues from the complementarity determining region (CDR) are replaced by residues from the CDR of a non-human species (e.g., mouse, rat, rabbit, hamster) that have the desired specificity, affinity, and capability. These humanized antibodies may contain one or more non-human species mutations, e.g., the heavy chain comprises about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 non-human species mutations in the framework region, and the light chain comprises about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15

non-human species mutations in the framework region. The humanized heavy chain variable domain may comprise IGHV1-46*02 framework with no or fewer than about 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid mutations. The humanized light chain variable domain may comprise IGKV3-20 framework with no or fewer than about 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid mutations.

[0121] In some embodiments, chimeric antibodies refer to antibodies wherein the sequence of the immunoglobulin molecule is derived from two or more species. As a non-limiting example, the variable region of both light and heavy chains corresponds to the variable region of antibodies derived from one species of mammals (e.g., mouse, rat, rabbit, etc.) with the desired specificity, affinity, and capability while the constant regions are homologous to the sequences in antibodies derived from another (usually human) to avoid eliciting an immune response in that species.

[0122] In certain aspects, antibodies are described herein that specifically bind to TL1A (Entrez Gene: 9966; UniProtKB: O95150). In some embodiments, the antibodies specifically bind to soluble TL1A. In some embodiments, the antibodies specifically bind to membrane bound TL1A. In some embodiments, an anti-TL1A antibody is provided having a heavy chain comprising four heavy chain framework regions (HCFR) and three heavy chain complementarity-determining regions (HCDR): HCFR1, HCDR1, HCFR2, HCDR2, HCFR3, HCDR3, and HCFR4; and a light chain comprising four light chain framework regions (LCFR) and three light chain complementarity-determining regions (LCDR): LCFR1, LCDR1, LCFR2, LCDR2, LCFR3, LCDR3, and LCFR4. An anti-TL1A antibody may comprise any region provided herein, for example, as provided in **Tables 15-21**, the examples, and the sequences.

Exemplary anti-TL1A CDRs

[0123] In certain embodiments, an anti-TL1A antibody comprises a HCDR1 as set forth by any one of SEQ ID NOS: 1 or 601-722. In certain embodiments, an anti-TL1A antibody comprises a HCDR2 as set forth by any one of SEQ ID NOS: 2-5 or 723-787. In certain embodiments, an anti-TL1A antibody comprises a HCDR3 as set forth by any one of SEQ ID NOS: 6-9 or 788-842. In certain embodiments, an anti-TL1A antibody comprises a LCDR1 as set forth by any one of SEQ ID NOS: 10 or 843-865. In certain embodiments, an anti-TL1A antibody comprises a LCDR2 as set forth by any one of SEQ ID NOS: 11 or 866-885. In certain embodiments, an anti-TL1A antibody comprises a LCDR3 as set forth by any one of SEQ ID NOS: 12-15 or 886-1101.

[0124] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising any one of SEQ ID NOS: 1 or 601-708, a HCDR2 comprising any one of SEQ ID NOS: 2-5 or 723-774, a HCDR3 comprising any one of SEQ ID NOS: 6-9 or 788-828, a LCDR1 comprising any one of SEQ ID NOS: 10 or 843-852, a LCDR2 comprising any one of SEQ ID NOS: 11 or 866-873, and a LCDR3 comprising any one of SEQ ID NOS: 12-15 or 886-1089.

[0125] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 709, a HCDR2 comprising SEQ ID NO: 775, a HCDR3 comprising SEQ ID NO: 829, a LCDR1 comprising SEQ ID NO: 853, a LCDR2 comprising SEQ ID NO: 874, and a LCDR3 comprising SEQ ID NO: 1090.

[0126] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 710, a HCDR2 comprising SEQ ID NO: 776, a HCDR3 comprising SEQ ID NO: 830, a LCDR1 comprising SEQ ID NO: 854, a LCDR2 comprising SEQ ID NO: 875, and a LCDR3 comprising SEQ ID NO: 1091.In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 711 or 712, a HCDR2 comprising SEQ ID NO: 777 or 778, a HCDR3 comprising SEQ ID NO: 831 or 832, a LCDR1 comprising SEQ ID NO: 855, a LCDR2 comprising SEQ ID NO: 876, and a LCDR3 comprising SEQ ID NO: 1092.

[0127] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 713, a HCDR2 comprising SEQ ID NO: 779, a HCDR3 comprising SEQ ID NO: 833, a LCDR1 comprising SEQ ID NO: 856, a LCDR2 comprising SEQ ID NO: 877, and a LCDR3 comprising SEQ ID NO: 1093.

[0128] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 714, a HCDR2 comprising SEQ ID NO: 780, a HCDR3 comprising SEQ ID NO: 834, a LCDR1 comprising SEQ ID NO: 857, a LCDR2 comprising SEQ ID NO: 878, and a LCDR3 comprising SEQ ID NO: 1094.

[0129] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 715 or 716, a HCDR2 comprising SEQ ID NO: 781, a HCDR3 comprising SEQ ID NO: 835 or 836, a LCDR1 comprising SEQ ID NO: 858 or 859, a LCDR2 comprising SEQ ID NO: 879, and a LCDR3 comprising SEQ ID NO: 1095.

[0130] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 717, a HCDR2 comprising SEQ ID NO: 782, a HCDR3 comprising SEQ ID NO: 837, a LCDR1 comprising SEQ ID NO: 860, a LCDR2 comprising SEQ ID NO: 880, and a LCDR3 comprising SEQ ID NO: 1096.

[0131] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 718, a HCDR2 comprising SEQ ID NO: 783, a HCDR3 comprising SEQ ID NO: 838, a LCDR1 comprising SEQ ID NO: 861, a LCDR2 comprising SEQ ID NO: 881, and a LCDR3 comprising SEQ ID NO: 1097.

[0132] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 719, a HCDR2 comprising SEQ ID NO: 784, a HCDR3 comprising SEQ ID NO: 839, a LCDR1 comprising SEQ ID NO: 862, a LCDR2 comprising SEQ ID NO: 882, and a LCDR3 comprising SEQ ID NO: 1098.

[0133] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 720, a HCDR2 comprising SEQ ID NO: 785, a HCDR3 comprising SEQ ID NO: 840, a LCDR1 comprising SEQ ID NO: 863, a LCDR2 comprising SEQ ID NO: 883, and a LCDR3 comprising SEQ ID NO: 1099.

[0134] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 721, a HCDR2 comprising SEQ ID NO: 786, a HCDR3 comprising SEQ ID NO: 841, a LCDR1 comprising SEQ ID NO: 864, a LCDR2 comprising SEQ ID NO: 884, and a LCDR3 comprising SEQ ID NO: 1100.

[0135] In one aspect, provided herein are anti-TL1A antibodies having a HCDR1 comprising SEQ ID NO: 722, a HCDR2 comprising SEQ ID NO: 787, a HCDR3 comprising SEQ ID NO: 842, a LCDR1 comprising SEQ ID NO: 865, a LCDR2 comprising SEQ ID NO: 885, and a LCDR3 comprising SEQ ID NO: 1101.

[0136] In certain embodiments, an anti-TL1A antibody comprises a HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, LCDR3 selected from **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody B as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody C as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody D as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody E as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody F as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody G as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody H as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody B2 as

shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody C2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody D2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody E2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody F2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody G2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody H2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody I as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody I2 as shown in **Table 20**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M1 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M2 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M3 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M4 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M5 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M6 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M7 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M8 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M9 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M10 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M11 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M12 as shown in **Table 15**. In certain embodiments, an anti-TL1A antibody comprises a P HCDR1 (any one of SEQ ID NOS: 1 or 601-708), a P HCDR2 (any one of SEQ ID NOS: 2-5 or 723-774), a P HCDR3 (any one of SEQ ID NOS: 6-9 or 788-828), a P LCDR1 (any one of SEQ ID NOS: 10 or 843-852), a P LCDR2 (any one of SEQ ID NOS: 11 or 866-873), and a P LCDR3 (any one of SEQ ID NOS: 12-15 or 886-1089) as shown in **Table 15**.

[0137] In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in any one of the antibodies in **Table 10**. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in any one of the heavy chain variable regions in **Table 16**. In

certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in any one of the light chain variable regions in **Table 17**. The CDRs may be defined by the Aho or Kabat, Chothia, or IMGT method. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A217. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A220. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A223. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A219. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A221. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A200. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A213. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A212. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A107. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A205. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A211. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A199. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A15. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A30. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A100. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A181. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A129. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A214. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A216. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A122. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A222. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A188. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A203. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A147. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A127. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A126. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A160. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A157. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A159. In certain embodiments, an anti-TL1A

antibody comprises the CDRs set forth in antibody A218. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A158. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A125. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A103. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A64. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A67. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A138. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A68. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A94. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A110. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A197. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A112. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A169. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A173. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A179. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A148. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A115. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A149. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A134. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A113. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A151. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A96. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A132. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A196. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A172. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A75. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A174. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A109. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A198. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody A170. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M1. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M2. In certain

embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M3. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M4. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M5. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M6. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M7. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M8. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M9. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M10. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M11. In certain embodiments, an anti-TL1A antibody comprises the CDRs set forth in antibody M12.

[0138] Exemplary anti-TL1A Framework Regions

[0139] **Tables 16-18** and **Table 21** provides exemplary framework and variable region sequences. In some embodiments, an anti-TL1A antibody comprises a HC FR1 of **Table 19** (SEQ ID NO: 304), a HC FR2 of **Table 19** (any one of SEQ ID NOS: 305, 313, 1317), a HC FR3 of **Table 19** (any one of SEQ ID NOS: 306, 307, 314, 315, 1318-1323), a HC FR4 of **Table 19** (SEQ ID NO: 308), a LC FR1 of **Table 19** (SEQ ID NO: 309), a LC FR2 of **Table 19** (SEQ ID NO: 310 or 1324), a LC FR3 of **Table 19** (SEQ ID NO: 311), and a LC FR4 of **Table 19** (SEQ ID NO: 312).

[0140] In some embodiments, an anti-TL1A antibody comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS). In some cases, X1 is Q. In some cases, X1 = E. In some cases, X2 = R. In some cases, X2 = K. In some cases, X3 = A. In some cases, X3 = R. In some cases, X4 = M. In some cases, X4 = I. In some cases, X5 = V. In some cases, X5 = A. In some cases, X6 = M. In some cases, X6 = I. In some cases, X7 = R. In some cases, X7 = T. In some cases, X8 = V. In some cases, X8 = A. In some cases, X9 = M. In some cases, X9 = L. In some embodiments, X1 is at position 1 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X2 is at position 45 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X3 is at position 47 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X4 is at position 55 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X5 is at position 78 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X6 is at position 80 of

IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X7 is at position 82 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X8 is at position 89 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X9 is at position 91 of IGHV1-46*02 as determined by Aho or Kabat numbering.

[0141] In one aspect, provided herein is a first embodiment of an anti-TL1A antibody comprising a heavy chain framework comprising IGHV1-46*02, or a variant thereof, wherein the variant comprises between about 1 and about 9 amino acid substitutions, or between about 1 and about 20 amino acid substitutions, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions from IGHV1-46*02 framework. Additional embodiments include: (2) The anti-TL1A of embodiment (1), wherein the heavy chain framework comprises SEQ ID NO: 301. (3) The anti-TL1A of embodiment 2, wherein X1 = Q. (4) The anti-TL1A of embodiment 2, wherein X1 = E. (5) The anti-TL1A of any one of embodiments 2-4, wherein X2 = R. (6) The anti-TL1A of any one of embodiments 2-4, wherein X2 = K. (7) The anti-TL1A of any one of embodiments 2-6, wherein X3 = A. (8) The anti-TL1A of any one of embodiments 2-6, wherein X3 = R. (9) The anti-TL1A of any one of embodiments 2-8, wherein X4 = M. (10) The anti-TL1A of any one of embodiments 2-8, wherein X4 = I. (11) The anti-TL1A of any one of embodiments 2-10, wherein X5 = V. (12) The anti-TL1A of any one of embodiments 2-10, wherein X5 = A. (13) The anti-TL1A of any one of embodiments 2-12, wherein X6 = M. (14) The anti-TL1A of any one of embodiments 2-12, wherein X6 = I. (15) The anti-TL1A of any one of embodiments 2-14, wherein X7 = R. (16) The anti-TL1A of any one of embodiments 2-14, wherein X7 = T. (17) The anti-TL1A of any one of embodiments 2-16, wherein X8 = V. (18) The anti-TL1A of any one of embodiments 2-16, wherein X8 = A. (19) The anti-TL1A of any one of embodiments 2-18, wherein X9 = M. (20) The anti-TL1A of any one of embodiments 2-4, wherein X9 = L. (21) The anti-TL1A of any one of embodiments 1-20, comprising antibody A. (22) The anti-TL1A of any one of embodiments 1-20, comprising antibody B. (23) The anti-TL1A of any one of embodiments 1-20, comprising antibody C. (24) The anti-TL1A of any one of embodiments 1-20, comprising antibody D. (25) The anti-TL1A of any one of embodiments 1-20, comprising antibody E. (26) The anti-TL1A of any one of embodiments 1-20, comprising antibody F. (27) The anti-TL1A of any one of embodiments 1-20, comprising antibody G or I. (28) The anti-TL1A of any one of embodiments 1-20, comprising antibody H. (29) The anti-TL1A of any one of embodiments 1-28, comprising a human IgG1 Fc region comprising: (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or

279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. As used herein, any combination of a group, such as (a) to (uu), includes at least about two or more items from the group, e.g., any combination of a group of (a) to (uu) includes 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and up to 47 or all of the members of the group. (30) The anti-TL1A of any one of embodiments 1-28, comprising a (i) human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P, (b) S228P and L235E, or (c) S228P, F234A, and L235A, per Kabat numbering. (31) The anti-TL1A of any one of embodiments 1-28, comprising a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ). (32) The anti-TL1A of any one of embodiments 1-31, comprising a heavy chain Fc region comprising any one of SEQ ID NOS: 320-362. (33) The anti-TL1A of any one of embodiments 1-32, comprising a light chain constant region comprising SEQ ID NO: 319. (34) The anti-TL1A of any one of embodiments 1-33, comprising a light chain comprising a light chain framework comprising IGKV3-20*01, or a variant thereof, wherein the variant comprises between about 1 and about 2 substitutions, or between about 1 and about 20 amino acid substitutions, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10,

11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. (35) The anti-TL1A antibody of embodiment 34, wherein X10 is L. (36) The anti-TL1A antibody of embodiment 34, wherein X10 is P. (37) The anti-TL1A antibody of any one of embodiments 34-36, wherein X11 is L. (38) The anti-TL1A antibody of any one of embodiments 34-36, wherein X11 is W.

[0142] In some embodiments, an anti-TL1A antibody comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS). In some cases, X1 is Q. In some cases, X1 = E. In some cases, X2 = R. In some cases, X2 = K. In some cases, X3 = A. In some cases, X3 = R. In some cases, X4 = M. In some cases, X4 = I. In some cases, X5 = V. In some cases, X5 = A. In some cases, X6 = M. In some cases, X6 = I. In some cases, X7 = R. In some cases, X7 = T. In some cases, X8 = V. In some cases, X8 = A. In some cases, X9 = M. In some cases, X9 = L. In some embodiments, X1 is at position 1 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X2 is at position 45 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X3 is at position 47 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X4 is at position 55 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X5 is at position 78 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X6 is at position 80 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X7 is at position 82 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X8 is at position 89 of IGHV1-46*02 as determined by Aho or Kabat numbering. In some embodiments, X9 is at position 91 of IGHV1-46*02 as determined by Aho or Kabat numbering.

[0143] In one aspect, provided herein is another first embodiment of an anti-TL1A antibody comprising a heavy chain framework comprising IGHV1-46*02, or a variant thereof, wherein the variant comprises between about 1 and about 9 amino acid substitutions, or between about 1 and about 20 amino acid substitutions, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions from IGHV1-46*02 framework. Additional embodiments include: (2) The anti-TL1A of embodiment (1), wherein the heavy chain framework comprises SEQ ID NO: 302. (3) The anti-TL1A of embodiment 2, wherein X1 = Q. (4) The anti-TL1A of embodiment 2, wherein X1 = E. (5) The anti-TL1A of any one of embodiments 2-4, wherein X2 = R. (6) The anti-TL1A of any one of

embodiments 2-4, wherein X2 = K. (7) The anti-TL1A of any one of embodiments 2-6, wherein X3 = A. (8) The anti-TL1A of any one of embodiments 2-6, wherein X3 = R. (9) The anti-TL1A of any one of embodiments 2-8, wherein X4 = M. (10) The anti-TL1A of any one of embodiments 2-8, wherein X4 = I. (11) The anti-TL1A of any one of embodiments 2-10, wherein X5 = V. (12) The anti-TL1A of any one of embodiments 2-10, wherein X5 = A. (13) The anti-TL1A of any one of embodiments 2-12, wherein X6 = M. (14) The anti-TL1A of any one of embodiments 2-12, wherein X6 = I. (15) The anti-TL1A of any one of embodiments 2-14, wherein X7 = R. (16) The anti-TL1A of any one of embodiments 2-14, wherein X7 = T. (17) The anti-TL1A of any one of embodiments 2-16, wherein X8 = V. (18) The anti-TL1A of any one of embodiments 2-16, wherein X8 = A. (19) The anti-TL1A of any one of embodiments 2-18, wherein X9 = M. (20) The anti-TL1A of any one of embodiments 2-4, wherein X9 = L. (21) The anti-TL1A of any one of embodiments 1-20, comprising antibody A. (22) The anti-TL1A of any one of embodiments 1-20, comprising antibody B. (23) The anti-TL1A of any one of embodiments 1-20, comprising antibody C. (24) The anti-TL1A of any one of embodiments 1-20, comprising antibody D. (25) The anti-TL1A of any one of embodiments 1-20, comprising antibody E. (26) The anti-TL1A of any one of embodiments 1-20, comprising antibody F. (27) The anti-TL1A of any one of embodiments 1-20, comprising antibody G or I. (28) The anti-TL1A of any one of embodiments 1-20, comprising antibody H. (29) The anti-TL1A of any one of embodiments 1-28, comprising a human IgG1 Fc region comprising: (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and

P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. (30) The anti-TL1A of any one of embodiments 1-28, comprising a (i) human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P and L235E, or (b) S228P, F234A, and L235A, per Kabat numbering. (31) The anti-TL1A of any one of embodiments 1-28, comprising a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ). (32) The anti-TL1A of any one of embodiments 1-31, comprising a heavy chain Fc region comprising any one of SEQ ID NOS: 320-362. (33) The anti-TL1A of any one of embodiments 1-32, comprising a light chain constant region comprising SEQ ID NO: 319. (34) The anti-TL1A of any one of embodiments 1-33, comprising a light chain comprising a light chain framework comprising IGKV3-20*01, or a variant thereof, wherein the variant comprises between about 1 and about 2 substitutions, or between about 1 and about 20 amino acid substitutions, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. (35) The anti-TL1A antibody of embodiment 34, wherein X10 is L. (36) The anti-TL1A antibody of embodiment 34, wherein X10 is P. (37) The anti-TL1A antibody of any one of embodiments 34-36, wherein X11 is L. (38) The anti-TL1A antibody of any one of embodiments 34-36, wherein X11 is W.

[0144] In some embodiments, an anti-TL1A antibody comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK). In some cases, X10 is L. In some cases, X10 is P. In some cases, X11 is L. In some cases, X11 is W. In some embodiments, X10 is at position 54 of IGKV3-20*01 as determined by Aho or Kabat numbering. In some embodiments, X11 is at position 55 of IGKV3-20*01 as determined by Aho or Kabat numbering.

[0145] In some embodiments, an anti-TL1A antibody comprises a heavy chain framework comprising IGHV1-46*02. In some embodiments, an anti-TL1A antibody comprises a heavy chain framework comprising a variant of IGHV1-46*02 comprising between about 1 and about 20 amino acid substitutions from SEQ ID NO: 316. In some embodiments, an anti-TL1A antibody comprises a heavy chain framework comprising a variant of IGHV1-46*02 comprising between about 1 and about 9 amino acid substitutions

from SEQ ID NO: 316. In some embodiments, an anti-TL1A antibody comprises a heavy chain framework comprising a variant of IGHV1-46*02 comprising about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions from SEQ ID NO: 316 in the framework. In some cases, the heavy chain framework substitution comprises Q1E, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises R45K, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises A47R, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises M55I, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises V78A, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises M80I, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises R82T, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises V89A, as determined by Aho or Kabat numbering. In some cases, the heavy chain framework substitution comprises M91L, as determined by Aho or Kabat numbering.

[0146] In some embodiments, an anti-TL1A antibody comprises a light chain framework comprising IGKV3-20*01. In some embodiments, an anti-TL1A antibody comprises a variant of IGKV3-20*01 comprising between about 1 and about 20 amino acid substitutions from SEQ ID NO: 317. In some embodiments, an anti-TL1A antibody comprises a variant of IGKV3-20*01 comprising about 1 amino acid substitution from SEQ ID NO: 317. In some embodiments, an anti-TL1A antibody comprises a light chain framework comprising a variant of IGKV3-20*01 comprising about 2 amino acid substitutions from SEQ ID NO: 317. In some embodiments, an anti-TL1A antibody comprises a light chain framework comprising a variant of IGKV3-20*01 comprising about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions from SEQ ID NO: 317 in the framework. In some cases, the light chain framework substitution comprises Q1E, as determined by Aho or Kabat numbering. In some cases, the light chain framework substitution comprises R45K, as determined by Aho or Kabat numbering.

[0147] In some embodiments, an anti-TL1A antibody comprises a heavy chain FR1 as set forth by SEQ ID NO: 304. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR2 as set forth by SEQ ID NO: 305. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR2 as set forth by SEQ ID NO: 313. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR2 as set forth by SEQ ID NO: 1317. In some

embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 306. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 307. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 314. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 315. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 1318. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 1319. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 1320. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 1321. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 1322. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR3 as set forth by SEQ ID NO: 1323. In some embodiments, an anti-TL1A antibody comprises a heavy chain FR4 as set forth by SEQ ID NO: 308. In some embodiments, an anti-TL1A antibody comprises a light chain FR1 as set forth by SEQ ID NO: 309. In some embodiments, an anti-TL1A antibody comprises a light chain FR2 as set forth by SEQ ID NO: 310. In some embodiments, an anti-TL1A antibody comprises a light chain FR2 as set forth by SEQ ID NO: 1324. In some embodiments, an anti-TL1A antibody comprises a light chain FR3 as set forth by SEQ ID NO: 311. In some embodiments, an anti-TL1A antibody comprises a light chain FR3 as set forth by SEQ ID NO: 1325. In some embodiments, an anti-TL1A antibody comprises a light chain FR4 as set forth by SEQ ID NO: 312.

[0148] In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in any one of the antibodies in **Table 1**, wherein the framework regions are defined by the Aho or Kabat, Chothia, or IMGT method. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A217. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A220. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A223. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A219. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A221. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A200. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A213. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A212. In certain embodiments, an anti-TL1A

antibody comprises the framework regions set forth in antibody A107. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A205. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A211. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A199. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A15. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A30. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A100. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A181. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A129. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A214. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A216. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A122. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A222. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A188. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A203. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A147. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A127. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A126. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A160. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A157. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A159. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A218. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A158. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A125. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A103. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A64. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A67. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody

A138. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A68. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A94. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A110. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A197. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A112. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A169. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A173. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A179. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A148. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A115. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A149. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A134. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A113. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A151. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A96. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A132. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A196. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A172. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A75. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A174. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A109. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A198. In certain embodiments, an anti-TL1A antibody comprises the framework regions set forth in antibody A170.

[0149] In certain embodiments, an anti-TL1A antibody comprises the heavy chain framework regions set forth in any one of the antibodies in **Table 16**, and the light chain framework regions set forth in any one of the antibodies in **Table 17**, wherein the framework regions are defined by the Aho or Kabat, Chothia, or IMGT method.

Exemplary anti-TL1A Variable Regions

[0150] In one aspect, provided herein is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 101-135; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 201-206.

[0151] Further provided herein is a first embodiment of an anti-TL1A antibody comprising a heavy chain variable region and a light chain variable region. Non-limiting additional embodiments include: (Embodiment 2) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 101. (Embodiment 3) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 101. (Embodiment 4) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 101. (Embodiment 5) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 102. (Embodiment 6) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 102. (Embodiment 7) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 102. (Embodiment 8) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 103. (Embodiment 9) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 103. (Embodiment 10) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 103.

[0152] (Embodiment 11) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 104. (Embodiment 12) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 104. (Embodiment 13) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid

substitutions or deletions as compared to SEQ ID NO: 104. (Embodiment 14) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 105. (Embodiment 15) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 105. (Embodiment 16) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 105. (Embodiment 17) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 106. (Embodiment 18) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 106. (Embodiment 19) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 106. (Embodiment 20) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 107. (Embodiment 21) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 107. (Embodiment 22) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 107.

[0153] (Embodiment 23) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 108. (Embodiment 24) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 108. (Embodiment 25) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 108. (Embodiment 26) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 109. (Embodiment 27) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 109. (Embodiment 28) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO:

109. (Embodiment 29) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 110. (Embodiment 30) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 110. (Embodiment 31) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 110. (Embodiment 32) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 111. (Embodiment 33) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 111. (Embodiment 34) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 111. (Embodiment 35) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 112. (Embodiment 36) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 112. (Embodiment 37) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 112. (Embodiment 38) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 113. (Embodiment 39) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 113. (Embodiment 40) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 113.

[0154] (Embodiment 41) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 114. (Embodiment 42) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 114. (Embodiment 43) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 114. (Embodiment 44) The anti-TL1A

antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 115. (Embodiment 45) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 115. (Embodiment 46) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 115. (Embodiment 47) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 116. (Embodiment 48) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 116. (Embodiment 49) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 116. (Embodiment 50) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 117. (Embodiment 51) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 117. (Embodiment 52) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 117.

[0155] (Embodiment 53) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 118. (Embodiment 54) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 118. (Embodiment 55) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 118. (Embodiment 56) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 119. (Embodiment 57) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 119. (Embodiment 58) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 119. (Embodiment 59) The anti-TL1A antibody of embodiment 1, wherein the heavy chain

variable region comprises SEQ ID NO: 120. (Embodiment 60) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 120. (Embodiment 61) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 120.

[0156] (Embodiment 62) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 121. (Embodiment 63) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 121. (Embodiment 64) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 121. (Embodiment 65) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 122. (Embodiment 66) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 122. (Embodiment 67) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 122. (Embodiment 68) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 123. (Embodiment 69) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 123. (Embodiment 70) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 123. (Embodiment 71) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 124. (Embodiment 72) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 124. (Embodiment 73) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 124.

[0157] (Embodiment 74) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 125. (Embodiment 75) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 125. (Embodiment 76) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 125. (Embodiment 77) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 126. (Embodiment 78) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 126. (Embodiment 79) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 126. (Embodiment 80) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 127. (Embodiment 81) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 127. (Embodiment 82) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 127. (Embodiment 83) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 128. (Embodiment 84) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 128. (Embodiment 85) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 128.

[0158] (Embodiment 86) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 129. (Embodiment 87) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 129. (Embodiment 88) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 129. (Embodiment 89) The anti-TL1A

antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 130. (Embodiment 90) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 130. (Embodiment 91) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 130. (Embodiment 92) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 131. (Embodiment 93) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 131. (Embodiment 94) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 131. (Embodiment 95) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 132. (Embodiment 96) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 132. (Embodiment 97) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 132.

[0159] (Embodiment 98) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 133. (Embodiment 99) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 133. (Embodiment 100) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 133. (Embodiment 101) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises SEQ ID NO: 134. (Embodiment 102) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 134. (Embodiment 103) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 134. (Embodiment 104) The anti-TL1A antibody of embodiment 1, wherein the heavy chain

variable region comprises SEQ ID NO: 135. (Embodiment 105) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 135. (Embodiment 106) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 135.

[0160] (Embodiment 107) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises SEQ ID NO: 201. (Embodiment 108) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 109) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 201. (Embodiment 110) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises SEQ ID NO: 202. (Embodiment 111) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202. (Embodiment 112) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 202. (Embodiment 113) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises SEQ ID NO: 203. (Embodiment 114) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203. (Embodiment 115) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 203. (Embodiment 116) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises SEQ ID NO: 204. (Embodiment 117) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204. (Embodiment 118) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ

ID NO: 204. (Embodiment 119) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises SEQ ID NO: 205. (Embodiment 120) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 121) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 205. (Embodiment 122) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises SEQ ID NO: 206. (Embodiment 123) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 206. (Embodiment 124) The anti-TL1A antibody of any one of embodiments 1-106, wherein the light chain variable region comprises a sequence having about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid substitutions or deletions as compared to SEQ ID NO: 206.

[0161] (Embodiment 125) The anti-TL1A antibody of embodiment 1, comprising A217. (Embodiment 126) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 101, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 127) The anti-TL1A antibody of embodiment 1, comprising A220. (Embodiment 128) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 102, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 129) The anti-TL1A antibody of embodiment 1, comprising A223. (Embodiment 130) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 103, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202. (Embodiment 131) The anti-TL1A antibody of embodiment 1, comprising A219. (Embodiment 132) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 104, and the light chain variable region comprises a sequence

at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 133) The anti-TL1A antibody of embodiment 1, comprising A221. (Embodiment 134) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 105, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.

[0162] (Embodiment 135) The anti-TL1A antibody of embodiment 1, comprising A200. (Embodiment 136) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 103, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 137) The anti-TL1A antibody of embodiment 1, comprising A213. (Embodiment 138) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 106, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 139) The anti-TL1A antibody of embodiment 1, comprising A212. (Embodiment 140) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 107, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202. (Embodiment 141) The anti-TL1A antibody of embodiment 1, comprising A107. (Embodiment 142) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 108, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202. (Embodiment 143) The anti-TL1A antibody of embodiment 1, comprising A205. (Embodiment 144) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 109, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202.

[0163] (Embodiment 145) The anti-TL1A antibody of embodiment 1, comprising A211. (Embodiment 146) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or

100% identical to SEQ ID NO: 108, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.
(Embodiment 147) The anti-TL1A antibody of embodiment 1, comprising A199.
(Embodiment 148) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 109, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.
(Embodiment 149) The anti-TL1A antibody of embodiment 1, comprising A15.
(Embodiment 150) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 108, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203.
(Embodiment 151) The anti-TL1A antibody of embodiment 1, comprising A30.
(Embodiment 152) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 108, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.
(Embodiment 153) The anti-TL1A antibody of embodiment 1, comprising A100.
(Embodiment 154) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 107, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.

[0164] (Embodiment 155) The anti-TL1A antibody of embodiment 1, comprising A181.
(Embodiment 156) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 107, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202.
(Embodiment 157) The anti-TL1A antibody of embodiment 1, comprising A129.
(Embodiment 158) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 110, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.
(Embodiment 159) The anti-TL1A antibody of embodiment 1, comprising A214.
(Embodiment 160) The anti-TL1A antibody of embodiment 1, wherein the heavy chain

variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 111, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.
(Embodiment 161) The anti-TL1A antibody of embodiment 1, comprising A216.
(Embodiment 162) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 112, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.
(Embodiment 163) The anti-TL1A antibody of embodiment 1, comprising A122.
(Embodiment 164) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 113, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.

[0165] (Embodiment 165) The anti-TL1A antibody of embodiment 1, comprising A222.
(Embodiment 166) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 114, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.
(Embodiment 167) The anti-TL1A antibody of embodiment 1, comprising A188.
(Embodiment 168) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 115, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202.
(Embodiment 169) The anti-TL1A antibody of embodiment 1, comprising A203.
(Embodiment 170) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 116, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.
(Embodiment 171) The anti-TL1A antibody of embodiment 1, comprising A147.
(Embodiment 172) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 117, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.
(Embodiment 173) The anti-TL1A antibody of embodiment 1, comprising A127.

(Embodiment 174) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 118, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.

[0166] (Embodiment 175) The anti-TL1A antibody of embodiment 1, comprising A126. (Embodiment 176) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 114, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204. (Embodiment 177) The anti-TL1A antibody of embodiment 1, comprising A160. (Embodiment 178) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 102, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204. (Embodiment 179) The anti-TL1A antibody of embodiment 1, comprising A157. (Embodiment 180) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 104, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204. (Embodiment 181) The anti-TL1A antibody of embodiment 1, comprising A159. (Embodiment 182) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 119, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204. (Embodiment 183) The anti-TL1A antibody of embodiment 1, comprising A218. (Embodiment 184) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 119, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.

[0167] (Embodiment 185) The anti-TL1A antibody of embodiment 1, comprising A158. (Embodiment 186) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 101, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.

(Embodiment 187) The anti-TL1A antibody of embodiment 1, comprising A125.
(Embodiment 188) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 105, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.
(Embodiment 189) The anti-TL1A antibody of embodiment 1, comprising A103.
(Embodiment 190) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 120, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.
(Embodiment 191) The anti-TL1A antibody of embodiment 1, comprising A64.
(Embodiment 192) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 121, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202.
(Embodiment 193) The anti-TL1A antibody of embodiment 1, comprising A67.
(Embodiment 194) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 122, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202.

[0168] (Embodiment 195) The anti-TL1A antibody of embodiment 1, comprising A138.
(Embodiment 196) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 122, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204.
(Embodiment 197) The anti-TL1A antibody of embodiment 1, comprising A68.
(Embodiment 198) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 123, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202.
(Embodiment 199) The anti-TL1A antibody of embodiment 1, comprising A94.
(Embodiment 200) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 124, and the light chain variable region comprises a sequence

at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202. (Embodiment 201) The anti-TL1A antibody of embodiment 1, comprising A110. (Embodiment 202) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 125, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 203) The anti-TL1A antibody of embodiment 1, comprising A197. (Embodiment 204) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 116, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205.

[0169] (Embodiment 205) The anti-TL1A antibody of embodiment 1, comprising A112. (Embodiment 206) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 117, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 207) The anti-TL1A antibody of embodiment 1, comprising A169. (Embodiment 208) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 126, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 209) The anti-TL1A antibody of embodiment 1, comprising A173. (Embodiment 210) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 127, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 211) The anti-TL1A antibody of embodiment 1, comprising A179. (Embodiment 212) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 127, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 213) The anti-TL1A antibody of embodiment 1, comprising A148. (Embodiment 214) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or

100% identical to SEQ ID NO: 121, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.

[0170] (Embodiment 215) The anti-TL1A antibody of embodiment 1, comprising A115. (Embodiment 216) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 122, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 217) The anti-TL1A antibody of embodiment 1, comprising A149. (Embodiment 218) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 122, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201. (Embodiment 219) The anti-TL1A antibody of embodiment 1, comprising A134. (Embodiment 220) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 122, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 206. (Embodiment 221) The anti-TL1A antibody of embodiment 1, comprising A113. (Embodiment 222) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 124, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 223) The anti-TL1A antibody of embodiment 1, comprising A151. (Embodiment 224) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 124, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 201.

[0171] (Embodiment 225) The anti-TL1A antibody of embodiment 1, comprising A96. (Embodiment 226) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 128, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 227) The anti-TL1A antibody of embodiment 1, comprising A132. (Embodiment 228) The anti-TL1A antibody of embodiment 1, wherein the heavy chain

variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 128, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 206.
(Embodiment 229) The anti-TL1A antibody of embodiment 1, comprising A196.
(Embodiment 230) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 129, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205.
(Embodiment 231) The anti-TL1A antibody of embodiment 1, comprising A172.
(Embodiment 232) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 130, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205.
(Embodiment 233) The anti-TL1A antibody of embodiment 1, comprising A75.
(Embodiment 234) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 131, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205.

[0172] (Embodiment 235) The anti-TL1A antibody of embodiment 1, comprising A174.
(Embodiment 236) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 132, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205.
(Embodiment 237) The anti-TL1A antibody of embodiment 1, comprising A109.
(Embodiment 238) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 133, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205.
(Embodiment 239) The anti-TL1A antibody of embodiment 1, comprising A198.
(Embodiment 240) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 134, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205.
(Embodiment 241) The anti-TL1A antibody of embodiment 1, comprising A170.

(Embodiment 242) The anti-TL1A antibody of embodiment 1, wherein the heavy chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 135, and the light chain variable region comprises a sequence at least about 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 205. (Embodiment 243) The anti-TL1A antibody of embodiment 1, comprising A500. (Embodiment 244) The anti-TL1A antibody of embodiment 1, comprising A501.

[0173] (Embodiment 245) The anti-TL1A of any one of embodiments 1-244, comprising a human IgG1 Fc region comprising: (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. (Embodiment 246) The anti-TL1A of any one of embodiments 1-244, comprising a (i) human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P and L235E, or (b) S228P, F234A, and L235A, per Kabat numbering. (Embodiment 247) The anti-TL1A of any one of embodiments 1-244, comprising a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ). (Embodiment 248) The anti-TL1A of any one of embodiments 1-247, comprising a heavy chain Fc region comprising any one of SEQ ID NOS: 320-362.

(Embodiment 249) The anti-TL1A of any one of embodiments 1-248, comprising a light chain constant region comprising SEQ ID NO: 319.

[0174] (Embodiment 250) The anti-TL1A of any one of embodiments 1-249, comprising at least about 80% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 251) The anti-TL1A of any one of embodiments 1-250, comprising at least about 81%, at least about 82%, at least about 83%, or at least about 84% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 252) The anti-TL1A of any one of embodiments 1-251, comprising at least about 85% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 253) The anti-TL1A of any one of embodiments 1-252, comprising at least about 86%, at least about 87%, at least about 88%, or at least about 89% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 254) The anti-TL1A of any one of embodiments 1-253, comprising at least about 90% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 255) The anti-TL1A of any one of embodiments 1-254, comprising at least about 91%, at least about 92%, at least about 93%, or at least about 94% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 256) The anti-TL1A of any one of embodiments 1-255, comprising at least about 95% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 257) The anti-TL1A of any one of embodiments 1-256, comprising at least about 96%, at least about 97%, at least about 98%, or at least about 99% monomeric fraction as determined by the size exclusion chromatography method described herein.

[0175] (Embodiment 258) The anti-TL1A of any one of embodiments 1-257, comprising at least about 2 μg/mL expression as determined by the method disclosed herein. (Embodiment 259) The anti-TL1A of any one of embodiments 1-258, comprising between about 2 μg/mL and about 60 μg/mL expression as determined by the method disclosed herein. (Embodiment 260) The anti-TL1A of any one of embodiments 1-259, comprising between about 5 μg/mL and about 60 μg/mL expression as determined by the method disclosed herein. (Embodiment 261) The anti-TL1A of any one of embodiments 1-260, comprising between about 10 μg/mL and about 60 μg/mL expression as determined by the method disclosed herein. (Embodiment 262) The anti-TL1A of any one of embodiments 1-261, comprising at least about 5 μg/mL expression as determined by the method disclosed herein. (Embodiment 263) The anti-TL1A of any one of embodiments 1-262, comprising at

least about 10 μg/mL expression as determined by the method disclosed herein. (Embodiment 264) The anti-TL1A of any one of embodiments 1-263, comprising at least about 15 μg/mL expression as determined by the method disclosed herein. (Embodiment 265) The anti-TL1A of any one of embodiments 1-264, comprising at least about 20 μg/mL expression as determined by the method disclosed herein.

[0176] In one aspect, provided herein is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1200-1263; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1264-1300, 1304-1316.

[0177] In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 136; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202 (clone 34). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1200; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 12646 (5C3D11). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1201; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1265 (9E12E5). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1202; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 208 (AS12824). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1203; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1266 (AS12823). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence

at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1204; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1267 (AS12819). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1205; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1268 (AS12816). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1206; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1269 (AS12825). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1207; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1270 (12835). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1208; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202 (18-7 S93E). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1208; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (18-7). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1208; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1272 (18-7 S92D). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1208; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%,

or 100% identical to SEQ ID NO: 1273 (18-7 S92H). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1208; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1274 (18-7 S92N). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1208; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1275 (18-7 S92Q). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1208; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1276 (18-7 CDRv). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1209; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1271 (21-3). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1210; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1271 (21-3 V102K). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1211; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1271 (21-3 V102M). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1212; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1271 (21-3 V102Q). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1213; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1271 (21-3 V102W). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1214; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1271 (21-3 CDRv). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1215; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1271 (21-3 CDRv). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1216; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202 (clone 2). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1216; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1277 (clone 52). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1217; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202 (clone 46). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1218; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202 (clone 47). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1219; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1275

(clone 14). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1220; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1275 (clone 16L). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1221; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1275 (clone 17L). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1222; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1275 (clone 17L-1). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1223; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202 (clone 23). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1224; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 202 (clone 53). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1224; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1277 (clone E1). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1225; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1275 (clone 3-17L V-A). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or

100% identical to SEQ ID NO: 1226; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1275 (clone 3-17L). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1227; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (clone L8mod). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1209; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (clone L8). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1228; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (clone X-V). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1229; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (clone X). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1229; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1278 (clone XL3-6). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1229; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1279 (clone XL3-10). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1229; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 207 (clone XL3-15). In one aspect, provided is

an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1229; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 204 (clone L3-13). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1230; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (clone H3-1). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1231; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (clone H2-2). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1232; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 203 (clone H2-5). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1233; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1280 (M1). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1234; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1281 (M2). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1235; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1282 (M3). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1235; and a light chain variable

region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1283 (M3). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1237; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1284 (M4). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1238; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1285 (M5). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1239-1242; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1286-1293 (M6). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1243-1247; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1294-1297 (M7). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1248-1259; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 1298-1312 (M8). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1260; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1313 (M9). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1261; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1314 (M10). In one aspect, provided is an anti-TL1A

antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1262; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1315 (M11). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1263; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1316 (M12). In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 301; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 303. In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 302; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 303. In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1301; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 303. In one aspect, provided is an anti-TL1A antibody comprising a heavy chain variable region comprising an amino acid sequence at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 1302; and a light chain variable region at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to SEQ ID NO: 303.

Exemplary anti-TL1A Constant Regions

[0178] In some embodiments, one or more amino acid modifications may be introduced into the Fragment crystallizable (Fc) region of a human or humanized antibody, thereby generating an Fc region variant. An Fc region may comprise a C-terminal region of an immunoglobulin heavy chain that comprises a hinge region, CH2 domain, CH3 domain, or any combination thereof. As used herein, an Fc region includes native sequence Fc regions and variant Fc regions. The Fc region variant may comprise a human Fc region sequence (*e.g.*, a human IgG1, IgG2, IgG3 or IgG4 Fc region) comprising an amino acid modification

(*e.g.*, a substitution, addition, or deletion) at one or more amino acid positions. In an exemplary embodiment, the Fc region comprises any one of SEQ ID NOS: 320-362, 401-413, 501-515.

[0179] In some embodiments, antibodies of this disclosure have a reduced effector function as compared to a human IgG. Effector function refers to a biological event resulting from the interaction of an antibody Fc region with an Fc receptor or ligand. Non-limiting effector functions include C1q binding, complement dependent cytotoxicity (CDC), Fc receptor binding, antibody-dependent cell-mediated cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), cytokine secretion, immune complex-mediated antigen uptake by antigen presenting cells, down regulation of cell surface receptors (e.g. B cell receptor), and B cell activation. In some cases, antibody-dependent cell-mediated cytotoxicity (ADCC) refers to a cell-mediated reaction in which nonspecific cytotoxic cells expressing Fc receptors (e.g., natural killer cells, neutrophils, macrophages) recognize bound antibody on a target cell, subsequently causing lysis of the target cell. In some cases, complement dependent cytotoxicity (CDC) refers to lysing of a target cells in the presence of complement, where the complement action pathway is initiated by the binding of C1q to antibody bound with the target.

[0180] Some Fc regions have a natural lack of effector function, and some Fc regions can comprise mutations that reduce effector functions. For instance, IgG4 has low ADCC and CDC activities and IgG2 has low ADCC activity.

[0181] The disclosure provides antibodies comprising Fc regions characterized by exhibiting ADCC that is reduced by at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70% or more as compared to an antibody comprising a non-variant Fc region, i.e., an antibody with the same sequence identity but for the substitution(s) that decrease ADCC (such as human IgG1, SEQ ID NO: 320). The disclosure provides antibodies comprising Fc regions characterized by exhibiting CDC that is reduced by at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70% or more as compared to an antibody comprising a non-variant Fc region, i.e., an antibody with the same sequence identity but for the substitution(s) that decrease CDC (such as human IgG1, SEQ ID NO: 320). In certain embodiments, the antibodies of this disclosure have reduced effector function as compared with human IgG1. Measurement of effector function may be performed as described in Example 3.

[0182] Non-limiting examples of Fc mutations in IgG1 that may reduce ADCC and/or CDC include substitutions at one or more of positions: 231, 232, 234, 235, 236, 237, 238,

239, 264, 265, 267, 269, 270, 297, 299, 318, 320, 322, 325, 327, 328, 329, 330, and 331 in IgG1, where the numbering system of the constant region is that of the EU index as set forth by Kabat. In certain embodiments, the antibodies of this disclosure have reduced effector function as compared with human IgG1.

[0183] In some embodiments, an antibody comprises an IgG1 Fc region comprising an N297A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an N297Q substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an N297D substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an D265A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an S228P substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an L235A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an L237A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an L234A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an E233P substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an L234V substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an C236 deletion, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising a P238A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an A327Q substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising a P329A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an P329G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an L235E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an P331S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an L234F substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising a 235G substitution,

according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 235Q substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 235R substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 235S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 236F substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 236R substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 237E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 237K substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 237N substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 237R substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238H substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238I substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238V substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238W substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 238Y substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 248A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254D substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254G substitution, according to the Kabat numbering system.

In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254H substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254I substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254N substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254P substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254Q substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254T substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 254V substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 255N substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 256H substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 256K substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 256R substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 256V substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 264S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 265H substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 265K substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 265S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 265Y substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 267G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 267H substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 267I substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 267K substitution, according to the Kabat numbering system. In some embodiments, an antibody

comprises an IgG1 Fc region comprising an 268K substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 269N substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 269Q substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 270A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 270G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 270M substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 270N substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 271T substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 272N substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 279F substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 279K substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 279L substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 292E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 292F substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 292G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 292I substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 293S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 301W substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 304E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 311E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 311G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region

comprising an 311S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 316F substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 327T substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 328V substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 329Y substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 330R substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 339E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 339L substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 343I substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 343V substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 373A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 373G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 373S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 376E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 376W substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 376Y substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 380D substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 382D substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 382P substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 385P substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 424H substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 424M substitution,

according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 424V substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 434I substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 438G substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 439E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 439H substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 439Q substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 440A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 440D substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 440E substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 440F substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 440M substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 440T Fc region substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising an 440V substitution, according to the Kabat numbering system.

[0184] In some embodiments, an antibody comprises a Fc region selected from the representative sequences disclosed in **Table 3 or 20** In some embodiments, an antibody comprises an IgG1 Fc region comprising E233P, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG4 Fc region comprising S228P and L235E. In some embodiments, an antibody comprises an IgG1 Fc region comprising L235E, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising L234A and L235A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising L234A, L235A, and G237A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising L234A, L235A, P329G, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising L234F, L235E, and P331S, according to the Kabat numbering system. In some

embodiments, an antibody comprises an IgG1 Fc region comprising L234A, L235E, and G237A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising L234A, L235E, G237A, and P331S, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising L234A, L235A, and P329A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising G236R and L328R, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising G237A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising F241A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising V264A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising D265A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising D265A and N297A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising D265A and N297G, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising D270A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising N297A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising N297G, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising N297D, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising N297Q, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising P329A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising P329G, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising P329R, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising A330L, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising P331A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG1 Fc region comprising P331S, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG2 Fc region. In some embodiments, an antibody

comprises an IgG4 Fc region. In some embodiments, an antibody comprises an IgG4 Fc region comprising S228P, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG4 Fc region comprising S228P, F234A, and L235A, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG2-IgG4 cross-subclass (IgG2/G4) Fc region. In some embodiments, an antibody comprises an IgG2-IgG3 cross-subclass Fc region. In some embodiments, an antibody comprises an IgG2 Fc region comprising H268Q, V309L, A330S, and P331S, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG2 Fc region comprising V234A, G237A, P238S, H268A, V309L, A330S, and P331S, according to the Kabat numbering system. In some embodiments, an antibody comprises a Fc region comprising high mannose glycosylation.

[0185] In some embodiments, an antibody comprises an IgG4 Fc region comprising a S228P substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG4 Fc region comprising an A330S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG4 Fc region comprising a P331S substitution, according to the Kabat numbering system.

[0186] In some embodiments, an antibody comprises an IgG2 Fc region comprising an A330S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG2 Fc region comprising an P331S substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG2 Fc region comprising an 234A substitution, according to the Kabat numbering system. In some embodiments, an antibody comprises an IgG2 Fc region comprising an 237A substitution, according to the Kabat numbering system.

[0187] In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising a sequence from **Table 19**. In certain embodiments, an anti-TL1A described herein comprises a Fc region as shown in **Table 3**.

Table 3. Exemplary Fc Mutations

Mutations	Constant Region (SEQ ID NO)		
	K_DL	R_EM	K_EM
Wild-type IgG1	320	321	322
L235E	323	324	325
L234A, L235A	326	327	328
L234A, L235A, G237A	329	330	331
L234A, L235A, P329G	332	333	334
L234F, L235E, P331S	335	336	337
L234A, L235E, G237A	338	339	340

L234A, L235E, G237A, P331S	341	342	343
L234A, L235A, P329A	344	345	346
D265A	347	348	349
N297G	350	351	352
D265A, N297A	353	354	355
D265A, N297G	356	357	358
L235A, G237A	359	360	361
Wild-type IgG4	362		

[0188] In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 320 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 320. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 321 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 321. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 322 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 322. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 323 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 323. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 324 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 324. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 325 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 325. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 326 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 326. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 327 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 327. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 328 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 328. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 329 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 329. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region

comprising SEQ ID NO: 330 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 330. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 331 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 331. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 332 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 332. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 333 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 333. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 334 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 334. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 335 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 335. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 336 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 336. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 337 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 337. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 338 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 338. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 339 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 339. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 340 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 340. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 341 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 341. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 342 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 342. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising

SEQ ID NO: 343 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 343. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 344 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 344. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 345 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 345. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 346 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 346. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 347 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 347. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 348 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 348. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 349 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 349. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 350 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 350. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 351 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 351. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 352 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 352. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 353 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 353. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 354 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 354. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 355 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 355. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 356 or a

sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 356. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 357 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 357. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 358 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 358. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 359 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 359. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 360 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 360. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 361 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 361. In certain embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 362 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 362.

[0189] In some embodiments, the antibodies of this disclosure are variants that possess some but not all effector functions, which make it a desirable candidate for applications in which the half-life of the antibody *in vivo* is important yet certain effector functions (such as complement and ADCC) are unnecessary or deleterious.

[0190] *In vitro* and/or *in vivo* cytotoxicity assays can be conducted to confirm the reduction/depletion of CDC and/or ADCC activities. For example, Fc receptor (FcR) binding assays can be conducted to ensure that the antibody lacks FcγR binding (hence likely lacking ADCC activity) but retains FcRn binding ability. Measurement of effector function may be performed as described in Example 3.

[0191] In some embodiments, antibodies are tested for binding to Fcγ receptors and complement C1q by ELISA. In some embodiments, antibodies are tested for the ability to activate primary human immune cells in vitro, for example, by assessing their ability to induce expression of activation markers.

[0192] In some embodiments, assessment of ADCC activity of an anti-TL1A antibody comprises adding the antibody to target cells in combination with immune effector cells, which may be activated by the antigen antibody complexes resulting in cytolysis of the target cell. Cytolysis may be detected by the release of label (e.g. radioactive substrates, fluorescent

dyes or natural intracellular proteins) from the lysed cells. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Specific examples of in vitro ADCC assays are described in Wisecarver et al., 1985 79:277-282; Bruggemann et al., 1987, J Exp Med 166:1351-1361; Wilkinson et al., 2001, J Immunol Methods 258:183-191; Patel et al., 1995 J Immunol Methods 184:29-38. Alternatively, or additionally, ADCC activity of the antibody of interest may be assessed in vivo, e.g., in an animal model such as that disclosed in Clynes et al., 1998, PNAS USA 95:652-656.

[0193] In some embodiments, antibodies comprising a Fc region herein exhibit decreased ADCC activities as compared to an unmodified antibody (e.g., an antibody with human IgG1). In some embodiments, the antibodies herein exhibit ADCC activities that are at least 2-fold, or at least 3-fold, or at least 5-fold or at least 10-fold or at least 50-fold or at least 100-fold less than that of an unmodified antibody. In some embodiments, antibodies herein exhibit ADCC activities that are reduced by at least 10%, or at least 20%, or by at least 30%, or by at least 40%, or by at least 50%, or by at least 60%, or by at least 70%, or by at least 80%, or by at least 90%, or by at least 100%, or by at least 200%, or by at least 300%, or by at least 400%, or by at least 500% relative to an unmodified antibody. In certain embodiments, antibodies herein have no detectable ADCC activity. In certain embodiments, the reduction and/or abatement of ADCC activity may be attributed to the reduced affinity antibodies of the invention exhibit for Fc ligands and/or receptors.

[0194] In some embodiments, an assessment of complement activation, a CDC assay, may be performed as described in Gazzano-Santoro et al., 1996, J. Immunol. Methods, 202:163.

[0195] In some embodiments, antibodies comprising Fc regions described herein exhibit decreased affinities to C1q relative to an unmodified antibody (e.g., human IgG1). In some embodiments, antibodies herein exhibit affinities for C1q receptor that are at least 2 fold, or at least 3 fold, or at least 5 fold, or at least 7 fold, or at least 10 fold, or at least 20 fold, or at least 30 fold, or at least 40 fold, or at least 50 fold, or at least 60 fold, or at least 70 fold, or at least 80 fold, or at least 90 fold, or at least 100 fold, or at least 200 fold less than an unmodified antibody. In some embodiments, antibodies herein exhibit affinities for C1q that are at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30%, at least 20%, at least 10%, or at least 5% less than an unmodified antibody. In some embodiments, antibodies herein exhibit affinities for C1q that are between about 100 nM to about 100 μM, or about 100 nM to about 10 μM, or about 100 nM to about 1 μM, or about 1 nM to about 100 μM, or about 10 nM to about 100 μM, or about 1 μM to about 100 μM, or

about 10 μM to about 100 μM. In certain embodiments, antibodies herein exhibit affinities for C1q that are greater than 1 μM, greater than 5 μM, greater than 10 μM, greater than 25 μM, greater than 50 μM, or greater than 100 μM.

[0196] In some embodiments, antibodies comprising Fc regions described herein exhibit decreased CDC activities as compared to an unmodified antibody (e.g., human IgG1). In some embodiments, antibodies herein exhibit CDC activities that are at least 2-fold, or at least 3-fold, or at least 5-fold or at least 10-fold or at least 50-fold or at least 100-fold less than that of an unmodified antibody. In some embodiments, antibodies herein exhibit CDC activities that are reduced by at least 10%, or at least 20%, or by at least 30%, or by at least 40%, or by at least 50%, or by at least 60%, or by at least 70%, or by at least 80%, or by at least 90%, or by at least 100%, or by at least 200%, or by at least 300%, or by at least 400%, or by at least 500% relative to an unmodified antibody. In certain embodiments, antibodies herein exhibit no detectable CDC activities. In some embodiments, the reduction and/or abatement of CDC activity may be attributed to the reduced affinity antibodies of the invention exhibit for Fc ligands and/or receptors.

[0197] Accordingly, further provided and described herein are anti-TL1A antibodies comprising a variant (e.g. harboring mutations) Fc region that reduce the cytotoxic response (e.g. ADCC or CDC) elicited by an anti-TL1A antibody. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 401 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 401. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 402 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 402. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 403 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 403. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 404 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 404. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 405 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 405. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 406 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 406. In some embodiments, an anti-TL1A antibody described herein comprises a Fc

region comprising SEQ ID NO: 407 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 407. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 408 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 408. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 409 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 409. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 410 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 410. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 411 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 411. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 412 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 412. In some embodiments, an anti-TL1A antibody described herein comprises a Fc region comprising SEQ ID NO: 413 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 413.

[0198] By way of further example, in certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 501 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 501. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 502 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 502. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 503 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 503. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 504 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 504. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 505 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 505. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 506 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO:

506. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 507 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 507. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 508 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 508. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 509 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 509. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 510 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 510. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 511 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 511. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 512 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 512. In certain embodiments, an anti-TL1A antibody described herein comprises a heavy chain comprising SEQ ID NO: 513 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 513. In certain embodiments, the heavy chain is paired with a light chain comprising SEQ ID NO: 514 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 514. In certain embodiments, the heavy chain is paired with the light chain variable region of SEQ ID NO: 514 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the light chain variable region of SEQ ID NO: 514. In certain embodiments, the heavy chain is paired with the light chain variable region of SEQ ID NO: 514 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the light chain variable region of SEQ ID NO: 515.

[0199] In some embodiments, anti-TL1A described herein comprise a light chain constant region comprising SEQ ID NO: 319 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to SEQ ID NO: 319.

Further Non-limiting Exemplary anti-TL1A Antibodies

[0200] In one aspect, provided herein is a first embodiment of an anti-TL1A antibody comprising a heavy chain comprising a HCDR1, a HCDR2, and a HCDR3, and a light chain comprising a LCDR1, a LCDR2, and a LCDR3. Non-limiting additional embodiments

include: (Embodiment 2) The anti-TL1A antibody of embodiment 1, comprising a HCDR1 comprising SEQ ID NO: 1. (Embodiment 3) The anti-TL1A antibody of embodiment 1 or embodiment 2, comprising a HCDR2 comprising SEQ ID NO: 2. (Embodiment 4) The anti-TL1A antibody of embodiment 1 or embodiment 2, comprising a HCDR2 comprising SEQ ID NO: 3. (Embodiment 5) The anti-TL1A antibody of embodiment 1 or embodiment 2, comprising a HCDR2 comprising SEQ ID NO: 4. (Embodiment 6) The anti-TL1A antibody of embodiment 1 or embodiment 2, comprising a HCDR2 comprising SEQ ID NO: 5. (Embodiment 7) The anti-TL1A antibody of any one of embodiments 1-6, comprising a HCDR3 comprising SEQ ID NO: 6. (Embodiment 8) The anti-TL1A antibody of any one of embodiments 1-6, comprising a HCDR3 comprising SEQ ID NO: 7. (Embodiment 9) The anti-TL1A antibody of any one of embodiments 1-6, comprising a HCDR3 comprising SEQ ID NO: 8. (Embodiment 10) The anti-TL1A antibody of any one of embodiments 1-6, comprising a HCDR3 comprising SEQ ID NO: 9. (Embodiment 11) The anti-TL1A antibody of any one of embodiments 1-10, comprising a LCDR1 comprising SEQ ID NO: 10. (Embodiment 12) The anti-TL1A antibody of any one of embodiments 1-11, comprising a LCDR2 comprising SEQ ID NO: 11. (Embodiment 13) The anti-TL1A antibody of any one of embodiments 1-12, comprising a LCDR3 comprising SEQ ID NO: 12. (Embodiment 14) The anti-TL1A antibody of any one of embodiments 1-12, comprising a LCDR3 comprising SEQ ID NO: 13. (Embodiment 15) The anti-TL1A antibody of any one of embodiments 1-12, comprising a LCDR3 comprising SEQ ID NO: 14 or 15.

[0201] (Embodiment 16) The anti-TL1A antibody of any one of embodiments 1-15, comprising a heavy chain framework comprising IGHV1-46*02. (Embodiment 17) The anti-TL1A antibody of any one of embodiments 1-15, comprising a heavy chain framework comprising a variant of IGHV1-46*02 comprising between about 1 and about 20 amino acid substitutions from SEQ ID NO: 316. (Embodiment 18) The anti-TL1A antibody of any one of embodiments 1-15, comprising a heavy chain framework comprising a variant of IGHV1-46*02 comprising between about 1 and about 9 amino acid substitutions from SEQ ID NO: 316. (Embodiment 19) The anti-TL1A antibody of any one of embodiments 1-15, comprising a heavy chain framework comprising a variant of IGHV1-46*02 comprising about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions from SEQ ID NO: 316 in the framework. (Embodiment 20) The anti-TL1A antibody of any one of embodiments 17-19, wherein the heavy chain framework substitution comprises Q1E, as determined by Aho or Kabat numbering. (Embodiment 21) The anti-TL1A antibody of any one of embodiments 17-20, wherein the heavy chain framework substitution comprises

R45K, as determined by Aho or Kabat numbering. (Embodiment 22) The anti-TL1A antibody of any one of embodiments 17-21, wherein the heavy chain framework substitution comprises A47R, as determined by Aho or Kabat numbering. (Embodiment 23) The anti-TL1A antibody of any one of embodiments 17-22, wherein the heavy chain framework substitution comprises M55I, as determined by Aho or Kabat numbering. (Embodiment 24) The anti-TL1A antibody of any one of embodiments 17-23, wherein the heavy chain framework substitution comprises V78A, as determined by Aho or Kabat numbering. (Embodiment 25) The anti-TL1A antibody of any one of embodiments 17-24, wherein the heavy chain framework substitution comprises M80I, as determined by Aho or Kabat numbering. (Embodiment 26) The anti-TL1A antibody of any one of embodiments 17-25, wherein the heavy chain framework substitution comprises R82T, as determined by Aho or Kabat numbering. (Embodiment 27) The anti-TL1A antibody of any one of embodiments 17-26, wherein the heavy chain framework substitution comprises V89A, as determined by Aho or Kabat numbering. (Embodiment 28) The anti-TL1A antibody of any one of embodiments 17-27, wherein the heavy chain framework substitution comprises M91L, as determined by Aho or Kabat numbering.

[0202] (Embodiment 29) The anti-TL1A antibody of any one of embodiments 1-15, comprising a heavy chain framework comprising SEQ ID NO: 301. (Embodiment 30) The anti-TL1A antibody of embodiment 29, wherein X1 is Q. (Embodiment 31) The anti-TL1A of embodiment 29, wherein X1 = E. (Embodiment 32) The anti-TL1A of any one of embodiments 29-31, wherein X2 = R. (Embodiment 33) The anti-TL1A of any one of embodiments 29-31, wherein X2 = K. (Embodiment 34) The anti-TL1A of any one of embodiments 29-33, wherein X3 = A. (Embodiment 35) The anti-TL1A of any one of embodiments 29-33, wherein X3 = R. (Embodiment 36) The anti-TL1A of any one of embodiments 29-35, wherein X4 = M. (Embodiment 37) The anti-TL1A of any one of embodiments 29-35, wherein X4 = I. (Embodiment 38) The anti-TL1A of any one of embodiments 29-37, wherein X5 = V. (Embodiment 39) The anti-TL1A of any one of embodiments 29-37, wherein X5 = A. (Embodiment 40) The anti-TL1A of any one of embodiments 29-39, wherein X6 = M. (Embodiment 41) The anti-TL1A of any one of embodiments 29-39, wherein X6 = I. (Embodiment 42) The anti-TL1A of any one of embodiments 29-41, wherein X7 = R. (Embodiment 43) The anti-TL1A of any one of embodiments 29-41, wherein X7 = T. (Embodiment 44) The anti-TL1A of any one of embodiments 29-43, wherein X8 = V. (Embodiment 45) The anti-TL1A of any one of embodiments 29-43, wherein X8 = A. (Embodiment 46) The anti-TL1A of any one of

embodiments 29-45, wherein X9 = M. (Embodiment 47) The anti-TL1A of any one of embodiments 29-45, wherein X9 = L.

[0203] (Embodiment 48) The anti-TL1A antibody of any one of embodiments 1-15, comprising a heavy chain framework comprising SEQ ID NO: 302. (Embodiment 49) The anti-TL1A antibody of embodiment 48, wherein X1 is Q. (Embodiment 50) The anti-TL1A of embodiment 48, wherein X1 = E. (Embodiment 51) The anti-TL1A of any one of embodiments 48-50, wherein X2 = R. (Embodiment 52) The anti-TL1A of any one of embodiments 48-50, wherein X2 = K. (Embodiment 53) The anti-TL1A of any one of embodiments 48-52, wherein X3 = A. (Embodiment 54) The anti-TL1A of any one of embodiments 48-52, wherein X3 = R. (Embodiment 55) The anti-TL1A of any one of embodiments 48-54, wherein X4 = M. (Embodiment 56) The anti-TL1A of any one of embodiments 48-54, wherein X4 = I. (Embodiment 57) The anti-TL1A of any one of embodiments 48-56, wherein X5 = V. (Embodiment 58) The anti-TL1A of any one of embodiments 48-56, wherein X5 = A. (Embodiment 59) The anti-TL1A of any one of embodiments 48-58, wherein X6 = M. (Embodiment 60) The anti-TL1A of any one of embodiments 48-58, wherein X6 = I. (Embodiment 61) The anti-TL1A of any one of embodiments 48-60, wherein X7 = R. (Embodiment 62) The anti-TL1A of any one of embodiments 48-60, wherein X7 = T. (Embodiment 63) The anti-TL1A of any one of embodiments 48-62, wherein X8 = V. (Embodiment 64) The anti-TL1A of any one of embodiments 48-62, wherein X8 = A. (Embodiment 65) The anti-TL1A of any one of embodiments 48-64, wherein X9 = M. (Embodiment 66) The anti-TL1A of any one of embodiments 48-64, wherein X9 = L.

[0204] (Embodiment 67) The anti-TL1A antibody of any one of embodiments 1-66, comprising a light chain framework comprising IGKV3-20*01. (Embodiment 68) The anti-TL1A antibody of any one of embodiments 1-66, comprising a light chain framework comprising a variant of IGKV3-20*01 comprising between about 1 and about 20 amino acid substitutions from SEQ ID NO: 317. (Embodiment 69) The anti-TL1A antibody of any one of embodiments 1-66, comprising a light chain framework comprising a variant of IGKV3-20*01 comprising about 1 amino acid substitution from SEQ ID NO: 317. (Embodiment 70) The anti-TL1A antibody of any one of embodiments 1-66, comprising a light chain framework comprising a variant of IGKV3-20*01 comprising about 2 amino acid substitutions from SEQ ID NO: 317. (Embodiment 71) The anti-TL1A antibody of any one of embodiments 1-66, comprising a light chain framework comprising a variant of IGKV3-20*01 comprising about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20

amino acid substitutions from SEQ ID NO: 317 in the framework. (Embodiment 72) The anti-TL1A antibody of any one of embodiments 69-71, wherein the light chain framework substitution comprises Q1E, as determined by Aho or Kabat numbering. (Embodiment 73) The anti-TL1A antibody of any one of embodiments 69-72, wherein the light chain framework substitution comprises R45K, as determined by Aho or Kabat numbering.

[0205] (Embodiment 74) The anti-TL1A antibody of any one of embodiments 1-66, comprising a light chain comprising a light chain framework comprising SEQ ID NO: 303. (Embodiment 75) The anti-TL1A antibody of embodiment 74, wherein X10 is L. (Embodiment 76) The anti-TL1A antibody of embodiment 74, wherein X10 is P. (Embodiment 77) The anti-TL1A antibody of any one of embodiments 74-76, wherein X11 is L. (Embodiment 78) The anti-TL1A antibody of any one of embodiments 74-76, wherein X11 is W.

[0206] (Embodiment 79) The anti-TL1A of any one of embodiments 1-78, comprising a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. (Embodiment 80) The anti-TL1A of any one of embodiments 1-78, comprising a (i) human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P and L235E, or (b) S228P, F234A, and L235A, per Kabat numbering. (Embodiment 81) The anti-TL1A of

any one of embodiments 1-78, comprising a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2□□□□ (Embodiment 82) The anti-TL1A of any one of embodiments 1-81, comprising a heavy chain Fc region comprising any one of SEQ ID NOS: 320-362. (Embodiment 83) The anti-TL1A antibody of any one of embodiments 1-82, comprising a light chain constant region comprising SEQ ID NO: 319.

[0207] (Embodiment 84) The anti-TL1A antibody of any one of embodiments 1-83, comprising at least about 80% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 85) The anti-TL1A antibody of any one of embodiments 1-84, comprising at least about 81%, at least about 82%, at least about 83%, or at least about 84% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 86) The anti-TL1A antibody of any one of embodiments 1-85, comprising at least about 85% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 87) The anti-TL1A antibody of any one of embodiments 1-86, comprising at least about 86%, at least about 87%, at least about 88%, or at least about 89% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 88) The anti-TL1A antibody of any one of embodiments 1-87, comprising at least about 90% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 89) The anti-TL1A antibody of any one of embodiments 1-88, comprising at least about 91%, at least about 92%, at least about 93%, or at least about 94% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 90) The anti-TL1A antibody of any one of embodiments 1-89, comprising at least about 95% monomeric fraction as determined by the size exclusion chromatography method described herein. (Embodiment 91) The anti-TL1A antibody of any one of embodiments 1-90, comprising at least about 96%, at least about 97%, at least about 98%, or at least about 99% monomeric fraction as determined by the size exclusion chromatography method described herein.

[0208] (Embodiment 92) The anti-TL1A antibody of any one of embodiments 1-91, comprising at least about 2 μg/mL expression as determined by the method disclosed herein. (Embodiment 93) The anti-TL1A antibody of any one of embodiments 1-92, comprising between about 2 μg/mL and about 60 μg/mL expression as determined by the method disclosed herein. (Embodiment 94) The anti-TL1A antibody of any one of embodiments 1-

93, comprising between about 5 μg/mL and about 60 μg/mL expression as determined by the method disclosed herein. (Embodiment 95) The anti-TL1A antibody of any one of embodiments 1-94, comprising between about 10 μg/mL and about 60 μg/mL expression as determined by the method disclosed herein. (Embodiment 96) The anti-TL1A antibody of any one of embodiments 1-95, comprising at least about 5 μg/mL expression as determined by the method disclosed herein. (Embodiment 97) The anti-TL1A antibody of any one of embodiments 1-96, comprising at least about 10 μg/mL expression as determined by the method disclosed herein. (Embodiment 98) The anti-TL1A antibody of any one of embodiments 1-97, comprising at least about 15 μg/mL expression as determined by the method disclosed herein. (Embodiment 99) The anti-TL1A antibody of any one of embodiments 1-98, comprising at least about 20 μg/mL expression as determined by the method disclosed herein. (Embodiment 100) The anti-TL1A antibody of any one of embodiments 1-91, comprising between about 2 μg/mL and about 50 μg/mL, between about 2 μg/mL and about 40 μg/mL, between about 2 μg/mL and about 30 μg/mL expression, between about 2 μg/mL and about 20 μg/mL, between about 5 μg/mL and about 50 μg/mL, between about 5 μg/mL and about 40 μg/mL, between about 5 μg/mL and about 30 μg/mL, between about 10 μg/mL and about 50 μg/mL, between about 10 μg/mL and about 40 μg/mL, or between about 10 μg/mL and about 30 μg/mL as determined by the method disclosed herein. (Embodiment 101) The anti-TL1A antibody of any one of embodiments 1-91, comprising about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 μg/mL expression as determined by the method disclosed herein.

[0209] In some embodiments, an anti-TL1A antibody comprises antibody A. As used herein, antibody A comprises the CDRs of antibody A in **Table 20**. In some cases, antibody A comprises a heavy chain framework comprising SEQ ID NO: 301 (Embodiment X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody A comprises a light chain framework comprising SEQ ID NO: 303 (Embodiment EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody A comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to

about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody A comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody A comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody A comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases,

antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO:

354. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody A comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody A comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody A is expressed from FreeStyle 293-F (*e.g.*, ThermoFisher Scientific #R79007) cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody A is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody A is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL. In some cases, antibody A comprises a viscosity less than about 30 mPa-s. In some cases, antibody A comprises a viscosity from about 4 mPa-s to about 30 mPa-s, or about 4, 5, 6, 7, 8, 9, 10. 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 mPa-s. In some cases, antibody A is formulated in a solution having a concentration of about 10 mg/ml to about 170 mg/ml, with a viscosity less than about 30 mPa-s. In some cases, the formulation has a pH of about 5 to about 7.5.

[0210] In some embodiments, an anti-TL1A antibody comprises antibody B. As used herein, antibody B comprises the CDRs of antibody B in **Table 20**. In some cases, antibody B comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2] RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody B comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody B comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody B comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody B comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody B comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb)

L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%,

94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases,

antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody B comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody B comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody B is expressed from

FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases, antibody B is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to about 60 μg/mL. In some cases, antibody B is expressed from FreeStyle 293-F cells at an expression level of between about 10 μg/mL to about 60 μg/mL.

[0211] In some embodiments, an anti-TL1A antibody comprises antibody C. As used herein, antibody C comprises the CDRs of antibody C in **Table 20**. In some cases, antibody C comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody C comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody C comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody C comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody C comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody C comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x)

271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody C comprises a constant region comprising at least about 85%,

87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity

to SEQ ID NO: 345. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody C comprises a constant region comprising at

least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody C comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody C comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody C is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody C is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody C is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0212] In some embodiments, an anti-TL1A antibody comprises antibody D. As used herein, antibody D comprises the CDRs of antibody D in **Table 20**. In some cases, antibody D comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody D comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody D comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody D comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody D comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody D comprises a human IgG1

Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody D comprises a constant region

comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody D comprises

a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody D comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody D comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody D is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody D is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody D is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0213] In some embodiments, an anti-TL1A antibody comprises antibody E. As used herein, antibody E comprises the CDRs of antibody E in **Table 20**. In some cases, antibody E comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody E comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody E comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to

about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody E comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody E comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody E comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases,

antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO:

354. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody E comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody E comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody E is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody E is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody E is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0214] In some embodiments, an anti-TL1A antibody comprises antibody F. As used herein, antibody F comprises the CDRs of antibody F in **Table 20**. In some cases, antibody F comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2] RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7

= R or T, X8 = V or A, and X9 = M or L. In some cases, antibody F comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody F comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody F comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody F comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody F comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID

NO: 320. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody F comprises a constant region comprising at

least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%,

or 100% identity to SEQ ID NO: 351. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody F comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody F comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody F is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases, antibody F is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to

about 60 µg/mL. In some cases, antibody F is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0215] In some embodiments, an anti-TL1A antibody comprises antibody G. As used herein, antibody G comprises the CDRs of antibody G in **Table 20**. In some cases, antibody G comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2] RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody G comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody G comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody G comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody G comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody G comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A,

(ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,

97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody G comprises

a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody G comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody G comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody G is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases, antibody G is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to about 60 μg/mL. In some cases, antibody G is expressed from FreeStyle 293-F cells at an expression level of between about 10 μg/mL to about 60 μg/mL.

[0216] In some embodiments, an anti-TL1A antibody comprises antibody H. As used herein, antibody H comprises the CDRs of antibody H in **Table 20**. In some cases, antibody H comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody H comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody H comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody H comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody H comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody H comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234 A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q)

256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO:

344. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody H comprises a constant region comprising at least about 85%,

87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody H comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody H comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody H is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody H is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody H is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0217] In some embodiments, an anti-TL1A antibody comprises antibody I. As used herein, antibody I comprises the CDRs of antibody I in **Table 20**. In some cases, antibody I comprises a heavy chain framework comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody I comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody I comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody I comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the

framework. In some cases, antibody I comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody I comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody I comprises a constant region comprising at least about

85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%

identity to SEQ ID NO: 341. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody I comprises a constant region

comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody I comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody I comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody I is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody I is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody I is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0218] In some embodiments, an anti-TL1A antibody comprises antibody A2. As used herein, antibody A2 comprises the CDRs of antibody A2 in **Table 20**. In some cases, antibody A2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody A2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody A2 comprises a heavy chain variable region

comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody A2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody A2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody A2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some

cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody A2

comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody A2 comprises a constant region

comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody A2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody A2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody A2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody A2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody A2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0219] In some embodiments, an anti-TL1A antibody comprises antibody B2. As used herein, antibody B2 comprises the CDRs of antibody B2 in **Table 20**. In some cases, antibody B2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2] RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody B2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody B2 comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody B2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody B2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody B2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb)

L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody B2 comprises a constant region comprising at least about

85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody B2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody B2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody B2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases, antibody B2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to about 60 μg/mL. In some cases, antibody B2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 μg/mL to about 60 μg/mL.

[0220] In some embodiments, an anti-TL1A antibody comprises antibody C2. As used herein, antibody C2 comprises the CDRs of antibody C2 in **Table 20**. In some cases, antibody C2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody C2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody C2 comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody C2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody C2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody C2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q)

256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody C2 comprises a constant region comprising at least about

85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody C2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody C2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody C2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases, antibody C2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to about 60 μg/mL. In some cases, antibody C2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 μg/mL to about 60 μg/mL.

[0221] In some embodiments, an anti-TL1A antibody comprises antibody D2. As used herein, antibody D2 comprises the CDRs of antibody D2 in **Table 20**. In some cases, antibody D2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody D2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody D2 comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody D2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework,

wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody D2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody D2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody D2 comprises a constant region

comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody D2 comprises a constant region comprising at least about

85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody D2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody D2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody D2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody D2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody D2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0222] In some embodiments, an anti-TL1A antibody comprises antibody E2. As used herein, antibody E2 comprises the CDRs of antibody E2 in **Table 20**. In some cases, antibody E2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or

T, X8 = V or A, and X9 = M or L. In some cases, antibody E2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDR FSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody E2 comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody E2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody E2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody E2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID

NO: 320. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some

cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody E2

comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody E2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody E2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody E2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases,

antibody E2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to about 60 μg/mL. In some cases, antibody E2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 μg/mL to about 60 μg/mL.

[0223] In some embodiments, an anti-TL1A antibody comprises antibody F2. As used herein, antibody F2 comprises the CDRs of antibody F2 in **Table 20**. In some cases, antibody F2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody F2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody F2 comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody F2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody F2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody F2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A,

440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody F2 comprises

a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody F2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%,

or 100% identity to SEQ ID NO: 362. In some cases, antibody F2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody F2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 µg/mL as determined by the method described in Example 2. In some cases, antibody F2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 µg/mL to about 60 µg/mL. In some cases, antibody F2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 µg/mL to about 60 µg/mL.

[0224] In some embodiments, an anti-TL1A antibody comprises antibody G2. As used herein, antibody G2 comprises the CDRs of antibody G2 in **Table 20**. In some cases, antibody G2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody G2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody G2 comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody G2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody G2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody G2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or

329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 323. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody G2 comprises a constant region comprising at least about

85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%,

89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%,

92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody G2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody G2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody G2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases, antibody G2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to about 60 μg/mL. In some cases, antibody G2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 μg/mL to about 60 μg/mL.

[0225] In some embodiments, an anti-TL1A antibody comprises antibody H2. As used herein, antibody H2 comprises the CDRs of antibody H2 in **Table 20**. In some cases, antibody H2 comprises a heavy chain framework comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), wherein X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, and X9 = M or L. In some cases, antibody H2 comprises a light chain framework comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein X10 = L or P and X11 = L or W. In some cases, antibody H2 comprises a heavy chain variable region comprising human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, wherein the modified human IGHV1-46*02 framework has less than or equal to

about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody H2 comprises a light chain variable region comprising human IGKV3-20 framework or a modified human IGKV3-20 framework, wherein the modified human IGKV3-20 framework has less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions in the framework. In some cases, antibody H2 comprises a constant region comprising reduced ADCC and/or CDC as compared to IgG1. For instance, antibody H2 comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 320. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 321. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 322. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID

NO: 323. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 324. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 325. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 326. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 327. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 328. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 329. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 330. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 331. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 332. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 333. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 334. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 335. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 336. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 337. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 338. In some

cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 339. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 340. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 341. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 342. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 343. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 344. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 345. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 346. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 347. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 348. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 349. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 350. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 351. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 352. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 353. In some cases, antibody H2

comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 354. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 355. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 356. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 357. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 358. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 359. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 360. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 361. In some cases, antibody H2 comprises a constant region comprising at least about 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 362. In some cases, antibody H2 comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction as measured by the size exclusion method described in Example 2. In some cases, antibody H2 is expressed from FreeStyle 293-F cells at an expression level of about or at least about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 5, 57, 58, 59 or 60 μg/mL as determined by the method described in Example 2. In some cases, antibody H2 is expressed from FreeStyle 293-F cells at an expression level of between about 2 μg/mL to about 60 μg/mL. In some cases, antibody H2 is expressed from FreeStyle 293-F cells at an expression level of between about 10 μg/mL to about 60 μg/mL.

[0226] The TL1A antibodies described herein bind to specific regions or epitopes of human TL1A demonstrated herein as useful to inhibit interferon gamma secretion from T lymphocytes. Various embodiments provide for an anti-TL1A antibody that binds to the same

region of a TL1A protein or portion thereof as a reference antibody such as the anti-TL1A antibodies described herein. In some embodiments, the reference antibody comprises antibody A, B, C, D, E, F, G, H, A2, B2, C2, D2, E2, F2, G2, or H2, or a combination thereof. In some embodiments, provided herein is an anti-TL1A antibody that binds specifically to the same region of TL1A as a reference antibody comprising a heavy chain sequence at least about 90%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 104, and a light chain comprising a sequence at least about 90%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 201. In some embodiments, provided herein is an anti-TL1A antibody that binds specifically to the same region of TL1A as a reference antibody comprising a heavy chain sequence at least about 90%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 107, and a light chain comprising a sequence at least about 90%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 201.

[0227] Non-limiting methods for determining whether an anti-TL1A antibody (i.e. test antibody) binds to the same region of a TL1A protein or portion thereof as an antibody described herein are provided. An exemplary embodiment comprises a competition assay. For instance, the method comprises determining whether the test antibody can compete with binding between the reference antibody and the TL1A protein or portion thereof, or determining whether the reference antibody can compete with binding between the test antibody and the TL1A protein or portion thereof. Exemplary methods include use of surface plasmon resonance to evaluate whether an anti-TL1A antibody can compete with the binding between TL1A and another anti-TL1A antibody. In some cases, surface plasmon resonance is utilized in the competition assay. Non-limiting methods are described in the examples.

[0228] In certain embodiments, disclosed herein are antibodies that compete for binding TL1A with the antibodies described herein. In certain embodiments, disclosed herein are antibodies that bind a discrete epitope that overlaps with an epitope of TL1A bound by an antibody described herein. In certain embodiments, disclosed herein are antibodies that bind the same epitope of TL1A, overlap with an epitope of TL1A by one or more amino acid residues, or that compete for binding to an epitope of TL1A with an antibody or fragment thereof that comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 104; and a light chain variable region comprising the amino acid of SEQ ID NO: 201. In certain embodiments, disclosed herein are antibodies that bind the same epitope of TL1A, overlap with an epitope of TL1A by one or more amino acid residues, or that compete for binding to an epitope of TL1A with an antibody or fragment thereof that

comprises a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 107; and a light chain variable region comprising the amino acid of SEQ ID NO: 201.

Additional Antibody Embodiments

[0229] In one aspect, provided herein, is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than 9 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework. In some embodiments, the amino acid modification comprises: (a) a modification at amino acid position 47 in the heavy chain variable region; (b) a modification at amino acid position 45 in the heavy chain variable region; (c) a modification at amino acid position 55 in the heavy chain variable region; (d) a modification at amino acid position 78 in the heavy chain variable region; (e) a modification at amino acid position 80 in the heavy chain variable region; (f) a modification at amino acid position 82 in the heavy chain variable region; (g) a modification at amino acid position 89 in the heavy chain variable region; or (h) a modification at amino acid position 91 in the heavy chain variable region; per Aho or Kabat numbering; or a combination of two or more modifications selected from (a) to (h). In some embodiments, (a) the amino acid modification is at position 47 in the heavy chain variable region, and the amino acid at position 47 is R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (b) the amino acid modification is at position 45 in the heavy chain variable region, and the amino acid at position 45 is A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (c) the amino acid modification is at position 55 in the heavy chain variable region, and the amino acid at position 55 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; (d) the amino acid modification is at position 78 in the heavy chain variable region, and the amino acid at position 78 is A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y; (e) the amino acid modification is at position 80 in the heavy chain variable region, and the amino acid at position 80 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; (f) the amino acid modification is at position 82 in the heavy chain variable region, and the amino acid at position 82 is A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (g) the amino acid modification is at position 89 in the heavy chain variable region, and the amino acid at position 89 is A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y; or (h) the amino acid modification is at position 91 in the heavy chain variable region, and the amino acid at

position 91 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; or a combination of two or more modifications selected from (a) to (h). In some embodiments, the amino acid modifications comprise one or more of: A47R, R45K, M55I, V78A, M80I, R82T, V89A, M91L in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid modification comprises: (a) a modification at amino acid position 54 in the light chain variable region; and/or (b) a modification at amino acid position 55 in the light chain variable region; per Aho or Kabat numbering. In some embodiments, (a) the amino acid modification is at position 54 of the light chain variable region, and the amino acid at position 54 is A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V; and/or (b) the amino acid modification is at position 55 of the light chain variable region, and the amino acid at position 55 is A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V. In some embodiments, the amino acid modifications comprise L54P and/or L55W in the light chain variable region, per Aho or Kabat numbering. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR1 as set forth by SEQ ID NO: 1, a heavy chain CDR2 as set forth by any one of SEQ ID NOS: 2-5, a heavy chain CDR3 as set forth by any one of SEQ ID NOS: 6-9, a light chain CDR1 as set forth by SEQ ID NO: 10, a light chain CDR2 as set forth by SEQ ID NO: 11, and a light chain CDR3 as set forth by any one of SEQ ID NOS: 12-15. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR1 as set forth by SEQ ID NO: 1, a heavy chain CDR2 as set forth by SEQ ID NO: 2, a heavy chain CDR3 as set forth by SEQ ID NO: 6, a light chain CDR1 as set forth by SEQ ID NO: 10, a light chain CDR2 as set forth by SEQ ID NO: 11, and a light chain CDR3 as set forth by SEQ ID NO: 12. In some embodiments, the antibody or antigen binding fragment comprises comprising a heavy chain framework (FR) 1 as set forth by SEQ ID NO: 304, a heavy chain FR2 as set forth by SEQ ID NO: 305 or SEQ ID NO: 313, a heavy chain FR3 as set forth by any one of SEQ ID NOS: 306, 307, 314, or 315, a heavy chain FR4 as set forth by SEQ ID NO: 308, a light chain FR1 as set forth by SEQ ID NO: 309, a light chain FR2 as set forth by SEQ ID NO: 310, a light chain FR3 as set forth by SEQ ID NO: 311, or a light chain FR4 as set forth by SEQ ID NO: 312, or a combination thereof. In some embodiments, the antibody or antigen binding fragment comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p)

255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of two or more selected from (a) – (uu), per Kabat numbering. In some embodiments, the antibody or antigen binding fragment comprises a human IgG4 Fc region. In some embodiments, the antibody or antigen binding fragment comprises a Fc region comprising a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362. In some embodiments, the antibody or antigen binding fragment comprises at least about 80% monomeric fraction as determined by size exclusion chromatography. In some embodiments, the antibody or antigen binding fragment expresses at least about 20 ug/ml total antibody, optionally about 20 ug/ml and 70 ug/mL total antibody.

[0230] In another aspect, provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least 96% identical to SEQ ID NO: 104, and a light chain variable domain comprising an amino acid sequence at least 97% identical to SEQ ID NO: 201. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least 97% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least 98% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least 99% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises SEQ ID NO: 104. In some embodiments, the light chain variable domain comprises an amino acid sequence at least 98% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain

comprises an amino acid sequence at least about 99% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain comprises SEQ ID NO: 201.

[0231] In another aspect, provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 99% identical to any one of SEQ ID NOS: 101-135, and a light chain variable domain comprising an amino acid sequence at least about 99% identical to any one of SEQ ID NOS: 201-206.

[0232] In some embodiments, antibodies or antigen binding fragments described herein comprise a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of two or more selected from (a) – (uu), per Kabat numbering. In some embodiments, antibodies or antigen binding fragments described herein comprise a human IgG4 Fc region. In some embodiments, antibodies or antigen binding fragments described herein comprise a Fc region comprising a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362. In some embodiments, antibodies or antigen binding fragments described herein comprise at least about 80% monomeric fraction as determined by size exclusion chromatography. In some embodiments,

antibodies or antigen binding fragments described herein express at least about 20 ug/ml total antibody, optionally about 20 ug/ml and 70 ug/mL total antibody.

[0233] In another aspect, provided herein is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15; and a fragment crystallizable (Fc) region comprising reduced antibody-dependent cell-mediated cytotoxicity (ADCC) function as compared to human IgG1 and/or reduced complement-dependent cytotoxicity (CDC) as compared to human IgG1. In some embodiments, the human IgG1 comprises SEQ ID NO: 320. In some embodiments, the ADCC function of the Fc region comprising reduced ADCC is at least about 50% reduced as compared to human IgG1. In some embodiments, the CDC function of the Fc region comprising reduced CDC is at least about 50% reduced as compared to human IgG1. In some embodiments, the Fc region comprises a human IgG1 comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and

N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some embodiments, the antibody or antigen binding fragment comprises a (i) human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P, (b) S228P and L235E, or (c) S228P, F234A, and L235A, per Kabat numbering. In some embodiments, the antibody or antigen binding fragment comprises a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ). In some embodiments, the Fc region comprises a human IgG1 with a substitution selected from 329A, 329G, 329Y, 331S, 236F, 236R, 238A, 238E, 238G, 238H, 238I, 238V, 238W, 238Y, 248A, 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, 254V, 264S, 265H, 265K, 265S, 265Y, 265A, 267G, 267H, 267I, 267K, 434I, 438G, 439E, 439H, 439Q, 440A, 440D, 440E, 440F, 440M, 440T, and 440V, per Kabat numbering. In some embodiments, the antibody or antigen binding fragment comprises a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362. In some embodiments, the HCDR1 comprises SEQ ID NO: 1, HCDR2 comprises any one of SEQ ID NOS: 2-5, HCDR3 comprises any one of SEQ ID NOS: 6-9, LCDR1 comprises SEQ ID NO: 10, LCDR2 comprises SEQ ID NO: 11, and LCDR3 comprises any one of SEQ ID NOS: 12-15. In some embodiments, the Fc region comprises any one of SEQ ID NOs: 401-413 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 401-413. In some embodiments, the heavy chain comprises any one of SEQ ID NOs: 501-513 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 501-513. In some embodiments, the light chain comprises any one of SEQ ID NO: 514 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NO: 514. In some embodiments, the HCDR2 comprises SEQ ID NO: 2, the HCDR3 comprises SEQ ID NO: 6, and the LCDR3 comprises SEQ ID NO: 12, and wherein the Fc region comprises any one of SEQ ID NOs: 401-413 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 401-413. In some embodiments, the antibody or antigen binding fragment comprises at least about 80% monomeric fraction as determined by size exclusion chromatography. In some embodiments, the antibody or antigen binding fragment expresses at least about 20 ug/ml total antibody, optionally about 20 ug/ml and 70 ug/mL total antibody.

[0234] Further provided are methods of treating fibrosis or an intestinal inflammatory condition, disease, or disorder in a subject in need thereof, the method comprising administering to the subject an antibody or antigen binding fragment of any antibody or antigen binding fragment disclosed herein. In some embodiments, the subject has fibrosis. In some embodiments, the subject has an intestinal inflammatory condition, disease, or disorder. In some embodiments, the intestinal inflammatory condition, disease, or disorder comprises inflammatory bowel disease (IBD). In some embodiments, the IBD comprises Crohn's Disease. In some embodiments, the IBD comprises ulcerative colitis.

[0235] In some embodiments, antibodies or antigen binding fragments described herein comprise are present in a liquid composition a concentration of the antibody or antigen binding fragment of 10 mg/ml to 170 mg/ml. In some embodiments, the antibody or antigen binding fragment thereof is at a concentration of 10 mg/ml to 170 mg/ml. In some embodiments, the viscosity is from about 4 to about 30 mPa-s (millipascal-second (mPa·s)). In some embodiments, the viscosity is from about 4 to about 10 mPa-s (millipascal-second (mPa·s)).

[0236] In another aspect, provided herein, is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than about 14 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework. In some embodiments, the heavy chain variable framework region and the light chain variable framework region collectively comprise 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or no amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework. In some embodiments, the amino acid modification comprises a modification at amino acid position 1 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 1 comprises A, R, N, D, C, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 1 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 1 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 1 comprises E. In some embodiments, the amino acid modification comprises a

modification at amino acid position 45 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 45 comprises A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 45 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 45 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 45 comprises K. In some embodiments, the amino acid modification comprises a modification at amino acid position 47 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 47 comprises R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 47 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 47 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 47 comprises R. In some embodiments, the amino acid modification comprises a modification at amino acid position 55 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 55 comprises A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 55 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 55 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 55 comprises I. In some embodiments, the amino acid modification comprises a modification at amino acid position 78 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 78 comprises A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y. In some embodiments, the amino acid at position 78 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 78 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 78 comprises A. In some embodiments, the amino acid modification comprises a modification at amino acid position 80 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 80 comprises A, R, N, D, C, Q,

E, G, H, I, L, K, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 80 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 80 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 80 comprises I. In some embodiments, the amino acid modification comprises a modification at amino acid position 82 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 82 comprises A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 82 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 82 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 82 comprises T. In some embodiments, the amino acid modification comprises a modification at amino acid position 89 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 89 comprises A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y. In some embodiments, the amino acid at position 89 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 89 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 89 comprises A. In some embodiments, the amino acid modification comprises a modification at amino acid position 91 in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 91 comprises A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 91 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 91 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 91 comprises L.

[0237] In some embodiments, the amino acid modifications comprise one or more of: Q1E, R45K, A47R, M55I, V78A, M80I, R82T, V89A, M91L in the heavy chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid modifications comprise Q1E. In some embodiments, the amino acid modifications comprise R45K. In some

embodiments, the amino acid modifications comprise A47R. In some embodiments, the amino acid modifications comprise M55I. In some embodiments, the amino acid modifications comprise V78A. In some embodiments, the amino acid modifications comprise M80I. In some embodiments, the amino acid modifications comprise R82T. In some embodiments, the amino acid modifications comprise V89A. In some embodiments, the amino acid modifications comprise M91L.

[0238] In some embodiments, the amino acid modification comprises a modification at amino acid position 54 in the light chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 54 comprises A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 54 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 54 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 54 comprises P. In some embodiments, the amino acid modification comprises a modification at amino acid position 55 in the light chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid at position 55 comprises A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V. In some embodiments, the amino acid at position 55 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, the amino acid at position 55 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, the amino acid at position 55 comprises W.

[0239] In some embodiments, the amino acid modifications comprise L54P and/or L55W in the light chain variable region, per Aho or Kabat numbering. In some embodiments, the amino acid modifications comprise L54P. In some embodiments, the amino acid modifications comprise L55W.

[0240] In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR1 as set forth by SEQ ID NO: 1. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR2 as set forth by SEQ ID NO: 2. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR2 as set forth by SEQ ID NO: 3. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR2 as set forth by SEQ ID NO: 4. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR2 as set

forth by SEQ ID NO: 5. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR3 as set forth by SEQ ID NO: 6. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR3 as set forth by SEQ ID NO: 7. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR3 as set forth by SEQ ID NO: 8. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain CDR3 as set forth by SEQ ID NO: 9. In some embodiments, the antibody or antigen binding fragment comprises a light chain CDR1 as set forth by SEQ ID NO: 10. In some embodiments, the antibody or antigen binding fragment comprises a light chain CDR2 as set forth by SEQ ID NO: 11. In some embodiments, the antibody or antigen binding fragment comprises a light chain CDR3 as set forth by SEQ ID NO: 12. In some embodiments, the antibody or antigen binding fragment comprises a light chain CDR3 as set forth by SEQ ID NO: 13. In some embodiments, the antibody or antigen binding fragment comprises a light chain CDR3 as set forth by SEQ ID NO: 14. In some embodiments, the antibody or antigen binding fragment comprises a light chain CDR3 as set forth by SEQ ID NO: 15.

[0241] In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR1 as set forth by SEQ ID NO: 304. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR2 as set forth by SEQ ID NO: 305. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR2 as set forth by SEQ ID NO: 313. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR3 as set forth by SEQ ID NO: 306. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR3 as set forth by SEQ ID NO: 307. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR3 as set forth by SEQ ID NO: 314. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR3 as set forth by SEQ ID NO: 315. In some embodiments, the antibody or antigen binding fragment comprises a heavy chain FR4 as set forth by SEQ ID NO: 308. In some embodiments, the antibody or antigen binding fragment comprises a light chain FR1 as set forth by SEQ ID NO: 309. In some embodiments, the antibody or antigen binding fragment comprises a light chain FR2 as set forth by SEQ ID NO: 310. In some embodiments, the antibody or antigen binding fragment comprises a light chain FR3 as set forth by SEQ ID NO: 311. In some embodiments, the antibody or antigen binding fragment comprises a light chain FR4 as set forth by SEQ ID NO: 312.

[0242] In another aspect, provided herein is an antibody or antigen binding fragment thereof that binds to TL1A, comprising: (a) a heavy chain variable region comprising SEQ ID NO: 301 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS), and (b) a light chain variable region comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V.

[0243] In some embodiments, X1 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X1 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X2 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X2 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X3 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X3 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X4 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X4 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X5 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X5 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X6 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X6 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X7 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X7 comprises an aliphatic amino

acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X8 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X8 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X9 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X9 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X10 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X10 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X11 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X11 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid.

[0244] In some embodiments, X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, X9 = M or L, X10 = L or P, and X11 = L or W. In some embodiments, X1 = Q. In some embodiments, X1 = E. In some embodiments, X2 = R. In some embodiments, X2 = K. In some embodiments, X3 = A. In some embodiments, X3 = R. In some embodiments, X4 = M. In some embodiments, X4 = I. In some embodiments, X5 = V. In some embodiments, X5 = A. In some embodiments, X6 = M. In some embodiments, X6 = I. In some embodiments, X7 = R. In some embodiments, X7 = T. In some embodiments, X8 = V. In some embodiments, X8 = A. In some embodiments, X9 = M. In some embodiments, X9 = L. In some embodiments, X10 = L. In some embodiments, X10 = P. In some embodiments, X11 = L. In some embodiments, X11 = W.

[0245] In some embodiments, HCDR1 comprises SEQ ID NO: 1. In some embodiments, HCDR2 comprises SEQ ID NO: 2. In some embodiments, HCDR2 comprises SEQ ID NO: 3. In some embodiments, HCDR2 comprises SEQ ID NO: 4. In some embodiments, HCDR2 comprises SEQ ID NO: 5. In some embodiments, HCDR3 comprises SEQ ID NO: 6. In some embodiments, HCDR3 comprises SEQ ID NO: 7. In some embodiments, HCDR3 comprises SEQ ID NO: 8. In some embodiments, HCDR3 comprises SEQ ID NO: 9. In some embodiments, LCDR1 comprises SEQ ID NO: 10. In some embodiments, LCDR2 comprises

SEQ ID NO: 11. In some embodiments, LCDR3 comprises SEQ ID NO: 12. In some embodiments, LCDR3 comprises SEQ ID NO: 13. In some embodiments, LCDR3 comprises SEQ ID NO: 14. In some embodiments, the antibody or antigen binding fragment comprises a light chain CDR3 as set forth by SEQ ID NO: 15.

[0246] In another aspect, provided herein is an antibody or antigen binding fragment thereof that binds to TL1A, comprising: (a) a heavy chain variable region comprising SEQ ID NO: 302 (X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS), and (b) a light chain variable region comprising SEQ ID NO: 303 (EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKLEIK), wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V.

[0247] In some embodiments, X1 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X1 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X2 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X2 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X3 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X3 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X4 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X4 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X5 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X5 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X6 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X6

comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X7 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X7 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X8 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X8 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X9 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X9 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X10 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X10 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid. In some embodiments, X11 comprises a hydrophobic amino acid, a hydrophilic amino acid, or an amphipathic amino acid. In some embodiments, X11 comprises an aliphatic amino acid, an aromatic amino acid, an acidic amino acid, a basic amino acid, a hydroxylic amino acid, a sulfur-containing amino acid, or an amidic amino acid.

[0248] In some embodiments, X1 = Q or E, X2 = R or K, X3 = A or R, X4 = M or I, X5 = V or A, X6 = M or I, X7 = R or T, X8 = V or A, X9 = M or L, X10 = L or P, and X11 = L or W. In some embodiments, X1 = Q. In some embodiments, X1 = E. In some embodiments, X2 = R. In some embodiments, X2 = K. In some embodiments, X3 = A. In some embodiments, X3 = R. In some embodiments, X4 = M. In some embodiments, X4 = I. In some embodiments, X5 = V. In some embodiments, X5 = A. In some embodiments, X6 = M. In some embodiments, X6 = I. In some embodiments, X7 = R. In some embodiments, X7 = T. In some embodiments, X8 = V. In some embodiments, X8 = A. In some embodiments, X9 = M. In some embodiments, X9 = L. In some embodiments, X10 = L. In some embodiments, X10 = P. In some embodiments, X11 = L. In some embodiments, X11 = W.

[0249] In some embodiments, HCDR1 comprises SEQ ID NO: 1. In some embodiments, HCDR2 comprises SEQ ID NO: 2. In some embodiments, HCDR2 comprises SEQ ID NO: 3. In some embodiments, HCDR2 comprises SEQ ID NO: 4. In some embodiments, HCDR2

comprises SEQ ID NO: 5. In some embodiments, HCDR3 comprises SEQ ID NO: 6. In some embodiments, HCDR3 comprises SEQ ID NO: 7. In some embodiments, HCDR3 comprises SEQ ID NO: 8. In some embodiments, HCDR3 comprises SEQ ID NO: 9. In some embodiments, LCDR1 comprises SEQ ID NO: 10. In some embodiments, LCDR2 comprises SEQ ID NO: 11. In some embodiments, LCDR3 comprises SEQ ID NO: 12. In some embodiments, LCDR3 comprises SEQ ID NO: 13. In some embodiments, LCDR3 comprises SEQ ID NO: 14. In some embodiments, LCDR3 comprises SEQ ID NO: 15.

[0250] Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 96% identical to SEQ ID NO: 104, and a light chain variable domain comprising an amino acid sequence at least about 97% identical to SEQ ID NO: 201. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least about 97% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least about 98% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least about 99% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises SEQ ID NO: 104. In some embodiments, the light chain variable domain comprises an amino acid sequence at least about 98% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain comprises an amino acid sequence at least about 99% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain comprises SEQ ID NO: 201.

[0251] Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 99% identical to SEQ ID NO: 107, and a light chain variable domain comprising an amino acid sequence at least about 97% identical to SEQ ID NO: 201. In some embodiments, the heavy chain variable domain comprises SEQ ID NO: 107. In some embodiments, the light chain variable domain comprises an amino acid sequence at least about 98% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain comprises an amino acid sequence at least about 99% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain comprises SEQ ID NO: 201.

[0252] Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 101, and a light chain variable domain comprising SEQ ID

NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 102, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 103, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 104, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 105, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 103, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 106, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 107, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 108, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 109, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 108, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 109, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that

binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 108, and a light chain variable domain comprising SEQ ID NOS: 203. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 108, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 107, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 107, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 110, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 111, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 112, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 113, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 114, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 115, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 116, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable

domain comprising SEQ ID NO: 117, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 118, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 114, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 102, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 104, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 119, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 119, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 101, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 105, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 120, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 121, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 122, and a light chain variable domain comprising SEQ ID

NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 122, and a light chain variable domain comprising SEQ ID NOS: 204. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 123, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 124, and a light chain variable domain comprising SEQ ID NOS: 202. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 125, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 116, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 117, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 126, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 127, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 127, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 121, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 122, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that

binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 122, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 122, and a light chain variable domain comprising SEQ ID NOS: 206. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 124, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 124, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 128, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 128, and a light chain variable domain comprising SEQ ID NOS: 206. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 129, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 130, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 131, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 132, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 133, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable

domain comprising SEQ ID NO: 134, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 135, and a light chain variable domain comprising SEQ ID NOS: 205. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 132, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 126, and a light chain variable domain comprising SEQ ID NOS: 201. Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising SEQ ID NO: 130, and a light chain variable domain comprising SEQ ID NOS: 201.

[0253] Further provided herein is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain domain comprising any one of SEQ ID NOs: 501-513, and a light chain domain comprising SEQ ID NOS: 514.

[0254] In another aspect, provided herein is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15; and a fragment crystallizable (Fc) region comprising reduced antibody-dependent cell-mediated cytotoxicity (ADCC) function as compared to human IgG1 and/or reduced complement-dependent cytotoxicity (CDC) as compared to human IgG1. In some embodiments, the human IgG1 comprises SEQ ID NO: 320. In some embodiments, the ADCC function of the Fc region comprising reduced ADCC is at least about 50% reduced as compared to human IgG1. In some embodiments, the CDC function of the Fc region comprising reduced ADCC is at least about 50% reduced as compared to human IgG1. In some embodiments, the Fc region comprises a human IgG1 comprising (a) 297A, 297Q, or

297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some embodiments, the antibody of antigen binding fragment comprises a (i) human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P and L235E, or (b) S228P, F234A, and L235A, per Kabat numbering. In some embodiments, the antibody of antigen binding fragment comprises a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ). In some embodiments, the antibody of antigen binding fragment comprises a human Fc region comprising high mannose glycosylation. In some embodiments, the Fc region comprises a human IgG1 with a substitution selected from 297A, 297Q, 297D, 279F, 279K, 279L, 228P, 235A, 235E, 235G, 235Q, 235R, 235S, 237A, 237E, 237K, 237N, 237R, 268K, 269N, 269Q, 270A, 270G, 270M, 270N, 424H, 424M, and 424V, per Kabat numbering. In some embodiments, the Fc region comprises a human IgG1 with a substitution selected from 271T, 272N, 292E, 292F, 292G, 292I, 293S, 301W, 304E, 311E, 311G, 311S, 255N, 256H, 256K, 256R, 256V, 316F, 328V, 330R, 339E, 339L, 343I, 343V, 373A, 373G, 373S, 376E, 376W, 376Y, 380D, 382D, 382P, 385P, 234A, 234V, 234F, 233P, 328A, 327Q and 327T, per Kabat numbering. In some embodiments, the Fc region comprises a human IgG1 with a substitution selected from 329A, 329G, 329Y, 331S, 236F, 236R,

238A, 238E, 238G, 238H, 238I, 238V, 238W, 238Y, 248A, 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, 254V, 264S, 265H, 265K, 265S, 265Y, 265A, 267G, 267H, 267I, 267K, 434I, 438G, 439E, 439H, 439Q, 440A, 440D, 440E, 440F, 440M, 440T, and 440V, per Kabat numbering. In some embodiments, the antibody or antigen binding fragment comprises a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362. In some embodiments, HCDR1 comprises SEQ ID NO: 1. In some embodiments, HCDR2 comprises SEQ ID NO: 2. In some embodiments, HCDR2 comprises SEQ ID NO: 3. In some embodiments, HCDR2 comprises SEQ ID NO: 4. In some embodiments, HCDR2 comprises SEQ ID NO: 5. In some embodiments, HCDR3 comprises SEQ ID NO: 6. In some embodiments, HCDR3 comprises SEQ ID NO: 7. In some embodiments, HCDR3 comprises SEQ ID NO: 8. In some embodiments, HCDR3 comprises SEQ ID NO: 9. In some embodiments, LCDR1 comprises SEQ ID NO: 10. In some embodiments, LCDR2 comprises SEQ ID NO: 11. In some embodiments, LCDR3 comprises SEQ ID NO: 12. In some embodiments, LCDR3 comprises SEQ ID NO: 13. In some embodiments, LCDR3 comprises SEQ ID NO: 14. In some embodiments, LCDR3 comprises SEQ ID NO: 15.

[0255] In another aspect, provided herein is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15. In some embodiments, the heavy chain variable region comprises human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework. In some embodiments, the light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework. In some embodiments, the heavy chain variable region comprises one of more of the following amino acids: 1E, 45K, 47R, 55I, 78A, 80I, 82T, 89A, 91L, per Aho or Kabat numbering. In some embodiments, the heavy chain variable region comprises 1E. In some embodiments, the heavy chain variable region comprises 45K. In some embodiments, the heavy chain variable region comprises 47R. In some embodiments, the heavy chain variable region comprises 55I. In some embodiments, the heavy chain variable region comprises 78A. In some embodiments, the heavy chain

variable region comprises 80I. In some embodiments, the heavy chain variable region comprises 82T. In some embodiments, the heavy chain variable region comprises 89A. In some embodiments, the heavy chain variable region comprises 91L. In some embodiments, the light chain variable region comprises one or more of the following amino acids: 54P and 55W, per Aho or Kabat numbering. In some embodiments, the light chain variable region comprises 54P. In some embodiments, the light chain variable region comprises 55W. In some embodiments, the HCDR2 comprises SEQ ID NO: 2. In some embodiments, the HCDR2 comprises SEQ ID NO: 3. In some embodiments, the HCDR2 comprises SEQ ID NO: 4. In some embodiments, the HCDR2 comprises SEQ ID NO: 5. In some embodiments, the HCDR3 comprises SEQ ID NO: 6. In some embodiments, the HCDR3 comprises SEQ ID NO: 7. In some embodiments, the HCDR3 comprises SEQ ID NO: 8. In some embodiments, the HCDR3 comprises SEQ ID NO: 9. In some embodiments, the LCDR3 comprises SEQ ID NO: 12. In some embodiments, the LCDR3 comprises SEQ ID NO: 13. In some embodiments, the LCDR3 comprises SEQ ID NO: 14. In some embodiments, LCDR3 comprises SEQ ID NO: 15.

[0256] In some embodiments, an antibody or antigen binding fragment described herein comprises a human IgG1 Fc region comprising (a) 297A, 297Q, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ), (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat

numbering. In some embodiments, an antibody of antigen binding fragment herein comprises a (i) human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P and L235E, or (b) S228P, F234A, and L235A, per Kabat numbering. In some embodiments, an antibody of antigen binding fragment herein comprises a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ). In some embodiments, an antibody of antigen binding fragment herein comprises a human Fc region comprising high mannose glycosylation. In some embodiments, any of the antibody or antigen binding fragments described herein comprise a human IgG4 Fc region.

[0257] In some embodiments, an antibody or antigen binding fragment described herein comprises a human IgG1 with a substitution selected from 297A, 297Q, 297D, 279F, 279K, 279L, 228P, 235A, 235E, 235G, 235Q, 235R, 235S, 237A, 237E, 237K, 237N, 237R, 268K, 269N, 269Q, 270A, 270G, 270M, 270N, 424H, 424M, and 424V, per Kabat numbering. In some embodiments, an antibody or antigen binding fragment described herein comprises a human IgG1 with a substitution selected from 271T, 272N, 292E, 292F, 292G, 292I, 293S, 301W, 304E, 311E, 311G, 311S, 255N, 256H, 256K, 256R, 256V, 316F, 328V, 330R, 339E, 339L, 343I, 343V, 373A, 373G, 373S, 376E, 376W, 376Y, 380D, 382D, 382P, 385P, 234A, 234V, 234F, 233P, 328A, 327Q and 327T, per Kabat numbering. In some embodiments, an antibody or antigen binding fragment described herein comprises a human IgG1 with a substitution selected from 329A, 329G, 329Y, 331S, 236F, 236R, 238A, 238E, 238G, 238H, 238I, 238V, 238W, 238Y, 248A, 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, 254V, 264S, 265H, 265K, 265S, 265Y, 265A, 267G, 267H, 267I, 267K, 434I, 438G, 439E, 439H, 439Q, 440A, 440D, 440E, 440F, 440M, 440T, and 440V, per Kabat numbering.

[0258] In some embodiments, an antibody or antigen binding fragment described herein comprises a Fc region comprising a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362.

[0259] In some embodiments, an antibody or antigen binding fragment described herein comprises at least about 80% monomeric fraction as determined by size exclusion chromatography. In some embodiments, an antibody or antigen binding fragment described herein comprises at least about 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% monomeric fraction. In some embodiments, the size exclusion chromatography comprises injecting purified antibody or antigen binding fragment onto a size exclusion column, wherein the antibody or antigen binding fragment is purified by protein A. In some

embodiments, the antibody or antigen binding fragment is purified as described in Example 2. In some embodiments, the antibody or antigen binding fragment is expressed under conditions described in Example 2. In some embodiments, the size exclusion chromatography column has an inner diameter of 4.6 mm. In some embodiments, the size exclusion chromatography column has a length of 150 mm. In some embodiments, the size exclusion chromatography column has a pore size of 200 Å. In some embodiments, the size exclusion chromatography column has a particle size of 1.7 micrometer. In some embodiments, the size exclusion chromatography column is ACQUITY UPLC BEH200 SEC column. In some embodiments, the antibody or antigen binding fragment is injected at a total volume of 15 µL. In some embodiments, the antibody or antigen binding fragment is injected at a concentration of about 0.1 µg/µL to about 1.0 µg/µL. In some embodiments, the size exclusion chromatography is performed on a Shimadzu UPLC instrument. In some embodiments, the size exclusion chromatography is performed at a flow rate of 0.2 mL/min. In some embodiments, the size exclusion chromatography is performed at a column oven temperature of 30°C. In some embodiments, the percentage of monomer is calculated using Shimadzu software. In some embodiments, the size exclusion chromatography is performed as described in Example 2.

[0260] In some embodiments, an antibody or antigen binding fragment described herein expresses at least about 20 ug/ml total antibody. In some embodiments, an antibody or antigen binding fragment described herein expresses between about 20 ug/ml and 70 ug/mL total antibody. In some embodiments, the antibody or antigen binding fragment is expressed in FreeStyle 293-F cells. In some embodiments, the antibody or antigen binding fragment is expressed as described in Example 2. In some embodiments, the antibody or antigen binding fragment expression level is quantified using Enzyme-Linked Immunosorbent assay (ELISA). In some embodiments, the ELISA comprises coating a surface of a substrate with a capture antibody that binds to a human or humanized antibody, applying the antibody or antigen binding fragment to the substrate, and applying to the substrate a second antibody that binds to a human or humanized antibody. In some embodiments, the capture antibody comprises an anti-kappa antibody. In some embodiments, the second antibody comprises an anti-Fc antibody. In some embodiments, the ELISA is performed as described in Example 2.

[0261] Further provided herein are methods of treating inflammatory bowel disease (IBD) in a subject in need thereof, the method comprising administering to the subject an antibody or antigen binding fragment described herein. In some embodiments, the IBD comprises Crohn's Disease. In some embodiments, the IBD comprises ulcerative colitis.

[0262] Also provided are antibodies or antigen binding fragments thereof that bind to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least 96% identical to SEQ ID NO: 104, and a light chain variable domain comprising an amino acid sequence at least 97% identical to SEQ ID NO: 201. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least 97% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least 98% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises an amino acid sequence at least 99% identical to SEQ ID NO: 104. In some embodiments, the heavy chain variable domain comprises SEQ ID NO: 104. In some embodiments, the light chain variable domain comprises an amino acid sequence at least 98% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain comprises an amino acid sequence at least about 99% identical to SEQ ID NO: 201. In some embodiments, the light chain variable domain comprises SEQ ID NO: 201.

[0263] Further provided are antibodies or antigen binding fragments thereof that bind to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 99% identical to any one of SEQ ID NOS: 101-135, and a light chain variable domain comprising an amino acid sequence at least about 99% identical to any one of SEQ ID NOS: 201-206. **Table 16** and **Table 17** set forth exemplary variable region amino acid sequences of anti-TL1A antibodies.

[0264] Provided are also antibodies or antigen binding fragments, as described herein, further comprising a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R, (m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and

P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of (a) – (uu), per Kabat numbering. In some embodiments, the antibodies comprise a human IgG4 Fc region. In some embodiments, the antibodies a Fc region comprising a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362. In some embodiments, the antibodies comprise at least about 80% monomeric fraction as determined by size exclusion chromatography. In some embodiments, the antibodies are expressed in an amount at least about 20 ug/ml total antibody, optionally about 20 ug/ml and 70 ug/mL total antibody.

Antibody Properties

[0265] In various embodiments, the anti-TL1A antibody is an antagonist of a TL1A receptor, such as, but not limited to, DR3 and TR6/DcR3. In certain embodiments, the antibody inhibits at least about 10%, at least about 20%, at least about 30%, at least about 50%, at least about 75%, at least about 90%, or about 100% of one or more activity of the bound TL1A receptor. In certain embodiments, the antibodies inhibit TL1A activation as measured by interferon gamma release in human blood. In certain embodiments, the antibody inhibits interferon gamma release in human blood at an IC_{50} of between about 1 nanomolar and about 30 picomolar. In certain embodiments, the antibody inhibits interferon gamma release in human blood at an IC_{50} of between about 500 picomolar and about 30 picomolar. In certain embodiments, the antibody inhibits interferon gamma release in human blood at an IC_{50} of between about 200 picomolar and about 30 picomolar. In certain embodiments, the antibody inhibits interferon gamma release in human blood at an IC_{50} of less than or equal to about 200 picomolar. In certain embodiments, the antibody inhibits interferon gamma release in human blood at an IC_{50} of less than or equal to about 100 picomolar.

[0266] In various embodiments, an anti-TL1A antibody provided herein has a binding affinity to human TL1A of less than about $1E^{-7}$, $1E^{-8}$, $1E^{-9}$, or $1E^{-10}$ Kd. In some cases, the binding affinity is from about $1E^{-9}$ to about $1E^{-10}$ Kd. In some embodiments, an anti-TL1A antibody provided herein has a binding affinity to murine TL1A and/or rat TL1A of less than about $1E^{-7}$, $1E^{-8}$, $1E^{-9}$, $1E^{-10}$, or $1E^{-11}$ Kd. Methods for determining binding affinity are exemplified herein, including in Example 2.

[0267] In various embodiments, an anti-TL1A antibody provided herein comprises at least about 80% monomeric fraction after expression and purification as described in Example 2 or elsewhere herein. In various embodiments, an anti-TL1A antibody provided herein comprises at least about 85% monomeric fraction after expression and purification as described in Example 2 or elsewhere herein. In various embodiments, an anti-TL1A antibody provided herein comprises at least about 90% monomeric fraction after expression and purification as described in Example 2 or elsewhere herein. In various embodiments, an anti-TL1A antibody provided herein comprises at least about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% monomeric fraction after expression and purification as described in Example 2 or elsewhere herein.

[0268] In various embodiments, an anti-TL1A antibody provided herein has at least about 2 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has about 2 μg/mL to about 60 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has about 5 μg/mL to about 60 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has about 10 μg/mL to about 60 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has at least about 5 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has at least about 10 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has at least about 15 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has at least about 20 μg/mL expression as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody expresses between about 2 μg/mL and about 50 μg/mL, between about 2 μg/mL and about 40 μg/mL, between about 2 μg/mL and about 30 μg/mL expression, between about 2 μg/mL and about 20 μg/mL, between about 5 μg/mL and about 50 μg/mL, between about 5 μg/mL and about 40 μg/mL, between about 5 μg/mL and about 30 μg/mL, between about 10 μg/mL and about 50 μg/mL, between about 10 μg/mL and about 40 μg/mL, or between about 10 μg/mL and about 30 μg/mL as determined by the method disclosed herein. In some embodiments, the anti-TL1A antibody has about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 μg/mL expression as determined by the method disclosed herein. Methods disclosed herein include those described in Example 2.

[0269] In various embodiments, an anti-TL1A antibody provided herein is humanized and has less than about 20% non-human sequence in the framework region of each of the

heavy chain and light chain variable regions. For instance, the humanized antibody comprises less than about 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% non-human sequence in the framework region of each of the heavy chain and light chain variable regions. As another example, the humanized antibody comprises about or less than about 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 non-human sequences in the framework region of each of the heavy chain and light chain variable regions. The humanized heavy chain variable domain may comprise IGHV1-46*02 framework with no or fewer than about 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 non-human mutations. The humanized light chain variable domain may comprise IGKV3-20 framework with no or fewer than about 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 non-human mutations.

Assays

[0270] An exemplary screening paradigm for identification of antibody variants that express well in mammalian cells and preserve TL1A binding activity while minimizing the propensity of the antibody to aggregate comprises a five-step process. This screen was performed as detailed in the examples. Briefly, (1) variants were cloned and transiently expressed as intact Ig in 293 cells using small-scale (3 mL, 6-well culture plates) transfections, (2) the expression level of the antibody was assessed in the culture supernatant 96-120 hours after transfection using an antibody quantitation ELISA, (3) the binding of the supernatant antibody variants to human TL1A was assessed by ELISA, (4) the antibody was purified in a single step using Protein A and (5) the material was analyzed by analytical SEC to assess monomer/aggregate content. This approach enabled identification of variants that expressed well, preserved binding to TL1A, and displayed high monomer content.

[0271] Further provided herein are methods for analyzing antibody solubility based on percentage of monomeric fraction. For example, as described in Example 2.

[0272] Further provided herein are assays for quantifying antibody expression. For example, as described in Example 2.

[0273] Further provided herein are assays for quantifying immunogenicity of an antibody.

[0274] The antibodies described herein can be assayed for specific binding by any method known in the art. The immunoassays which can be used include, but are not limited to, competitive and non-competitive assay systems using techniques such as BIAcore analysis, FACS analysis, immunofluorescence, immunocytochemistry, Western blots, radioimmunoassays, ELISA, "sandwich" immunoassays, immunoprecipitation assays, precipitation reactions, gel diffusion precipitin reactions, immunodiffusion assays,

agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, and protein A immunoassays. Such assays are provided in for e.g., Ausubel et al., eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York.

Additional Therapeutic Agent

[0275] A therapeutic agent may be used alone or in combination with an additional therapeutic agent. 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.

[0276] In some embodiments, the additional therapeutic agent comprises an anti-TNF therapy, e.g., an anti-TNFα 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).

[0277] 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).

Methods of Generating Antibodies

[0278] In various embodiments, monoclonal antibodies are prepared using methods known in the art, such as, but not limited to the hybridoma method, where a host animal is immunized to elicit the production by lymphocytes of antibodies that will specifically bind to an immunizing antigen (Kohler and Milstein (1975) Nature 256:495). Hybridomas produce monoclonal antibodies directed specifically against a chosen antigen. The monoclonal

antibodies are purified from the culture medium or ascites fluid by techniques known in the art, when propagated either in vitro or in vivo.

[0279] In some embodiments, monoclonal antibodies are made using recombinant DNA methods. The polynucleotides encoding a monoclonal antibody are isolated from mature B-cells or hybridoma cells. The isolated polynucleotides encoding the heavy and light chains are then cloned into suitable expression vectors, which when transfected into host cells (e.g., *E. coli* cells, simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells) generate monoclonal antibodies. The polynucleotide(s) encoding a monoclonal antibody can further be modified in a number of different manners using recombinant DNA technology to generate alternative antibodies.

[0280] In various embodiments, a chimeric antibody, a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region (e.g., humanized antibodies) can be generated.

[0281] In some embodiments, the anti-TL1A monoclonal antibody is a humanized antibody, to reduce antigenicity and HAMA (human anti-mouse antibody) responses when administered to a human subject. Humanized antibodies can be produced using various techniques known in the art. For example, an antibody is humanized by (1) determining the nucleotide and predicted amino acid sequence of the starting antibody light and heavy variable domains; (2) designing the humanized antibody, e.g., deciding which antibody framework region to use during the humanizing process; (3) the actual humanizing methodologies/techniques; and (4) the transfection and expression of the humanized antibody. In various embodiments, a humanized antibody can be further optimized to decrease potential immunogenicity, while maintaining functional activity, for therapy in humans.

[0282] Humanized antibodies can also be made in transgenic mice containing human immunoglobulin loci that are capable, upon immunization, of producing the full repertoire of human antibodies in the absence of endogenous immunoglobulin production. A humanized antibody may also be obtained by a genetic engineering approach that enables production of affinity-matured human-like polyclonal antibodies in large animals.

[0283] A fully humanized antibody may be created by first designing a variable region amino acid sequence that contains non-human, e.g., rodent-derived CDRs, embedded in human-derived framework sequences. The non-human CDRs provide the desired specificity. Accordingly, in some cases these residues are included in the design of the reshaped variable

region essentially unchanged. In some cases, modifications should therefore be restricted to a minimum and closely watched for changes in the specificity and affinity of the antibody. On the other hand, framework residues in theory can be derived from any human variable region. A human framework sequences should be chosen, which is equally suitable for creating a reshaped variable region and for retaining antibody affinity, in order to create a reshaped antibody which shows an acceptable or an even improved affinity. The human framework may be of germline origin, or may be derived from non-germline (e.g., mutated or affinity matured) sequences. Genetic engineering techniques well known to those in the art, for example, but not limited to, phage display of libraries of human antibodies, transgenic mice, human-human hybridoma, hybrid hybridoma, B cell immortalization and cloning, single-cell RT–PCR or HuRAb Technology, may be used to generate a humanized antibody with a hybrid DNA sequence containing a human framework and a non-human CDR.

[0284] In certain embodiments, the anti-TL1A antibody is a human antibody. Human antibodies can be directly prepared using various techniques known in the art. Immortalized human B lymphocytes immunized in vitro or isolated from an immunized individual that produce an antibody directed against a target antigen can be generated.

[0285] Chimeric, humanized and human antibodies may be produced by recombinant expression. Recombinant polynucleotide constructs typically include an expression control sequence operably linked to the coding sequences of antibody chains, including naturally associated or heterologous promoter regions. In certain embodiments, it may be desirable to generate amino acid sequence variants of these humanized antibodies, particularly where these improve the binding affinity or other biological properties of the antibody.

[0286] In certain embodiments, an antibody fragment is used to treat and/or ameliorate IBD. Various techniques are known for the production of antibody fragments. Generally, these fragments are derived via proteolytic digestion of intact antibodies (for example Morimoto et al., 1993, Journal of Biochemical and Biophysical Methods 24:107-117; Brennan et al., 1985, Science, 229:81). Fab, Fv, and scFv antibody fragments can all be expressed in and secreted from E. coli or other host cells, thus allowing the production of large amounts of these fragments. Other techniques for the production of antibody fragments will be apparent to the skilled practitioner.

[0287] According to the present disclosure, techniques can be adapted for the production of single-chain antibodies specific to TL1A. In addition, methods can be adapted for the construction of Fab expression libraries to allow rapid and effective identification of monoclonal Fab fragments with the desired specificity for TL1A, or derivatives, fragments,

analogs or homologs thereof. Antibody fragments may be produced by techniques in the art including, but not limited to: (a) a F(ab')2 fragment produced by pepsin digestion of an antibody molecule; (b) a Fab fragment generated by reducing the disulfide bridges of an F(ab')2 fragment, (c) a Fab fragment generated by the treatment of the antibody molecule with papain and a reducing agent, and (d) Fv fragments.

[0288] Also provided herein are modified antibodies comprising any type of variable region that provides for the association of the antibody with TL1A. Those skilled in the art will appreciate that the modified antibodies may comprise antibodies (e.g., full-length antibodies or immunoreactive fragments thereof) in which at least a fraction of one or more of the constant region domains has been deleted or otherwise altered so as to provide desired biochemical characteristics such as decreasing TL1A. In certain embodiments, the variable regions in both the heavy and light chains are altered by at least partial replacement of one or more CDRs and, if necessary, by partial framework region replacement and sequence changing. In some embodiments, the replaced CDRs may be derived from an antibody of the same class, subclass, from an antibody of a different class, for instance, from an antibody from a different species and/or a combination thereof. In some embodiments, the constant region of the modified antibodies will comprise a human constant region. Modifications to the constant region compatible with this disclosure comprise additions, deletions or substitutions of one or more amino acids in one or more domains.

[0289] In various embodiments, the expression of an antibody or antigen-binding fragment thereof as described herein can occur in either prokaryotic or eukaryotic cells. Suitable hosts include bacterial or eukaryotic hosts, including yeast, insects, fungi, bird and mammalian cells either in vivo, or in situ, or host cells of mammalian, insect, bird or yeast origin. The mammalian cell or tissue can be of human, primate, hamster, rabbit, rodent, cow, pig, sheep, horse, goat, dog or cat origin, but any other mammalian cell may be used. In other embodiments, the antibody or antigen-fragment thereof as described herein may be transfected into the host.

[0290] In some embodiments, the expression vectors are transfected into the recipient cell line for the production of the chimeric, humanized, or composite human antibodies described herein. In various embodiments, mammalian cells can be useful as hosts for the production of antibody proteins, which can include, but are not limited to cells of fibroblast origin, such as Vero (ATCC CRL 81) or CHO-K1 (ATCC CRL 61) cells, HeLa cells and L cells. Exemplary eukaryotic cells that can be used to express polypeptides include, but are not limited to, COS cells, including COS 7 cells; 293 cells, including 293-6E cells; CHO cells, including CHO—

S and DG44 cells; PER.C6™ cells (Crucell); and NSO cells. In some embodiments, a particular eukaryotic host cell is selected based on its ability to make desired post-translational modifications to the heavy chains and/or light chains.

[0291] A number of suitable host cell lines capable of secreting intact heterologous proteins have been developed in the art, and include, but are not limited to CHO cell lines, various COS cell lines, HeLa cells, L cells and multiple myeloma cell lines.

[0292] An expression vector carrying a chimeric, humanized, or composite human antibody construct, antibody or antigen-binding fragment thereof as described herein can be introduced into an appropriate host cell by any of a variety of suitable means, depending on the type of cellular host including, but not limited to transformation, transfection, lipofection, conjugation, electroporation, direct microinjection, and microprojectile bombardment, as known to one of ordinary skill in the art. Expression vectors for these cells can include expression control sequences, such as an origin of replication sites, a promoter, an enhancer and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences.

[0293] In various embodiments, yeast can also be utilized as hosts for the production of the antibody molecules or peptides described herein. In various other embodiments, bacterial strains can also be utilized as hosts for the production of the antibody molecules or peptides described herein. Examples of bacterial strains include, but are not limited to *E. coli*, *Bacillus* species, enterobacteria, and various *Pseudomonas* species.

[0294] In some embodiments, one or more antibodies or antigen-binding fragments thereof as described herein can be produced in vivo in an animal that has been engineered (transgenic) or transfected with one or more nucleic acid molecules encoding the polypeptides, according to any suitable method. For production of transgenic animals, transgenes can be microinjected into fertilized oocytes, or can be incorporated into the genome of embryonic stem cells, and the nuclei of such cells transferred into enucleated oocytes. Once expressed, antibodies can be purified according to standard procedures of the art, including HPLC purification, column chromatography, gel electrophoresis and the like (see generally, Scopes, Protein Purification (Springer-Verlag, NY, 1982)).

[0295] Once expressed in the host, the whole antibodies, antibody-fragments (e.g., individual light and heavy chains), or other immunoglobulin forms of the present disclosure can be recovered and purified by known techniques, e.g., immunoabsorption or immunoaffinity chromatography, chromatographic methods such as HPLC (high performance liquid chromatography), ammonium sulfate precipitation, gel electrophoresis, or

any combination of these. See generally, Scopes, PROTEIN PURIF. (Springer- Verlag, NY, 1982). Substantially pure immunoglobulins of at least about 90% to 95% homogeneity are advantageous, as are those with 98% to 99% or more homogeneity, particularly for pharmaceutical uses. Once purified, partially or to homogeneity as desired, a humanized or composite human antibody can then be used therapeutically or in developing and performing assay procedures, immunofluorescent stainings, etc. See generally, Vols. I & II Immunol. Meth. (Lefkovits & Pernis, eds., Acad. Press, NY, 1979 and 1981).

[0296] Various embodiments provide for a genetic construct comprising a nucleic acid encoding an anti-TL1A antibody or fragment provided herein. Genetic constructs of the antibody can be in the form of expression cassettes, which can be suitable for expression of the encoded anti-TL1A antibody or fragment. The genetic construct may be introduced into a host cell with or without being incorporated in a vector. For example, the genetic construct can be incorporated within a liposome or a virus particle. Alternatively, a purified nucleic acid molecule can be inserted directly into a host cell by methods known in the art. The genetic construct can be introduced directly into cells of a host subject by transfection, infection, electroporation, cell fusion, protoplast fusion, microinjection or ballistic bombardment.

[0297] Various embodiments provide a recombinant vector comprising the genetic construct of an antibody provided herein. The recombinant vector can be a plasmid, cosmid or phage. The recombinant vectors can include other functional elements; for example, a suitable promoter to initiate gene expression.

[0298] Various embodiments provide a host cell comprising a genetic construct and/or recombinant vector described herein.

[0299] Various host systems are also advantageously employed to express recombinant protein. Examples of suitable mammalian host cell lines include the COS-7 lines of monkey kidney cells, and other cell lines capable of expressing an appropriate vector including, for example, L cells, C127, 3T3, Chinese hamster ovary (CHO), HeLa and BHK cell lines. Mammalian expression vectors can comprise non-transcribed elements such as an origin of replication, a suitable promoter and enhancer linked to the gene to be expressed, and other 5' or 3' flanking non-transcribed sequences, and 5' or 3' non-translated sequences, such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences.

[0300] The proteins produced by a transformed host can be purified according to any suitable method. Such standard methods include chromatography (e.g., ion exchange, affinity

and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for protein purification. Affinity tags such as hexahistidine (SEQ ID NO: 1303), maltose binding domain, influenza coat sequence and glutathione-S-transferase can be attached to the protein to allow easy purification by passage over an appropriate affinity column. Isolated proteins can also be physically characterized using such techniques as proteolysis, nuclear magnetic resonance and x-ray crystallography. Recombinant protein produced in bacterial culture can be isolated.

[0301] One of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid and retain the ability to specifically bind the target antigen. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles consistent with the disclosure.

[0302] A given amino acid can be replaced by a residue having similar physiochemical characteristics, e.g., substituting one aliphatic residue for another (such as He, Val, Leu, or Ala for one another), or substitution of one polar residue for another (such as between Lys and Arg; Glu and Asp; or Gln and Asn). Other such conservative substitutions, e.g., substitutions of entire regions having similar hydrophobicity characteristics, are well known. Polypeptides comprising conservative amino acid substitutions can be tested in any one of the assays described herein to confirm that a desired activity, e.g. antigen-binding activity and specificity of a native or reference polypeptide is retained.

[0303] Particular conservative substitutions include, for example; Ala into Gly or into Ser; Arg into Lys; Asn into Gin or into H is; Asp into Glu; Cys into Ser; Gin into Asn; Glu into Asp; Gly into Ala or into Pro; His into Asn or into Gin; lie into Leu or into Val; Leu into lie or into Val; Lys into Arg, into Gin or into Glu; Met into Leu, into Tyr or into lie; Phe into Met, into Leu or into Tyr; Ser into Thr; Thr into Ser; Trp into Tyr; Tyr into Trp; and/or Phe into Val, into lie or into Leu.

[0304] In some embodiments, the antibody and/or antigen-binding fragment thereof described herein can be a variant of a sequence described herein, e.g., a conservative substitution variant of an antibody polypeptide. In some embodiments, the variant is a conservatively modified variant. A variant may refer to a polypeptide substantially homologous to a native or reference polypeptide, but which has an amino acid sequence different from that of the native or reference polypeptide because of one or a plurality of

deletions, insertions or substitutions. Variant polypeptide-encoding DNA sequences encompass sequences that comprise one or more additions, deletions, or substitutions of nucleotides when compared to a native or reference DNA sequence, but that encode a variant protein or fragment thereof that retains activity, e.g., antigen-specific binding activity for the relevant target polypeptide.

[0305] Alterations of the native amino acid sequence can be accomplished by any of a number of techniques known to one of skill in the art. Mutations can be introduced at particular loci or by oligonucleotide-directed site-specific mutagenesis procedures. Techniques for making such alterations are very well established and include, for example, those disclosed by Walder et al. (Gene 42: 133, 1986); Bauer et al. (Gene 37:73, 1985); Craik (BioTechniques, January 1985, 12-19); Smith et al. (Genetic Engineering: Principles and Methods, Plenum Press, 1981).

[0306] Nucleic acid molecules encoding amino acid sequence variants of antibodies are prepared by a variety of methods known in the art. These methods include, but are not limited to, preparation by oligonucleotide-mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant version of the antibody. A nucleic acid sequence encoding at least one antibody, portion or polypeptide as described herein can be recombined with vector DNA in accordance with conventional techniques, including but not limited to, blunt-ended or staggered-ended termini for ligation and restriction enzyme digestion. Techniques for such manipulations are disclosed, e.g., by Maniatis et al., Molecular Cloning, Lab. Manual (Cold Spring Harbor Lab. Press, NY, 1982 and 1989), and can be used to construct nucleic acid sequences which encode a monoclonal antibody molecule or antigen-binding region.

[0307] In some embodiments, a nucleic acid encoding an antibody or antigen-binding fragment thereof as described herein is comprised by a vector. In some of the aspects described herein, a nucleic acid sequence encoding an antibody or antigen-binding fragment thereof as described herein, or any module thereof, is operably linked to a vector. The term "vector," as used herein, refers to a nucleic acid construct designed for delivery to a host cell or for transfer between different host cells. As used herein, a vector can be viral or non-viral. The term "vector" encompasses any genetic element that is capable of replication when associated with the proper control elements and that can transfer gene sequences to cells. A vector can include, but is not limited to, a cloning vector, an expression vector, a plasmid, phage, transposon, cosmid, chromosome, virus, virion, etc.

[0308] As used herein, the term "expression vector" refers to a vector that directs expression of an RNA or polypeptide from sequences linked to transcriptional regulatory sequences on the vector. The term "expression" refers to the cellular processes involved in producing RNA and proteins and as appropriate, secreting proteins, including where applicable, but not limited to, for example, transcription, transcript processing, translation and protein folding, modification and processing. "Expression products" include RNA transcribed from a gene, and polypeptides obtained by translation of mRNA transcribed from a gene. The term "gene" means the nucleic acid sequence which is transcribed (DNA) to RNA in vitro or in vivo when operably linked to appropriate regulatory sequences. The gene may or may not include regions preceding and following the coding region, e.g., 5' untranslated (5'UTR) or "leader" sequences and 3' UTR or "trailer" sequences, as well as intervening sequences (introns) between individual coding segments (exons).

[0309] As used herein, the term "viral vector" refers to a nucleic acid vector construct that includes at least one element of viral origin and has the capacity to be packaged into a viral vector particle. The viral vector can contain the nucleic acid encoding an antibody or antigen-binding portion thereof as described herein in place of non-essential viral genes. The vector and/or particle may be utilized for the purpose of transferring any nucleic acids into cells either in vitro or in vivo. Numerous forms of viral vectors are known in the art.

[0310] By "recombinant vector," it is meant that the vector includes a heterologous nucleic acid sequence, or "transgene" that is capable of expression in vivo.

Pharmaceutical Compositions, Administration and Dosage

[0311] The anti-TL1A antibodies provided are useful in a variety of applications including, but not limited to, therapeutic treatment methods, such as the treatment of IBD. The methods of use may be *in vitro*, *ex vivo*, or *in vivo* methods. In certain embodiments, the anti-TL1A antibody is an antagonist for TL1A receptors.

[0312] In certain embodiments, the disease treated with anti-TL1A antibody or TL1A receptor antagonist is IBD, CD, UC and/or MR-UC.

[0313] In various embodiments, the pharmaceutical compositions are formulated for delivery via any route of administration. "Route of administration" may refer to any administration pathway known in the art, including but not limited to aerosol, nasal, oral, transmucosal, transdermal or parenteral.

[0314] The pharmaceutical compositions can also contain any pharmaceutically acceptable carrier. "Pharmaceutically acceptable carrier" refers to a pharmaceutically acceptable material, composition, or vehicle that is involved in carrying or transporting a

compound of interest from one tissue, organ, or portion of the body to another tissue, organ, or portion of the body. For example, the carrier may be a liquid or solid filler, diluent, excipient, solvent, or encapsulating material, or a combination thereof. Each component of the carrier must be "pharmaceutically acceptable" in that it must be compatible with the other ingredients of the formulation. It must also be suitable for use in contact with any tissues or organs with which it may come in contact, meaning that it must not carry a risk of toxicity, irritation, allergic response, immunogenicity, or any other complication that excessively outweighs its therapeutic benefits.

[0315] In various embodiments, provided are pharmaceutical compositions including a pharmaceutically acceptable excipient along with a therapeutically effective amount of an anti-TL1A antibody. "Pharmaceutically acceptable excipient" means an excipient that is useful in preparing a pharmaceutical composition that is generally safe, non-toxic, and desirable, and includes excipients that are acceptable for veterinary use as well as for human pharmaceutical use. The active ingredient can be mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient and in amounts suitable for use in therapeutic methods described herein. Such excipients may be solid, liquid, semisolid, or, in the case of an aerosol composition, gaseous. Suitable excipients are, for example, starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, water, saline, dextrose, propylene glycol, glycerol, ethanol, mannitol, polysorbate or the like and combinations thereof. In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents and the like which enhance or maintain the effectiveness of the active ingredient. Therapeutic compositions as described herein can include pharmaceutically acceptable salts. Pharmaceutically acceptable salts include the acid addition salts formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, organic acids, for example, acetic, tartaric or mandelic, salts formed from inorganic bases such as, for example, sodium, potassium, ammonium, calcium or ferric hydroxides, and salts formed from organic bases such as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine and the like. Liquid compositions can contain liquid phases in addition to and in the exclusion of water, for example, glycerin, vegetable oils such as cottonseed oil, and water-oil emulsions. Physiologically tolerable carriers are well known in the art. The amount of an active agent (i.e. antibody or fragment thereof) used that will be effective in the treatment of a particular

disorder or condition will depend on the nature of the disorder or condition and can be determined by one of skill in the art with standard clinical techniques.

[0316] The pharmaceutical compositions may be delivered in a therapeutically effective amount. The precise therapeutically effective amount is that amount of the composition that will yield the most effective results in terms of efficacy of treatment in a given subject. This amount will vary depending upon a variety of factors, including but not limited to the characteristics of therapeutic compound (including activity, pharmacokinetics, pharmacodynamics, and bioavailability), the physiological condition of the subject (including age, sex, disease type and stage, general physical condition, responsiveness to a given dosage, and type of medication), the nature of the pharmaceutically acceptable carrier or carriers in the formulation, and the route of administration. One skilled in the clinical and pharmacological arts will be able to determine a therapeutically effective amount through routine experimentation, for instance, by monitoring a subject's response to administration of a compound and adjusting the dosage accordingly. For additional guidance, see *Remington: The Science and Practice of Pharmacy* (Gennaro ed. 20th edition, Williams & Wilkins PA, USA) (2000).

[0317] For the treatment of the disease, the appropriate dosage of an antibody depends on the type of disease to be treated, the severity and course of the disease, the responsiveness of the disease, whether the antibody is administered for therapeutic or preventative purposes, previous therapy, and patient's clinical history. The dosage can also be adjusted by the individual physician in the event of any complication and at the discretion of the treating physician. The administering physician can determine optimum dosages, dosing methodologies and repetition rates. The TL1A antibody can be administered one time or over a series of treatments lasting from several days to several months, or until a cure is effected or a diminution of the disease state is achieved (e.g., treatment or amelioration of IBD). The duration of treatment depends upon the subject's clinical progress and responsiveness to therapy. In certain embodiments, dosage is from 0.01 μg to 100 mg per kg of body weight, and can be given once or more daily, weekly, monthly or yearly.

[0318] Antibody therapeutics suitable for injection and/or administration are important to realizing the full therapeutic potential of mAbs (monoclonal antibodies, e.g. an anti-TL1A monoclonal antibody). However, administration is generally restricted by volume. This, in turn, elucidates the importance developing of high concentration mAb formulations of greater than, for example in some cases, 100 mg/ml. Problems associated with mAb development include high solution viscosity and opalescence, which are commonly encountered during the

development of high-concentration (e.g. greater than 100 mg/ml). Both viscosity and opalescence impact mAb developability broadly, affecting manufacturability, stability, and delivery. High solution viscosities (e.g. greater than 30 mPa-s) cause limiting back-pressures in ultrafiltration/diafiltration during the mAb concentration unit operation. Similarly, viscous mAb solutions also result in forbidding or incompatible injection forces when administering via injection, including via patient friendly autoinjectors. In effect, solution viscosity can be a determining factor for the maximum mAb dose possible via injection. Solution opalescence in therapeutic mAbs can be equally problematic as opalescence can indicate predisposition for liquid-liquid phase separation, precipitation, or aggregation

[0319] The anti-TL1A antibodies provided herein demonstrate advantageous viscosity and aggregation properties at high antibody concentrations (e.g. greater than 100 mg/mL or greater than 150 mg/mL). Notably, anti-TL1A antibodies provided herein are characterized by low viscosity (e.g. less than 10 mPa-s) and low aggregation (e.g. less than 5% high molecular weight species) at high concentrations (**FIGS. 7A-7C**).

[0320] For example, for an antibody or antigen binding fragment wherein HCDR1 comprises SEQ ID NO: 1, HCDR2 comprises SEQ ID NO: 2, HCDR3 comprises SEQ ID NO: 6, LCDR1 comprises SEQ ID NO: 10, LCDR2 comprises SEQ ID NO: 11, and LCDR3 comprises SEQ ID NO: 12 or an antibody or antigen binding fragment wherein the heavy chain variable region comprises SEQ ID NO: 104 and the light chain variable region comprises SEQ ID NO: 201, in some embodiments, the anti-T1LA antibody is characterized by a viscosity less than about 30, 20, 15, or 10 mPa-s at a concentration greater than about 100 mg/mL, e.g., up to about 170 mg/mL. In some embodiments, the anti-T1LA antibody is characterized by a viscosity less than about 30, 20, 15, or 10 mPa-s at a concentration greater than at least about 100 mg/mL. In some embodiments, the anti-T1LA antibody is characterized by a viscosity less than about 30, 20, 15, or 10 mPa-s at a concentration up to about 170 mg/mL. In some embodiments, the anti-T1LA antibody is characterized by a viscosity less than about 30, 20, 15, or 10 mPa-s at a concentration from about 100 mg/mL to about 125 mg/mL, about 100 mg/mL to about 150 mg/mL, about 100 mg/mL to about 160 mg/mL, about 100 mg/mL to about 170 mg/mL, about 125 mg/mL to about 150 mg/mL, about 125 mg/mL to about 160 mg/mL, about 125 mg/mL to about 170 mg/mL, about 150 mg/mL to about 160 mg/mL, about 150 mg/mL to about 170 mg/mL, or about 160 mg/mL to about 170 mg/mL. In some embodiments, the anti-T1LA antibodies is characterized by a viscosity less than about 30, 20, 15, or 10 mPa-s at a concentration about or greater than about 100 mg/mL, about 125 mg/mL, about 150 mg/mL, about 160 mg/mL, or about 170

mg/mL. In some embodiments, less than about 10 mPa-s includes from about 4 to about 10 mPa-s, from about 4 to about 9 mPa-s, from about 4 to about 8 mPa-s, from about 4 to about 7 mPa-s, from about 4 to about 6 mPa-s, from about 4 to about 5 mPa-s, from about 5 to about 10 mPa-s, from about 5 to about 9 mPa-s, from about 5 to about 8 mPa-s, from about 5 to about 7 mPa-s, from about 5 to about 6 mPa-s, from about 6 to about 10 mPa-s, from about 6 to about 9 mPa-s, from about 6 to about 8 mPa-s, or from about 6 to about 7 mPa-s. In some embodiments, greater than about 100, 125, 150, or 160 mg/ml is up to about 170 mg/ml.

[0321] Additionally, for example, for an antibody or antigen binding fragment wherein HCDR1 comprises SEQ ID NO: 1, HCDR2 comprises SEQ ID NO: 2, HCDR3 comprises SEQ ID NO: 6, LCDR1 comprises SEQ ID NO: 10, LCDR2 comprises SEQ ID NO: 11, and LCDR3 comprises SEQ ID NO: 12 or an antibody or antigen binding fragment wherein the heavy chain variable region comprises SEQ ID NO: 104 and the light chain variable region comprises SEQ ID NO: 201, in some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration greater than about 100 mg/mL to about 170 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration greater than at least about 100 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration up to about 170 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration from about 100 mg/mL to about 125 mg/mL, about 100 mg/mL to about 150 mg/mL, about 100 mg/mL to about 160 mg/mL, about 100 mg/mL to about 170 mg/mL, about 125 mg/mL to about 150 mg/mL, about 125 mg/mL to about 160 mg/mL, about 125 mg/mL to about 170 mg/mL, about 150 mg/mL to about 160 mg/mL, about 150 mg/mL to about 170 mg/mL, or about 160 mg/mL to about 170 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration at or greater than about 100 mg/mL, about 125 mg/mL, about 150 mg/mL, about 160 mg/mL, or about 170 mg/mL.

[0322] By way of further example, for an antibody or antigen binding fragment wherein HCDR1 comprises SEQ ID NO: 1, HCDR2 comprises SEQ ID NO: 2, HCDR3 comprises SEQ ID NO: 6, LCDR1 comprises SEQ ID NO: 10, LCDR2 comprises SEQ ID NO: 11, and LCDR3 comprises SEQ ID NO: 12 or an antibody or antigen binding fragment wherein the heavy chain variable region comprises SEQ ID NO: 104 and the light chain variable region

comprises SEQ ID NO: 201, in some embodiments, the anti-T1LA antibody at a concentration from about 150 mg/mL to about or greater than about 170 mg/mL is characterized by a viscosity less than about 10 mPa-s to about 30 mPa-s. In some embodiments, the anti-T1LA antibody at a concentration from about 150 mg/mL to about or greater than about 170 mg/mL is characterized by a viscosity less than about 30 mPa-s. In some embodiments, the anti-T1LA antibody at a concentration from about 150 mg/mL to about or greater than about 170 mg/mL is characterized by a viscosity less than about 5 mPa-s to about 10 mPa-s, about 5 mPa-s to about 15 mPa-s, about 5 mPa-s to about 20 mPa-s, about 5 mPa-s to about 30 mPa-s, about 10 mPa-s to about 15 mPa-s, about 10 mPa-s to about 20 mPa-s, about 10 mPa-s to about 30 mPa-s, about 15 mPa-s to about 20 mPa-s, about 15 mPa-s to about 30 mPa-s, about 20 mPa-s to about 30 mPa-s, about 5 mPa-s to about 9 mPa-s, about 4 to about 10 mPa-s, about 4 to about 9 mPa-s, about 4 to about 8 mPa-s, about 4 to about 7 mPa-s, about 4 to about 6 mPa-s, about 4 to about 5 mPa-s, about 5 to about 10 mPa-s, about 5 to about 9 mPa-s, about 5 to about 8 mPa-s, about 5 to about 7 mPa-s, about 5 to about 6 mPa-s, about 6 to about 10 mPa-s, about 6 to about 9 mPa-s, about 6 to about 8 mPa-s, or about 6 to about 7 mPa-s. In some embodiments, the anti-T1LA antibody at a concentration of about 150 mg/mL to about or greater than about 170 mg/mL is characterized by a viscosity less than about 5 mPa-s, about 10 mPa-s, about 15 mPa-s, about 20 mPa-s, or about 30 mPa-s. In some embodiments, less than about 5, 10, 15, 20, or 30 mPa-s is at least about 1 mPa-s.

[0323] Additionally, for example, for an antibody or antigen binding fragment wherein HCDR1 comprises SEQ ID NO: 1, HCDR2 comprises SEQ ID NO: 2, HCDR3 comprises SEQ ID NO: 6, LCDR1 comprises SEQ ID NO: 10, LCDR2 comprises SEQ ID NO: 11, and LCDR3 comprises SEQ ID NO: 12 or an antibody or antigen binding fragment wherein the heavy chain variable region comprises SEQ ID NO: 104 and the light chain variable region comprises SEQ ID NO: 201, in some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than about 5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than at least about 5 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than at most about 15 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than about 5

Nephelometric Turbidity Units (NTU) to about 7.5 Nephelometric Turbidity Units (NTU), about 5 Nephelometric Turbidity Units (NTU) to about 10 Nephelometric Turbidity Units (NTU), about 5 Nephelometric Turbidity Units (NTU) to about 12.5 Nephelometric Turbidity Units (NTU), about 5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU) to about 10 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU) to about 12.5 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU), about 10 Nephelometric Turbidity Units (NTU) to about 12.5 Nephelometric Turbidity Units (NTU), about 10 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU), or about 12.5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than about 5 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU), about 10 Nephelometric Turbidity Units (NTU), about 12.5 Nephelometric Turbidity Units (NTU), or about 15 Nephelometric Turbidity Units (NTU).

[0324] The anti-TL1A antibodies described herein also demonstrate advantageous aggregation properties. For an antibody or antigen binding fragment wherein HCDR1 comprises SEQ ID NO: 1, HCDR2 comprises SEQ ID NO: 2, HCDR3 comprises SEQ ID NO: 6, LCDR1 comprises SEQ ID NO: 10, LCDR2 comprises SEQ ID NO: 11, and LCDR3 comprises SEQ ID NO: 12 or an antibody or antigen binding fragment wherein the heavy chain variable region comprises SEQ ID NO: 104 and the light chain variable region comprises SEQ ID NO: 201, in some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species (e.g. a species having a molecular weight greater than the molecular weight of the monomer)) less than 10% when at a concentration greater than about 100 mg/mL to about greater than 170 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration greater than at least about 100 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration up to about 170 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration from about 100 mg/mL to about 125 mg/mL, about 100 mg/mL to about 150 mg/mL, about 100 mg/mL to about 160 mg/mL, about 100 mg/mL to about 170 mg/mL, about 125 mg/mL to about 150

mg/mL, about 125 mg/mL to about 160 mg/mL, about 125 mg/mL to about 170 mg/mL, about 150 mg/mL to about 160 mg/mL, about 150 mg/mL to about 170 mg/mL, or about 160 mg/mL to about 170 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration about or greater than about 100 mg/mL, about 125 mg/mL, about 150 mg/mL, about 160 mg/mL, or about 170 mg/mL. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than about 5 % to about 15 %. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than at most about 15 %. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than about 5 % to about 7.5 %, about 5 % to about 10 %, about 5 % to about 15 %, about 5 % to about 17.5 %, about 5% to about 20 %, about 5% to about 25 %, about 7.5 % to about 10 %, about 7.5 % to about 15 %, about 7.5 % to about 17.5 %, about 7.5 % to about 20 %, about 7.5 % to about 25 %, about 10 % to about 15 %, about 10 % to about 17.5 %, about 10 % to about 20 %, about 10 % to about 25 %, about 15 % to about 17.5 %, about 15 % to about 20 %, about 15 % to about 25 %, about 17.5 % to about 20 %, about 17.5 % to about 25 %, or about 20 % to about 25 %. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than about 5%, about 7.5 %, about 10 %, about 15 %, about 17.5 %, about 20 %, or about 25 %.

[0325] By way of further example, for an antibody or antigen binding fragment comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than 9 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework, in some embodiments, the anti-T1LA antibodies is characterized by a viscosity less than 10 mPa-s at a concentration greater than about 100 mg/mL to about greater than 170 mg/mL. In some embodiments, the anti-T1LA antibodies is characterized by a viscosity less than 10 mPa-s at a concentration greater than at least about 100 mg/mL. In some embodiments, the anti-T1LA antibodies is characterized by a viscosity less than 10 mPa-s at a concentration greater than at

most about 170 mg/mL. In some embodiments, the anti-T1LA antibodies is characterized by a viscosity less than 10 mPa-s at a concentration greater than about 100 mg/mL to about 125 mg/mL, about 100 mg/mL to about 150 mg/mL, about 100 mg/mL to about 160 mg/mL, about 100 mg/mL to about 170 mg/mL, about 125 mg/mL to about 150 mg/mL, about 125 mg/mL to about 160 mg/mL, about 125 mg/mL to about 170 mg/mL, about 150 mg/mL to about 160 mg/mL, about 150 mg/mL to about 170 mg/mL, or about 160 mg/mL to about 170 mg/mL. In some embodiments, the anti-T1LA antibodies is characterized by a viscosity less than 10 mPa-s at a concentration greater than about 100 mg/mL, about 125 mg/mL, about 150 mg/mL, about 160 mg/mL, or about 170 mg/mL.

[0326] Additionally, for example, for an antibody or antigen binding fragment comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than 9 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework, in some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration greater than about 100 mg/mL to about greater than 170 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration greater than at least about 100 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration greater than at most about 170 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration greater than about 100 mg/mL to about 125 mg/mL, about 100 mg/mL to about 150 mg/mL, about 100 mg/mL to about 160 mg/mL, about 100 mg/mL to about 170 mg/mL, about 125 mg/mL to about 150 mg/mL, about 125 mg/mL to about 160 mg/mL, about 125 mg/mL to about 170 mg/mL, about 150 mg/mL to about 160 mg/mL, about 150 mg/mL to about 170 mg/mL, or about 160 mg/mL to about 170 mg/mL. In some embodiments, the anti-TL1A antibody is characterized by a turbidity less than 12 Nephelometric Turbidity Units (NTU) when at a concentration greater than about 100 mg/mL, about 125 mg/mL, about 150 mg/mL, about 160 mg/mL, or about 170 mg/mL.

[0327] Additionally, for an antibody or antigen binding fragment comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a

modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than 9 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework, in some embodiments, the anti-T1LA antibody at a concentration greater than 150 mg/mL to greater than about 170 mg/mL is characterized by a viscosity less than about 10 mPa-s to about 30 mPa-s. In some embodiments, the anti-T1LA antibody at a concentration greater than 150 mg/mL to greater than about 170 mg/mL is characterized by a viscosity less than at most about 30 mPa-s. In some embodiments, the anti-T1LA antibody at a concentration greater than 150 mg/mL to greater than about 170 mg/mL is characterized by a viscosity less than about 5 mPa-s to about 10 mPa-s, about 5 mPa-s to about 15 mPa-s, about 5 mPa-s to about 20 mPa-s, about 5 mPa-s to about 30 mPa-s, about 10 mPa-s to about 15 mPa-s, about 10 mPa-s to about 20 mPa-s, about 10 mPa-s to about 30 mPa-s, about 15 mPa-s to about 20 mPa-s, about 15 mPa-s to about 30 mPa-s, or about 20 mPa-s to about 30 mPa-s. In some embodiments, the anti-T1LA antibody at a concentration greater than 150 mg/mL to greater than about 170 mg/mL is characterized by a viscosity less than about 5 mPa-s, about 10 mPa-s, about 15 mPa-s, about 20 mPa-s, or about 30 mPa-s.

[0328] Additionally, for example, for an antibody or antigen binding fragment comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than 9 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework, in some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than about 5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than at least about 5 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than at most about 15 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than about 5 Nephelometric Turbidity Units (NTU) to about 7.5 Nephelometric

Turbidity Units (NTU), about 5 Nephelometric Turbidity Units (NTU) to about 10 Nephelometric Turbidity Units (NTU), about 5 Nephelometric Turbidity Units (NTU) to about 12.5 Nephelometric Turbidity Units (NTU), about 5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU) to about 10 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU) to about 12.5 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU), about 10 Nephelometric Turbidity Units (NTU) to about 12.5 Nephelometric Turbidity Units (NTU), about 10 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU), or about 12.5 Nephelometric Turbidity Units (NTU) to about 15 Nephelometric Turbidity Units (NTU). In some embodiments, the anti-TL1A antibody having a concentration greater than 150 mg/mL is characterized by a turbidity less than about 5 Nephelometric Turbidity Units (NTU), about 7.5 Nephelometric Turbidity Units (NTU), about 10 Nephelometric Turbidity Units (NTU), about 12.5 Nephelometric Turbidity Units (NTU), or about 15 Nephelometric Turbidity Units (NTU).

[0329] The anti-TL1A antibodies described herein also demonstrate advantageous aggregation properties. For an antibody or antigen binding fragment comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than 9 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework, in some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species (e.g. a species having a molecular weight greater than the molecular weight of the monomer)) less than 10% when at a concentration greater than about 100 mg/mL to about greater than 170 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration greater than at least about 100 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration greater than at most about 170 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration greater than about 100 mg/mL to about 125 mg/mL, about 100 mg/mL to about 150 mg/mL, about 100 mg/mL to about 160 mg/mL, about 100 mg/mL to

about 170 mg/mL, about 125 mg/mL to about 150 mg/mL, about 125 mg/mL to about 160 mg/mL, about 125 mg/mL to about 170 mg/mL, about 150 mg/mL to about 160 mg/mL, about 150 mg/mL to about 170 mg/mL, or about 160 mg/mL to about 170 mg/mL. In some embodiments, the anti-TL1A antibody composition is characterized by percent high molecular weight species less than 10% when at a concentration greater than about 100 mg/mL, about 125 mg/mL, about 150 mg/mL, about 160 mg/mL, or about 170 mg/mL. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than about 5 % to about 15 %. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than at most about 15 %. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than about 5 % to about 7.5 %, about 5 % to about 10 %, about 5 % to about 15 %, about 5 % to about 17.5 %, about 5% to about 20 %, about 5% to about 25 %, about 7.5 % to about 10 %, about 7.5 % to about 15 %, about 7.5 % to about 17.5 %, about 7.5 % to about 20 %, about 7.5 % to about 25 %, about 10 % to about 15 %, about 10 % to about 17.5 %, about 10 % to about 20 %, about 10 % to about 25 %, about 15 % to about 17.5 %, about 15 % to about 20 %, about 15 % to about 25 %, about 17.5 % to about 20 %, about 17.5 % to about 25 %, or about 20 % to about 25 %. In some embodiments, the anti-TL1A antibody composition having an antibody concentration greater than 150 mg/mL is characterized by a high molecular weight species less than about 5%, about 7.5 %, about 10 %, about 15 %, about 17.5 %, about 20 %, or about 25 %.

Dosages and Routes of Administration

[0330] 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 renteral 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

administrating 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.

[0331] 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.

[0332] Suitable dose and dosage administrated to a subject is determined by factors including, but no 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.

[0333] 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.

[0334] 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.

[0335] 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.

[0336] 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.

Numbered Embodiments

[0337] In certain embodiments, described herein are methods for evaluating an effect of a treatment described herein. In some instances, the treatment comprises administration with an inhibitor of TL1A activity or expression and optionally, one or more additional therapeutic agents. In some instances, the treatment is monitored by evaluating the quantity of TL1A in the subject prior to and/or after administration of a therapeutic agent.

1. A method of inhibiting or reducing TL1A activity or expression in a subject having or suspected of having at least one of an inflammatory, fibrostenotic, and fibrotic, disease or condition the method comprising:

a) identifying the subject as being a carrier of a genotype comprising a polymorphism provided in **Table 1** or **Table 4**, or a polymorphism in linkage disequilibrium (LD) therewith; and

b) administering to the subject a therapeutically effective amount of an anti-TL1A antibody from **Tables 16-17 or 20**, thereby inhibiting or reducing TL1A activity or expression in the subject.

2. The method of embodiment 1, provided that the inflammatory, fibrostenotic, and fibrotic, disease or condition comprises Crohn's disease, scleroderma, or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis).
3. The method of embodiment 2, provided that the Crohn's disease comprises ileal, ileocolonic, or colonic Crohn's disease.
4. The method of embodiment 1, provided that the inflammatory disease comprises ulcerative colitis (UC).
5. The method of embodiment 4, provided that the UC is medically refractory UC.
6. The method of any of embodiments 1-5, wherein identifying the subject as being a carrier of the genotype of step (a) comprises:

a) contacting a sample comprising genetic material from the subject with a nucleic acid sequence capable of hybridizing to at least 10 contiguous nucleobases comprising a risk allele located at nucleoposition 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059; and

b) detecting binding between the nucleic acid sequence and the at least 10 contiguous nucleobases comprising the risk allele.

7. The method of embodiment 6, provided that the standard hybridization conditions comprise an annealing temperature between about 35 °C and about 65 °C.
8. The method of embodiment 6 or embodiment 7, provided that the standard hybridization conditions are performed with a TaqMan master mix solution.
9. The method of any of embodiments 6-8, provided that the nucleic acid sequence is conjugated to a detectable molecule.
10. The method of embodiment 9, provided that the detectable molecule comprises a fluorophore.
11. The method of any of embodiments 6-10, provided that the nucleic acid sequence is conjugated to a quencher.

12. The method of any of embodiments 6-11, provided that the sample comprising genetic material from the subject is amplified genetic material obtained from a nucleic acid amplification assay.
13. The method of embodiment 12, provided that the nucleic acid amplification assay comprises amplification of DNA from the subject with a pair of primers capable of amplifying at least 15 contiguous nucleobases comprising the risk allele located at nucleoposition 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059, the pair of primers comprising a first primer and a second primer.
14. The method of embodiment 12, provided that the first primer comprises a nucleic acid sequence complimentary to at least 15 contiguous nucleobases upstream of the risk allele located at nucleobase 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059, and the second primer comprises a nucleic acid sequence complimentary to at least 15 contiguous nucleobases downstream of the risk allele located at nucleobase 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059.
15. The method of any of embodiments 1-14, provided that the subject has been determined to be a carrier of the genotype by a process comprising DNA sequencing.
16. The method of any of embodiments 1-15, provided that the subject further comprises soluble TL1A at a level greater than a control level derived from a non-diseased individual or population of non-diseased individuals.
17. The method of any of embodiments 1-16, provided that the subject is homozygous for the genotype.
18. The method of any of embodiments 1-17, wherein the genotype comprises at least two polymorphisms provided in **Table 1** or **Table 4**.
19. The method of any of embodiments 1-17, wherein the genotype comprises at least three polymorphisms provided in **Table 1** or **Table 4**.
20. The method of any of embodiments 1-17, wherein the genotype comprises at least four polymorphisms provided in **Table 1** or **Table 4**.
21. The method of any of embodiments 1-17, wherein the genotype comprises at least five polymorphisms provided in **Table 1** or **Table 4**.
22. The method of any of embodiments 1-17, wherein the genotype comprises at least six polymorphisms provided in **Table 1** or **Table 4**.
23. The method of any of embodiments 1-17, wherein the genotype comprises at least seven polymorphisms provided in **Table 1** or **Table 4**.

24. The method of any of embodiments 1-17, wherein the genotype comprises at least eight polymorphisms provided in **Table 1** or **Table 4**.
25. The method of any of embodiments 1-24, wherein the genotype comprises a polymorphism selected from the group consisting of a "G" allele at rs11897732 (SEQ ID NO: 2001), an "A" allele at rs6740739 (SEQ ID NO: 2002), a "G" allele at rs17796285 (SEQ ID NO: 2003), an "A" allele at rs7935393 (SEQ ID NO: 2004), a "G" allele at rs12934476 (SEQ ID NO: 2005), an "A" allele at rs12457255 (SEQ ID NO: 2006), an "A" allele at rs2070557 (SEQ ID NO: 2007), an "A" allele at rs4246905 (SEQ ID NO: 2008), an "A" allele at rs10974900 (SEQ ID NO: 2009), a "C" allele at rs12434976 (SEQ ID NO: 2010), an "A" allele at rrs16901748 (SEQ ID NO: 20011), an "A" allele at rs2815844 (SEQ ID NO: 20012), a "G" allele at rs889702 (SEQ ID NO: 20013), a "C" allele at rs2409750 (SEQ ID NO: 20014), an "A" allele at rs1541020 (SEQ ID NO: 20015), a "T" allele at rs4942248 (SEQ ID NO: 20016), a "G" allele at rs12934476 (SEQ ID NO: 20017), an "A" allele at rs12457255 (SEQ ID NO: 20018), an "A" allele at rs2297437 (SEQ ID NO: 20019), a "G" allele at rs41309367 (SEQ ID NO: 20020), an "A" allele at rs10733509 (SEQ ID NO: 20021), a "G" allele at rs10750376 (SEQ ID NO: 20022), a "G" allele at rs10932456 (SEQ ID NO: 20023), an "A" allele at rs1326860 (SEQ ID NO: 20024), a "G" allele at rs1528663 (SEQ ID NO: 20025), a "C" allele at rs1892231 (SEQ ID NO: 20026), an "A" allele at rs951279 (SEQ ID NO: 20027), an "A" allele at rs9806914 (SEQ ID NO: 20028), an "A" allele at rs7935393 (SEQ ID NO: 20029), a "G" allele at rs1690492 (SEQ ID NO: 20030), an "A" allele at rs420726 (SEQ ID NO: 20031), a "T" allele at rs7759385 (SEQ ID NO: 20032), an "A" allele at rs10974900 (SEQ ID NO: 20033), an "A" allele at rs1326860 (SEQ ID NO: 20034), a "C" allele at rs2548147 (SEQ ID NO: 20035), an "A" allele at rs2815844 (SEQ ID NO: 20036), a "G" allele at rs889702 (SEQ ID NO: 20037), an "A" allele at rs9806914 (SEQ ID NO: 20038), an "A" allele at rs6478109 (SEQ ID NO: 20039), a "C" allele at rs7278257 (SEQ ID NO: 20040), an "A" allele at rs11221332 (SEQ ID NO: 20041), an "A" allele at rs56124762 (SEQ ID NO: 20057), a "G" at rs2070558 (SEQ ID NO: 20058), and a "T" allele at rs2070561 (SEQ ID NO: 20059).
26. The method of embodiments 1-25, wherein the inhibitor of TL1A activity or expression is an anti-TL1A antibody.
27. The method of embodiment 26, wherein the anti-TL1A antibody is selected from **Table 20.**

28. The method of embodiment 26, wherein the anti-TL1A antibody comprises an amino acid sequence provided in **Tables 16-17**.
29. The method of embodiment 26, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody selected from **Table 20**.
30. The method of embodiment 26, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody, the reference antibody comprising an amino acid sequence provided in **Tables 16-17**.
31. The method of embodiments 26-30, wherein the anti-TL1A antibody is a neutralizing TL1A antibody.
32. The method of embodiments 26-31, wherein the anti-TL1A antibody is an antagonist of TL1A.
33. A method of treating an inflammatory, fibrostenotic, and fibrotic, disease or condition in a subject comprising administering to the subject a therapeutically effective amount of an inhibitor of TL1A activity or expression, provided a presence of a genotype is detected in a sample obtained from the subject.
34. A method of treating an inflammatory, fibrostenotic, or fibrotic, disease or condition in a subject comprising:
    a) analyzing a sample obtained from a subject to detect a presence or an absence of a genotype;
    b) detect the presence of the genotype in the sample obtained from the subject;
    c) administering to the subject a therapeutically effective amount of a TL1A antibody or antigen binding fragment from **Tables 16-17 or 21**.
35. The method of embodiment 33-34, provided that the inflammatory, fibrostenotic, or fibrotic disease or condition comprises Crohn's disease, scleroderma, or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis).
36. The method of embodiment 35, provided that the Crohn's disease comprises ileal, ileocolonic, or colonic Crohn's disease.
37. The method of embodiment 33-34, provided that the inflammatory disease is ulcerative colitis (UC).
38. The method of embodiment 37, provided that the UC is medically refractory UC.
39. The method of any of embodiments 33-38, wherein the presence of the genotype is detected in the sample obtained from the subject by:
    a) contacting the sample comprising genetic material from the subject with a nucleic acid sequence capable of hybridizing to at least 10 contiguous

nucleobases comprising a risk allele located at nucleoposition 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059; and

b) detecting binding between the nucleic acid sequence and the at least 10 contiguous nucleobases comprising the risk allele.

40. The method of embodiment 39, provided that the standard hybridization conditions comprise an annealing temperature between about 35 °C and about 65 °C.
41. The method of embodiment 39 or embodiment 40, provided that the standard hybridization conditions are performed with a TaqMan master mix solution.
42. The method of any of embodiments 39-37, provided that the nucleic acid sequence is conjugated to a detectable molecule.
43. The method of embodiment 42, provided that the detectable molecule comprises a fluorophore.
44. The method of any of embodiments 39-43, provided that the nucleic acid sequence is conjugated to a quencher.
45. The method of any of embodiments 39-44, provided that the sample comprising genetic material from the subject is amplified genetic material obtained from a nucleic acid amplification assay.
46. The method of embodiment 45, provided that the nucleic acid amplification assay comprises amplification of DNA from the subject with a pair of primers capable of amplifying at least 15 contiguous nucleobases comprising the risk allele located at nucleoposition 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059, the pair of primers comprising a first primer and a second primer.
47. The method of embodiment 46, provided that the first primer comprises a nucleic acid sequence complimentary to at least 15 contiguous nucleobases upstream of the risk allele located at nucleobase 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059, and the second primer comprises a nucleic acid sequence complimentary to at least 15 contiguous nucleobases downstream of the risk allele located at nucleobase 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059.
48. The method of any of embodiments 34-47, the presence of the genotype is detected in the sample obtained from the subject by a process comprising DNA sequencing.
49. The method of any of embodiments 34-48, provided that the subject further comprises soluble TL1A at a level greater than a control level derived from a non-diseased individual or population of non-diseased individuals.

50. The method of any of embodiments 34-49, provided that the subject is homozygous for the genotype.
51. The method of any of embodiments 34-50, wherein the genotype comprises at least two polymorphisms provided in **Table 1** or **Table 4**.
52. The method of any of embodiments 34-51, wherein the genotype comprises at least three polymorphisms provided in **Table 1** or **Table 4**.
53. The method of any of embodiments 34-52, wherein the genotype comprises at least four polymorphisms provided in **Table 1** or **Table 4**.
54. The method of any of embodiments 34-53, wherein the genotype comprises at least five polymorphisms provided in **Table 1** or **Table 4**.
55. The method of any of embodiments 34-54, wherein the genotype comprises at least six polymorphisms provided in **Table 1** or **Table 4**.
56. The method of any of embodiments 34-55, wherein the genotype comprises at least seven polymorphisms provided in **Table 1** or **Table 4**.
57. The method of any of embodiments 34-56, wherein the genotype comprises at least eight polymorphisms provided in **Table 1** or **Table 4**.
58. The method of any of embodiments 34-57, wherein the genotype comprises a polymorphism selected from the group consisting of a "G" allele at rs11897732 (SEQ ID NO: 2001), an "A" allele at rs6740739 (SEQ ID NO: 2002), a "G" allele at rs17796285 (SEQ ID NO: 2003), an "A" allele at rs7935393 (SEQ ID NO: 2004), a "G" allele at rs12934476 (SEQ ID NO: 2005), an "A" allele at rs12457255 (SEQ ID NO: 2006), an "A" allele at rs2070557 (SEQ ID NO: 2007), an "A" allele at rs4246905 (SEQ ID NO: 2008), an "A" allele at rs10974900 (SEQ ID NO: 2009), a "C" allele at rs12434976 (SEQ ID NO: 2010), an "A" allele at rrs16901748 (SEQ ID NO: 20011), an "A" allele at rs2815844 (SEQ ID NO: 20012), a "G" allele at rs889702 (SEQ ID NO: 20013), a "C" allele at rs2409750 (SEQ ID NO: 20014), an "A" allele at rs1541020 (SEQ ID NO: 20015), a "T" allele at rs4942248 (SEQ ID NO: 20016), a "G" allele at rs12934476 (SEQ ID NO: 20017), an "A" allele at rs12457255 (SEQ ID NO: 20018), an "A" allele at rs2297437 (SEQ ID NO: 20019), a "G" allele at rs41309367 (SEQ ID NO: 20020), an "A" allele at rs10733509 (SEQ ID NO: 20021), a "G" allele at rs10750376 (SEQ ID NO: 20022), a "G" allele at rs10932456 (SEQ ID NO: 20023), an "A" allele at rs1326860 (SEQ ID NO: 20024), a "G" allele at rs1528663 (SEQ ID NO: 20025), a "C" allele at rs1892231 (SEQ ID NO: 20026), an "A" allele at rs951279 (SEQ ID NO: 2027), an "A" allele at rs9806914 (SEQ ID NO: 20028), an "A" allele at rs7935393 (SEQ ID NO:

20029), a "G" allele at rs1690492 (SEQ ID NO: 20030), an "A" allele at rs420726 (SEQ ID NO: 20031), a "T" allele at rs7759385 (SEQ ID NO: 20032), an "A" allele at rs10974900 (SEQ ID NO: 20033), an "A" allele at rs1326860 (SEQ ID NO: 20034), a "C" allele at rs2548147 (SEQ ID NO: 20035), an "A" allele at rs2815844 (SEQ ID NO: 20036), a "G" allele at rs889702 (SEQ ID NO: 20037), an "A" allele at rs9806914 (SEQ ID NO: 20038), an "A" allele at rs6478109 (SEQ ID NO: 20039), a "C" allele at rs7278257 (SEQ ID NO: 20040), an "A" allele at rs11221332 (SEQ ID NO: 20041)an "A" allele at rs56124762 (SEQ ID NO: 20057), a "G" at rs2070558 (SEQ ID NO: 20058), and a "T" allele at rs2070561 (SEQ ID NO: 20059).

59. The method of embodiments 34-58, wherein the inhibitor of TL1A activity or expression is an anti-TL1A antibody.
60. The method of embodiment 59, wherein the anti-TL1A antibody is selected from **Table 20.**
61. The method of embodiment 59, wherein the anti-TL1A antibody comprises an amino acid sequence provided in **Tables 16-17**.
62. The method of embodiment 59, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody selected from **Table 20**.
63. The method of embodiment 59, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody, the reference antibody comprising an amino acid sequence provided in **Tables 16-17**.
64. The method of embodiments 59-643, wherein the anti-TL1A antibody is a neutralizing TL1A antibody.
65. The method of embodiments 59-64, wherein the anti-TL1A antibody is an antagonist of TL1A.
66. A method of characterizing at least one of an inflammatory, fibrostenotic, and fibrotic, disease or condition of a subject, the method comprising assaying genetic material from the subject to identify the presence or absence of a genotype comprising a polymorphism provided in **Table 1** or **Table 4**.
67. The method of embodiment 66, further comprising assigning a more favorable prognosis to treatment with an inhibitor of TL1A activity or expression when the genotype is present.
68. The method of embodiment 66, further comprising assigning a less favorable prognosis to with an inhibitor of TL1A activity or expression when the genotype is absent.

69. The method of embodiment 66, further comprising assigning the subject to treatment with an inhibitor of TL1A activity or expression when the genotype is present.
70. The method of embodiment 66, further comprising prescribing to the subject an inhibitor of TL1A activity or expression when the genotype is present.
71. The method of embodiment 66, further comprising administering to the subject an inhibitor of anti-CD30 ligand activity or expression when the genotype is present.
72. The method of any of embodiments 67-71, provided that the inhibitor of TL1A activity or expression is an anti-TL1A antibody or antigen-binding fragment thereof.
73. The method of any of embodiments 67-72, provided that assaying comprises amplifying from the genetic material comprising at least 15 contiguous nucleobases including a risk allele located at nucleoposition 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059 using a pair of primers comprising a first primer and a second primer.
74. The method of any of embodiment 73, provided that the first primer comprises a nucleic acid sequence complimentary to at least 15 contiguous nucleobases upstream of the risk allele located at nucleobase 501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059, and the second primer comprises a nucleic acid sequence complimentary to at least 15 contiguous nucleobases downstream of the risk allele located at nucleobase501 within any one of SEQ ID NOS: 2001-2048, or 2057-2059.
75. The method of any of embodiments 66-74, provided that assaying comprises hybridizing to the genetic material a nucleic acid comprising any one of SEQ ID NOS: 2001-2048, or 2057-2059.
76. The method of embodiment 75, provided that the nucleic acid sequence is conjugated to a detectable molecule.
77. The method of embodiment 76, provided that the detectable molecule comprises a fluorophore.
78. The method of any of embodiments 75-77, provided that the nucleic acid sequence is conjugated to a quencher.
79. The method of any of embodiments 66-78, provided that assaying comprises DNA sequencing.
80. The method of any of embodiments 66-79, further comprising measuring the level of TL1A in the subject.
81. The method of any of embodiments 66-80, provided that the subject is homozygous for the genotype.

82. The method of embodiments 66-81, wherein the genotype comprises at least two polymorphisms provided in **Table 1** or **Table 4**.
83. The method of any of embodiments 66-82, wherein the genotype comprises at least three polymorphisms provided in **Table 1** or **Table 4**
84. The method of any one of embodiments 66-83, wherein the genotype comprises at least one polymorphism comprising a non-reference allele.
85. The method of any of embodiments 66-84, further comprising characterizing the at least one of the inflammatory, the fibrostenotic, and the fibrotic, disease or condition as Crohn's disease (CD) provided the genotype is present.
86. The method of embodiment 85, provided that the CD comprises ileal, ileocolonic, or colonic CD.
87. The method of any of embodiments 66-86, further comprising characterizing the at least one of the inflammatory, the fibrostenotic, and the fibrotic, disease or condition as a ulcerative colitis (UC), provided the genotype is present.
88. The method of embodiment 87, provided that the fibrotic disease is medically refractory UC.
89. The method of embodiment 72, wherein the anti-TL1A antibody is selected from **Table 20.**
90. The method of embodiment 72, wherein the anti-TL1A antibody comprises an amino acid sequence provided in **Tables 16-17**.
91. The method of embodiment 72, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody selected from **Table 20**.
92. The method of embodiment 72, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody, the reference antibody comprising an amino acid sequence provided in **Tables 16-17**.
93. The method of embodiments 89-92, wherein the anti-TL1A antibody is a neutralizing TL1A antibody.
94. The method of embodiments 89-93, wherein the anti-TL1A antibody is an antagonist of TL1A.
95. A method for detecting a genotype of interest in a subject comprising at least one of an inflammatory, a fibrostenotic, and a fibrotic, disease or condition, the method comprising:
    (a) contacting genetic material from the subject with a composition sufficiently complementary to and capable of hybridizing to the genotype of interest, the composition comprising:

(i) a detectably labeled oligonucleotide probe comprising at least 10 contiguous nucleobases provided in any one of SEQ ID NOS: 2001-2048, or 2057-2059,

(ii) a detectably labeled oligonucleotide probe comprising at least 10 contiguous nucleobases provided in any one of SEQ ID NOS: 2001-2048, or 2057-2059,

(iii) a detectably labeled oligonucleotide probe comprising at least 10 contiguous nucleobases provided in any one of SEQ ID NOS: 2001-2048, or 2057-2059,

(iv) a detectably labeled oligonucleotide probe comprising a nucleic acid sequence that differs from a probe selected from the group consisting of (i)-(iii) by up to three nucleobases, provided the detectably labeled oligonucleotide probe of (iv) hybridizes to the genotype of interest,

(v) a detectably labeled oligonucleotide probe comprising a nucleic acid sequence complementary to a probe selected from the group consisting of (i)-(iv), or

(vi) a combination of probes selected from the group consisting of (i)-(v),

wherein the detectably labeled oligonucleotide probe of (i), (ii), and (iii) are different,

(b) detecting the presence or absence of hybridization of the genetic material with the composition using the detectably labeled probe, whereby hybridization of the genetic material with the composition is indicative of the presence of the genotype of interest in the subject.

96. The method of embodiment 95, provided that the presence of the genotype of interest is indicative of the subject comprising elevated levels of TL1A.

97. The method of embodiment 95 or embodiment 96, provided that the inflammatory, fibrostenotic, or fibrotic disease or condition comprises Crohn's disease (CD), scleroderma, or pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis).

98. The method of embodiment 97, provided that the CD comprises ileal, ileocolonic, or colonic CD.

99. The method of embodiments 99 or 92, provided that the inflammatory disease is ulcerative colitis (UC).

100. A method of treating the at least one of an inflammatory disease, a fibrostenotic disease, in the subject of any one of embodiments 95-99, the method comprising:

a) administering to the subject of any of embodiments 95-89 a therapeutically effective amount of an inhibitor of TL1A activity or expression, provided that the subject comprises the genotype of interest.

101. The method of embodiment 100, provided that the inhibitor of TL1A activity comprises an anti-TL1A ligand antibody or antigen binding fragment thereof.

102. A composition comprising at least 10 but less than 50 contiguous nucleobase residues of any one of SEQ ID NOS: 2001-2048, or 2057-2059 or its complement, wherein the contiguous nucleobase residues comprise the nucleobase at position 501 of the any one of SEQ ID NOS: 2001-2048, or 2057-2059, and wherein the contiguous nucleobase residues are connected to a detectable molecule.

103. The composition of embodiment 102, provided that the detectable molecule is a fluorophore.

104. The composition of embodiments 102-103, wherein the contiguous nucleobase residues comprise the nucleobase at position 501 of any one of SEQ ID NOS: 2001-2048, or 2057-2059.

105. The composition of embodiments 102-104, wherein the contiguous nucleobase residues comprise the nucleobase at position 501 of any one of SEQ ID NOS: 2060-2108, or 364141-364142.

106. The composition of embodiments 102-105, provided that the contiguous nucleobase residues are connected to a quencher.

107. A kit comprising the composition of any of embodiments 102-106, and a primer pair capable of amplifying at least 15 contiguous nucleic acid molecules of any one of SEQ ID NOS: 2001-2048, or 2057-2059, the at least 15 contiguous nucleic acid molecules comprising the nucleic acid located at position 501 of any one of SEQ ID NOS: 2001-2048, or 2057-2059.

108. A method comprising contacting DNA from a subject with the composition of any of embodiments 102-106 or the kit of any of embodiment 107 under conditions configured to hybridize the composition to the DNA if the DNA comprises a sequence complementary to the composition.

109. A method comprising treating the subject of embodiment 108 with an inhibitor of TL1A activity or expression, provided that the DNA from the subject comprises the sequence complementary to the composition.

110. The method of embodiment 109, provided that the inhibitor of TL1A comprises an anti-TL1A antibody or antigen binding fragment thereof.

111. A method of identifying a risk of developing a TL1A mediated disease or condition comprising at least one of an inflammatory, a fibrostenotic, and a fibrotic, disease or condition in a subject, the method comprising:

a) assaying a sample obtained from the subject to identify the presence of a genotype comprising a polymorphism provided in **Table 1** or **Table 4**, or a polymorphism in linkage disequilibrium (LD) therewith; and

b) identifying the risk of developing at least one of an inflammatory, a fibrostenotic, and a fibrotic, disease or condition in the subject, provided the presence of the genotype is identified in step (a).

112. A method of selecting a subject for treatment, the method comprising:

a) assaying a sample obtained from the subject to identify the presence of a genotype comprising a polymorphism provided in **Table 1** or **Table 4**, or a polymorphism in linkage disequilibrium (LD) therewith; and

b) selecting the subject for treatment with an inhibitor of TL1A activity or expression, provided the presence of the genotype is identified in step (a).

113. The method of any of embodiments 111-112, provided that the subject is homozygous for the genotype.

114. The method of any of embodiments 111-113, wherein the genotype comprises at least two polymorphisms provided in **Table 1** or **Table 4**.

115. The method of any of embodiments 111-114, wherein the genotype comprises at least three polymorphisms provided in **Table 1** or **Table 4**.

116. The method of any of embodiments 111-115, wherein the genotype comprises at least four polymorphisms provided in **Table 1** or **Table 4**.

117. The method of any of embodiments 111-116, wherein the genotype comprises at least five polymorphisms provided in **Table 1** or **Table 4**.

118. The method of any of embodiments 111-117, wherein the genotype comprises at least six polymorphisms provided in **Table 1** or **Table 4**.

119. The method of any of embodiments 111-118, wherein the genotype comprises at least seven polymorphisms provided in **Table 1** or **Table 4**.

120. The method of any of embodiments 111-119, wherein the genotype comprises at least eight polymorphisms provided in **Table 1** or **Table 4**.

121. The method of any of embodiments 111-1220, wherein the genotype comprises at least one polymorphism comprising a non-reference allele.

122. The method of embodiments 111-121, further comprising treating the subject by administering to the subject a therapeutically effective amount of an inhibitor of TL1A activity or expression.

123. The method of embodiment 122, wherein the inhibitor of TL1A activity or expression is an anti-TL1A antibody.

124. The method of embodiment 123, wherein the anti-TL1A antibody is selected from **Table 20.**

125. The method of embodiment 123, wherein the anti-TL1A antibody comprises an amino acid sequence provided in **Tables 16-17**.

126. The method of embodiment 123, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody selected from **Table 20**.

127. The method of embodiment 123, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody, the reference antibody comprising an amino acid sequence provided in **Tables 16-17**.

128. The method of embodiments 123-128, wherein the anti-TL1A antibody is a neutralizing TL1A antibody.

129. The method of embodiments 123-129, wherein the anti-TL1A antibody is an antagonist of TL1A.

130. The methods of embodiments 33-65 or 111-121, further comprising administering a therapeutically effective amount of an additional therapeutic agent.

131. The method of embodiment 130, wherein the additional therapeutic agent is a modulator of Receptor Interacting Serine/Threonine Kinase 2 (RIPK2).

132. The method of embodiment 130, wherein the additional therapeutic agent is a modulator of G Protein-Coupled Receptor 35 (GPR35).

133. The method of embodiment 130, wherein the additional therapeutic agent is a modulator of CD30 ligand (CD30L)

134. The method of any one of embodiments 1-134, further comprising predicting a positive therapeutic response in a subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.

135. The method of any one of embodiments 1-135, further comprising predicting a positive therapeutic response in a subject to a treatment with the inhibitor of TL1A activity or expression with a specificity of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.

136. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a

therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression, provided at least three polymorphisms comprising rs1892231, rs56124762, rs6478109, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs16901748, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject; wherein the inhibitor of TL1A activity is an antibody or antigen binding fragment as described herein.

137. The method of embodiment 136, wherein the at least three polymorphisms are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression at a positive predictive value of at least about 70%.

138. The method of embodiment 136, wherein the at least three polymorphisms are predictive of positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a specificity of at least about 70%.

139. The method of embodiment 136, wherein the at least three polymorphisms comprise:

(a) rs6478109, rs56124762, and rs1892231;

(b) rs6478109, rs56124762, and rs16901748;

(c) rs6478109, rs1892231, and rs16901748;

(d) rs56124762, rs1892231, and rs16901748;

(e) rs6478109, rs2070558, and rs1892231;

(f) rs6478109, rs2070558, and rs16901748;

(g) rs6478109, rs1892231, and rs16901748;

(h) rs2070558, rs1892231, and rs16901748;

(i) rs6478109, rs2070561, and rs1892231;

(j) rs6478109, rs2070561 , and rs16901748;

(k) rs6478109, rs1892231, and rs16901748;

(l) rs2070561, rs1892231, and rs16901748;

(m)rs6478109, rs7935393, and rs1892231;

(n) rs6478109, rs7935393, and rs9806914;

(o) rs6478109, rs7935393, and rs7278257;

(p) rs6478109, rs7935393, and rs2070557;

(q) rs6478109, rs1892231, and rs9806914;

(r) rs6478109, rs1892231, and rs7278257;

(s) rs6478109, rs1892231, and rs2070557;

(t) rs6478109, rs9806914, and rs7278257;

(u) rs6478109, rs9806914, and rs2070557;

(v) rs6478109, rs7278257, and rs2070557;

(w) rs7935393, rs1892231, and rs9806914;

(x) rs7935393, rs1892231, and rs7278257;

(y) rs7935393, rs1892231, and rs2070557;

(z) rs7935393, rs9806914, and rs7278257;

(aa) rs7935393, rs9806914, and rs2070557;

(bb) rs7935393, rs7278257, and rs2070557;

(cc) rs1892231, rs9806914, and rs7278257;

(dd) rs1892231, rs9806914, and rs2070557;

(ee) rs1892231, rs7278257, and rs2070557; or

(ff) rs9806914, rs7278257, and rs2070557.

140. The method of embodiment 136, wherein the at least three polymorphisms further comprises a fourth polymorphism comprising rs16901748, rs1892231, rs56124762, rs6478109, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.

141. The method of method of embodiment 136, wherein the at least three polymorphisms are detected in the sample by subjecting the sample to an assay configured to detect a presence of at least three nucleotides corresponding to nucleic acid position 501 within at least three of SEQ ID NOS: 2001-2041, or 2057-2059.

142. The method of embodiment 136, wherein the at least eight polymorphisms are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression at a positive predictive value of at least about 70%.

143. The method of embodiment 136, wherein the at least eight polymorphisms are predictive of positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a specificity of at least about 70%.

144. The method of embodiment 136, wherein the at least eight polymorphisms comprise a set of polymorphisms selected from **Table 25.**

145. The method of embodiment 1, wherein the inflammatory, fibrotic, or fibrostenotic disease or condition comprises inflammatory bowel disease, Crohn's disease, obstructive Crohn's disease, ulcerative colitis, intestinal fibrosis, intestinal fibrostenosis, rheumatoid arthritis, pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis), scleroderma, or primary sclerosing cholangitis.

146. The method of embodiment 145, wherein the Crohn's disease is ileal, ileocolonic, or colonic Crohn's disease.

147. The method of embodiment 136, wherein the subject has, or is at risk for developing, a non-response or loss-of-response to a standard therapy comprising glucocorticosteriods, anti-TNF therapy, anti-a4-b7 therapy, anti-IL12p40 therapy, or a combination thereof.

148. The method of embodiment 136, wherein the inhibitor of TL1A is an anti-TL1A antibody or antigen-binding fragment.

149. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising:

(a) determining whether the subject with an inflammatory, a fibrotic, or a fibrostenotic disease or condition is suitable for treatment with an inhibitor of TL1A activity or expression by:

(i) obtaining or having obtained a sample from the subject; and

(ii) subjecting the sample to an assay adapted to detect at least three polymorphisms comprising rs1892231, rs56124762, rs6478109, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs16901748, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509,

rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof; and

(b) treating the subject by administering a therapeutically effective amount of the inhibitor of TL1A activity or expression to the subject;
wherein the inhibitor of TL1A activity or expression is an anti-TL1A antibody or antigen as described herein.

150. The method of embodiment 149, wherein the at least three polymorphisms are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression at a positive predictive value of at least about 70%.

151. The method of embodiment 149, wherein the at least three polymorphisms are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression at a specificity of at least about 70%.

152. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising:

(c) determining whether the subject with an inflammatory, a fibrotic, or a fibrostenotic disease or condition is suitable for treatment with an inhibitor of TL1A activity or expression by:

(iii) obtaining or having obtained a sample from the subject; and

(iv) subjecting the sample to an assay adapted to detect at least eight polymorphisms comprising rs1892231, rs56124762, rs6478109, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs16901748, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof; and

(d) treating the subject by administering a therapeutically effective amount of the inhibitor of TL1A activity or expression to the subject;
wherein the inhibitor of TL1A activity or expression is an anti-TL1A antibody or antigen as described herein.

153. The method of embodiment 152, wherein the at least eight polymorphisms are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression at a positive predictive value of at least about 70%.

154. The method of embodiment 152, wherein the at least eight polymorphisms are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression at a specificity of at least about 70%.

155. The method of embodiment 136, wherein the inflammatory, fibrotic, or fibrostenotic disease or condition comprises inflammatory bowel disease, Crohn's disease, obstructive Crohn's disease, ulcerative colitis, intestinal fibrosis, intestinal fibrostenosis, rheumatoid arthritis, pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis), scleroderma, or primary sclerosing cholangitis.

156. The method of embodiment 156, wherein the Crohn's disease is ileal, ileocolonic, or colonic Crohn's disease.

157. The method of embodiment 149, wherein the wherein the inhibitor of TL1A activity or expression is an anti-TL1A antibody or antigen-binding fragment.

158. The method of embodiment 149, wherein the at least three polymorphisms comprise:

(a) rs6478109, rs56124762, and rs1892231;
(b) rs6478109, rs56124762, and rs16901748;
(c) rs6478109, rs1892231, and rs16901748;
(d) rs56124762, rs1892231, and rs16901748;
(e) rs6478109, rs2070558, and rs1892231;
(f) rs6478109, rs2070558, and rs16901748;
(g) rs6478109, rs1892231, and rs16901748;
(h) rs2070558, rs1892231, and rs16901748;
(i) rs6478109, rs2070561, and rs1892231;
(j) rs6478109, rs2070561 , and rs16901748;
(k) rs6478109, rs1892231, and rs16901748;
(l) rs2070561, rs1892231, and rs16901748;

(m) rs6478109, rs7935393, and rs1892231;

(n) rs6478109, rs7935393, and rs9806914;

(o) rs6478109, rs7935393, and rs7278257;

(p) rs6478109, rs7935393, and rs2070557;

(q) rs6478109, rs1892231, and rs9806914;

(r) rs6478109, rs1892231, and rs7278257;

(s) rs6478109, rs1892231, and rs2070557;

(t) rs6478109, rs9806914, and rs7278257;

(u) rs6478109, rs9806914, and rs2070557;

(v) rs6478109, rs7278257, and rs2070557;

(w) rs7935393, rs1892231, and rs9806914;

(x) rs7935393, rs1892231, and rs7278257;

(y) rs7935393, rs1892231, and rs2070557;

(z) rs7935393, rs9806914, and rs7278257;

(aa) rs7935393, rs9806914, and rs2070557;

(bb) rs7935393, rs7278257, and rs2070557;

(cc) rs1892231, rs9806914, and rs7278257;

(dd) rs1892231, rs9806914, and rs2070557;

(ee) rs1892231, rs7278257, and rs2070557; or

(ff) rs9806914, rs7278257, and rs2070557.

159. The method of embodiment 136, wherein the at least three polymorphisms further comprises a fourth polymorphism comprising rs16901748, rs1892231, rs56124762, rs6478109, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332 or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.

160. The method of embodiment 136, wherein the subject is at risk of developing a non-response or loss-of-response to a standard therapy comprising glucocorticosteriods, anti-TNF therapy, anti-a4-b7 therapy, anti-IL12p40 therapy, or a combination thereof.

161. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of TL1A activity or expression, wherein the subject expresses at least three polymorphisms comprising rs16901748, rs6478109, rs56124762, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85;
wherein the inhibitor of TL1A activity of expression is an nti-TL1A antibody or antigen-binding fragment as described herein.

162. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, wherein said antibody or antigen-binding fragment comprises:

a) a heavy chain comprising a heavy chain complementarity determining region 1 (HCDR1), a heavy chain complementarity determining region 2 (HCDR2), and a heavy chain complementarity determining region 3 (HCDR3), wherein the HCDR1 comprises a first amino acid sequence of DTYMH of SEQ ID NO: 601; the HCDR2 comprises a second amino acid sequence of PASGH of SEQ ID NO: 768; and the HCDR3 comprises a third amino acid sequence of SGGLPD of SEQ ID NO: 805; and

b) a light chain comprising a light chain complementarity determining region 1 (LCDR1), a light chain complementarity determining region 2 (LCDR2), and a light chain complementarity determining region 3 (LCDR3), wherein the LCDR1 comprises a fourth amino acid sequence of ASSSVSYMY of SEQ ID NO: 851; the LCDR2 comprises a fifth amino acid sequence of ATSNLAS of SEQ ID NO: 11; and the LCDR3 comprises a sixth amino acid sequence of GNPRT of SEQ ID NO: 921.

163. The method of embodiment 163, provided that the antibody or antigen-binding fragment is a chimeric antibody, a CDR-grafted antibody, a humanized 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, a bispecific antibody, or a combination thereof.

164. The method of embodiment 163, provided that the antibody or antigen-binding fragment is a humanized antibody.

165. The method of embodiment 163, where the antibody or antigen-binding fragment of embodiment 141 is administered with a pharmaceutically acceptable carrier.

166. The method of embodiment 163, provided the antibody or antigen binding fragment is an immunoglobulin G (IgG).

167. The method of embodiment 165, provided the IgG comprises an IgG1.

168. The method of embodiment 164, provided the IgG comprises an IgG2.

169. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, wherein said antibody or antigen-binding fragment comprises an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3002, and 3006; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3013.

170. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least eight polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or

expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, wherein said antibody or antigen-binding fragment comprises an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3002, and 3006; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3013.

171. The method of embodiment 170 or 171, wherein the light chain variable region comprises SEQ ID NO: 3204.

172. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3005, and 3008; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3012.

173. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least eight polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that

specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3005, and 3008; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3012.

174. The method of embodiment 173 or 174, wherein the light chain variable region comprises SEQ ID NO: 3202.

175. The method of any one of embodiments 173-175, wherein the heavy chain variable region comprises SEQ ID NO: 3121.

176. The method of any one of embodiments 173-175, wherein the heavy chain variable region comprises SEQ ID NO: 3122.

177. The method of any one of embodiments 173-175, wherein the heavy chain variable region comprises SEQ ID NO: 3123.

178. The method of any one of embodiments 173-175, wherein the heavy chain variable region comprises SEQ ID NO: 3124.

179. The method of embodiments 173 or 174, wherein the light chain variable region comprises SEQ ID NO: 3205.

180. The method of embodiment 173 or embodiment 174, wherein the heavy chain variable region comprises SEQ ID NO: 3122.

181. The method of embodiment 173 or embodiment 174, wherein the heavy chain variable region comprises SEQ ID NO: 3124.

182. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3005, and 3008; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3013.

183. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least eight polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3005, and 3008; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3013.

184. The method of embodiment 183 or 184, wherein the heavy chain variable region comprises SEQ ID NO: 3122.

185. The method of embodiment 183 or embodiment 184, wherein the light chain variable region comprises SEQ ID NO: 3204.

186. The method of embodiment 183 or embodiment 184, wherein the light chain variable region comprises SEQ ID NO: 3206.

187. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3003, and 3008; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3013.

188. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a

therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least eight polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable region comprising complementarity determining regions (CDRs) as set forth in SEQ ID NOS: 3001, 3003, and 3008; and a light chain variable region comprising CDRs as set forth in SEQ ID NOS: 3010, 3011, and 3013.

189. The method of embodiment 188 or 189, wherein the heavy chain variable region comprises SEQ ID NO: 3128.

190. The method of embodiment 188 or 189, wherein the light chain variable region comprises SEQ ID NO: 3206.

191. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than about 14 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework.

192. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a

therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least eight polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and wherein the inhibitor of TL1A activity or expression comprises a antibody or antigen-binding fragment that specifically binds to a tumor necrosis factor-like protein 1A (TL1A) polypeptide, comprising a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework, and a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than about 14 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework.

193. The method of embodiment 193 or 194, wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or no amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework.

194. The method of any one of embodiments 170-193, wherein the antibody is humanized.

195. The method of any one of embodiments 170-194, wherein the antibody comprises a human IgG1 fragment crystallizable (Fc) region.

196. The method of any one of embodiments 170-194, wherein the antibody comprises a human IgG4 fragment crystallizable (Fc) region.

197. The method of embodiments 170-197, wherein the disease or condition comprises inflammatory bowel disease.

198. The method of embodiments 170-198, wherein the disease or condition comprises Crohn's disease.

199. The method of embodiments 170-199, wherein the disease or condition comprises ulcerative colitis.

200. The method of any one of embodiments 170-200, further comprising predicting a positive therapeutic response in a subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value of at least or about

50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.

201. The method of any one of embodiments 169-201, further comprising predicting a positive therapeutic response in a subject to a treatment with the inhibitor of TL1A activity or expression with a specificity of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.

202. The method of any one of embodiments, 162-201, inflammatory, fibrotic, or fibrostenotic disease or condition comprises inflammatory bowel disease, Crohn's disease, obstructive Crohn's disease, ulcerative colitis, intestinal fibrosis, intestinal fibrostenosis, rheumatoid arthritis, pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis), scleroderma, or primary sclerosing cholangitis.

[0338] In some embodiments, the at least three polymorphisms is eight polymorphisms. Non-limiting examples of eight polymorphism combinations are provided in paragraph [045], embodiment 54 (495 combinations).

Kits

[0339] Further provided is a kit to treat IBD (e.g., CD, UC and/or mrUC). The kit comprises of the antibodies described herein, which can be used to perform the methods described herein. The kit is useful for practicing the inventive method of providing treatment to an IBD, CD, UC and/or mrUC patient by administering an anti-TL1A antibody. The kit is an assemblage of materials or components, including at least one of the inventive compositions. Thus, in some embodiments, the kit contains a composition including anti-TL1A antibodies, for the treatment of IBD, CD, UC and/or MR-UC, as described above. In other embodiments, the kits contain all of the components necessary and/or sufficient to perform a detection assay for TL1A, including all controls, directions for performing assays, and any necessary software for analysis and presentation of results.

[0340] The exact nature of the components configured in the inventive kit depends on its intended purpose. For example, some embodiments are configured for the purpose of treating IBD, CD, UC and/or MR-UC. In one embodiment, the kit is configured particularly for the purpose of treating mammalian subjects. In another embodiment, 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.

[0341] Instructions for use may be included in the kit. "Instructions for use" typically include a tangible expression describing the technique to be employed in using the components of the kit to effect a desired outcome, such as to treat or alleviate IBD, CD, UC and/or MR-UC. 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 as will be readily recognized by those of skill in the art.

[0342] 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 inventive 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 an inventive composition containing anti-TL1A antibodies and/or primers and probes for TL1A. The packaging material generally has an external label which indicates the contents and/or purpose of the kit and/or its components.

[0343] Disclosed herein, 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.

[0344] In some instances, the kits described herein comprise components for detecting the presence, absence, and/or quantity of a target nucleic acid and/or protein 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.

[0345] In some embodiments, the kits described herein are configured for the purpose of treating and/or characterizing a disease or condition (*e.g.*, Crohn's disease, pulmonary fibrosis, scleroderma, ulcerative colitis), or subclinical phenotype thereof (*e.g.,* stricturing, penetrating, or stricturing and penetrating disease phenotypes) in a subject. In some embodiments, the kits described herein are configured for the purpose of identifying a subject suitable for treatment with an inhibitor of TL1A activity or expression (*e.g.,* anti-TL1A antibody). 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 a therapeutic agent disclosed herein. An exemplary therapeutic agent is an anti-TL1A antibody.

[0346] 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

[0347] Disclosed herein are systems for treating a subject with an inhibitor of TL1A activity or expression (e.g., anti-TL1A antibody), wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject. In some embodiments, the systems described herein comprise kits and compositions for detecting the genotypes described herein in a biological sample of a subject. The system may comprise a computer system for implementing one or more methods of the disclosure, such as for example, receiving genotype data of a subject 201, inputting the genotype data into an algorithm to produce a TNFSF15 profile 202, and generating a report comprising the TNFSF15 profile of the subject 203, and displaying the report to a user on a graphical user interface 204, as shown in **FIG. 2**. A "TNFSF15 profile" as used herein refers to a profile of one or more genotypes described herein of a subject that is detected in a biological sample obtained from the subject. In some embodiments, a TNFSF15 profile comprises a positive, a negative, or an indeterminate result (e.g., therapeutic response to treatment with an inhibitor of TL1A activity or expression).

Computer systems

[0348] **FIG. 3** shows a computer system 301 that is programmed or otherwise configured to generate a TNFSF15 profile for a subject in need thereof. The computer system 301 can regulate various aspects of producing the TNFSF15 profile (e.g., receiving genotype data, generating a report with the TNFSF15 profile of the biological sample, and displaying the report to a user), of the present disclosure, such as, for example, by including permissions or encryption of genotype data and/or TNFSF15 profile of the subject to ensure patient privacy.

[0349] The computer system 301 can be an electronic device of a user or a computer system that is remotely located with respect to the electronic device. The electronic device

can be a mobile electronic device, such as a mobile electronic device belonging to a physician.

[0350] The computer system 301 includes a central processing unit (CPU, also "processor" and "computer processor" herein) 305, which can be a single core or multi core processor, or a plurality of processors for parallel processing. The computer system 301 also includes memory or memory location 310 (e.g., random-access memory, read-only memory, flash memory), electronic storage unit 315 (e.g., hard disk), communication interface 320 (e.g., network adapter) for communicating with one or more other systems, and peripheral devices 325, such as cache, other memory, data storage and/or electronic display adapters. The memory 310, storage unit 315, interface 320 and peripheral devices 325 are in communication with the CPU 305 through a communication bus (solid lines), such as a motherboard. The storage unit 315 can be a data storage unit (or data repository) for storing data. The computer system 301 can be operatively coupled to a computer network ("network") 330 with the aid of the communication interface 320. The network 330 can be the Internet, an internet and/or extranet, or an intranet and/or extranet that is in communication with the Internet. The network 330 in some cases is a telecommunication and/or data network. The network 330 can include one or more computer servers, which can enable distributed computing, such as cloud computing. The network 330, in some cases with the aid of the computer system 301, can implement a peer-to-peer network, which may enable devices coupled to the computer system 301 to behave as a client or a server.

[0351] The CPU 305 can execute a sequence of machine-readable instructions, which can be embodied in a program or software. The instructions may be stored in a memory location, such as the memory 310. The instructions can be directed to the CPU 305, which can subsequently program or otherwise configure the CPU 305 to implement methods of the present disclosure. Examples of operations performed by the CPU 305 can include fetch, decode, execute, and writeback.

[0352] The CPU 305 can be part of a circuit, such as an integrated circuit. One or more other components of the system 301 can be included in the circuit. In some cases, the circuit is an application specific integrated circuit (ASIC).

[0353] The storage unit 315 can store files, such as drivers, libraries and saved programs. The storage unit 315 can store user data, e.g., user preferences and user programs. The computer system 301 in some cases can include one or more additional data storage units that are external to the computer system 301, such as located on a remote server that is in communication with the computer system 301 through an intranet or the Internet.

[0354] The computer system 301 can communicate with one or more remote computer systems through the network 330. For instance, the computer system 301 can communicate with a remote computer system of a user. Examples of remote computer systems include personal computers (e.g., portable PC), slate or tablet PC's (e.g., Apple® iPad, Samsung® Galaxy Tab), telephones, Smart phones (e.g., Apple® iPhone, Android-enabled device, Blackberry®), or personal digital assistants. The user can access the computer system 301 via the network 330.

[0355] Methods as described herein can be implemented by way of machine (e.g., computer processor) executable code stored on an electronic storage location of the computer system 301, such as, for example, on the memory 310 or electronic storage unit 315. The machine executable or machine readable code can be provided in the form of software. During use, the code can be executed by the processor 305. In some cases, the code can be retrieved from the storage unit 315 and stored on the memory 310 for ready access by the processor 305. In some situations, the electronic storage unit 315 can be precluded, and machine-executable instructions are stored on memory 310.

[0356] The code can be pre-compiled and configured for use with a machine having a processer adapted to execute the code, or can be compiled during runtime. The code can be supplied in a programming language that can be selected to enable the code to execute in a pre-compiled or as-compiled fashion.

[0357] Aspects of the systems and methods provided herein, such as the computer system 301, can be embodied in programming. Various aspects of the technology may be thought of as "products" or "articles of manufacture" typically in the form of machine (or processor) executable code and/or associated data that is carried on or embodied in a type of machine readable medium. Machine-executable code can be stored on an electronic storage unit, such as memory (e.g., read-only memory, random-access memory, flash memory) or a hard disk. "Storage" type media can include any or all of the tangible memory of the computers, processors or the like, or associated modules thereof, such as various semiconductor memories, tape drives, disk drives and the like, which may provide non-transitory storage at any time for the software programming. All or portions of the software may at times be communicated through the Internet or various other telecommunication networks. Such communications, for example, may enable loading of the software from one computer or processor into another, for example, from a management server or host computer into the computer platform of an application server. Thus, another type of media that may bear the software elements includes optical, electrical and electromagnetic waves, such as used across

physical interfaces between local devices, through wired and optical landline networks and over various air-links. The physical elements that carry such waves, such as wired or wireless links, optical links or the like, also may be considered as media bearing the software. As used herein, unless restricted to non-transitory, tangible "storage" media, terms such as computer or machine "readable medium" refer to any medium that participates in providing instructions to a processor for execution.

[0358] Hence, a machine readable medium, such as computer-executable code, may take many forms, including but not limited to, a tangible storage medium, a carrier wave medium or physical transmission medium. Non-volatile storage media include, for example, optical or magnetic disks, such as any of the storage devices in any computer(s) or the like, such as may be used to implement the databases, etc. shown in the drawings. Volatile storage media include dynamic memory, such as main memory of such a computer platform. Tangible transmission media include coaxial cables; copper wire and fiber optics, including the wires that comprise a bus within a computer system. Carrier-wave transmission media may take the form of electric or electromagnetic signals, or acoustic or light waves such as those generated during radio frequency (RF) and infrared (IR) data communications. Common forms of computer-readable media therefore include for example: a floppy disk, a flexible disk, hard disk, magnetic tape, any other magnetic medium, a CD-ROM, DVD or DVD-ROM, any other optical medium, punch cards paper tape, any other physical storage medium with patterns of holes, a RAM, a ROM, a PROM and EPROM, a FLASH-EPROM, any other memory chip or cartridge, a carrier wave transporting data or instructions, cables or links transporting such a carrier wave, or any other medium from which a computer may read programming code and/or data. Many of these forms of computer readable media may be involved in carrying one or more sequences of one or more instructions to a processor for execution.

[0359] The computer system 301 can include or be in communication with an electronic display 335 that comprises a user interface (UI) 340 for providing, for example, a report comprising the TNFSF15 profile of the subject or other relevant clinical information for purposes of informing a selection of a therapeutic agent (e.g., anti-TL1A antibody) to treat a disease or condition of the subject described herein. Examples of UI's include, without limitation, a graphical user interface (GUI) and web-based user interface.

[0360] Methods and systems of the present disclosure can be implemented by way of one or more algorithms. An algorithm can be implemented by way of software upon execution by the central processing unit 305. The algorithm can, for example, perform: (a) receiving

genotype data of a subject 401, (b) determining whether the genotypes are heterozygous or homozygous for at least three polymorphisms 402, (c) generating an outcome using predetermined parameters 403, and (d) displaying the outcome to a user (e.g., physician) on a user interface of an electronic device 404, as shown in **FIG. 4**. In some embodiments, the outcome is positive, negative or indeterminant. In some embodiments, the predetermined parameters are genotype combinations known to be predictive of a therapeutic response to a treatment, such as with an inhibitor of TL1A activity or expression.

Web application

[0361] In some embodiments, the computer system comprises software for 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®.

Mobile application

[0362] In some embodiments, the computer system comprises software for a mobile application. 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.

[0363] 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.

[0364] 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.

[0365] 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.

Standalone application

[0366] In some embodiments, the computer system comprises software 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 complied applications.

Web browser plug-in

[0367] In some embodiments, the computer system comprises software that comprises 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.

[0368] 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.

[0369] 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.

Software modules

[0370] 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.

Databases

[0371] 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.

Data transmission

[0372] The subject matter described herein, including methods for producing a TNFSF15 profile 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 genotype in a biological 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.

[0373] 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 (e.g., anti-TL1A therapy), or the like, in the same or different location or country.

Business Methods Utilizing a Computer

[0374] The methods described herein may utilize one or more computers. The computer may be used for managing customer and biological 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 user 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 (e.g., physician) 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.

[0375] The entity obtaining a report with the TNFSF15 profile may enter biological 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.

[0376] 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.

Systems Embodiments

[0377] Among the exemplary embodiments are:

1. A computer system for evaluating a 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 sample;
   c) an algorithm executed by said central computing environment, wherein the algorithm is configured to use the presence or absence of the genotype to classify said sample as at least one of (i) a disease or normal sample, and (ii) a response or a non-response to an anti-TL1A therapy; 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 at least one of an inflammatory, a fibrostenotic, and a fibrotic, disease or condition.
3. The computer system of embodiment 1 or embodiment 2, wherein the disease state is a TL1A mediated disease state selected from the group consisting of inflammatory bowel disease (IBD), Crohn's disease (CD), obstructive CD, ulcerative colitis (UC), intestinal fibrosis, intestinal fibrostenosis, rheumatoid arthritis, and primary sclerosing cholangitis.
4. The computer system of any previous embodiment, herein the sample comprises whole blood, plasma, serum, or tissue.
5. The computer system of any previous embodiment, wherein the genotype comprises at least one polymorphism selected from **Table 1** or **Table 4**, a polymorphism in linkage disequilibrium (LD) therewith, and any combination thereof.
6. The computer system of any previous embodiment, wherein the genotype comprises at least one polymorphism comprising a non-reference allele.
7. The computer system of any previous embodiment, wherein the genotype comprises at least two polymorphisms provided in **Table 1** or **Table 4**.

8. The computer system of any previous embodiment, wherein the genotype comprises at least three polymorphisms provided in **Table 1** or **Table 4**.
9. The computer system of any previous embodiment, wherein the genotype comprises at least four polymorphisms provided in **Table 1** or **Table 4**.
10. The computer system of any previous embodiment, wherein the genotype comprises at least five polymorphisms provided in **Table 1** or **Table 4**.
11. The computer system of any previous embodiment, wherein the genotype comprises at least six polymorphisms provided in **Table 1** or **Table 4**.
12. The computer system of any previous embodiment, wherein the genotype comprises at least seven polymorphisms provided in **Table 1** or **Table 4**.
13. The computer system of any previous embodiment, wherein the genotype comprises at least eight polymorphisms provided in **Table 1** or **Table 4**.
14. The computer system of any previous embodiment, further comprising the genotype is homozygous.
15. The computer system of embodiment 5-13, where LD is defined by an r^2 value of at least 0.80, 0.85, 0.90, 0.95, or 1.0.
16. The computer system of any previous embodiment, wherein the genotype is associated with a risk that a subject has, or will develop, the disease state 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}.
17. The computer system of any previous embodiment, wherein said output device provides a report summarizing said information on said classification.
18. The computer system of any previous embodiment, wherein said report comprises a recommendation for treatment of said disease state.
19. The computer system of embodiment 18, wherein the treatment comprises administration of an inhibitor of TL1A activity or expression.
20. The computer system of embodiment 19, wherein the inhibitor of TL1A activity or expression comprises an antibody or antigen-binding fragment, peptide, or small molecule.
21. 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.

22. Use of a composition comprising one or more binding agents for generating a report that classifies a sample from a subject as at least one of (i) a disease or non-disease state and (ii) a response or a non-response to an anti-TL1A therapy, wherein the one or more binding agents specifically bind to a risk allele provided in **Table 1** corresponding to a polymorphism provided in **Table 1**, their compliment, a polymorphism in linkage disequilibrium therewith, and any combination thereof.
23. The use of embodiment 22, wherein generating the report further comprises:
    a) providing the sample from the subject;
    b) assaying the sample from the subject for detecting the presence of a polymorphism provided in **Table 1**;
    c) generating the report based on the result of step (b); and
    d) determining whether said subject has or is likely to exhibit a positive therapeutic response to a treatment with an inhibitor of TL1A activity or expression based on the results of step (b).
24. The use of embodiment 22 or 23, wherein the disease state comprises at least one of an inflammatory, a fibrostenotic, and a fibrotic, disease or condition.
25. The use of embodiment 22-24, wherein the disease state is a TL1A-mediated disease state selected from the group consisting of inflammatory bowel disease (IBD), Crohn's disease (CD), obstructive CD, ulcerative colitis (UC), intestinal fibrosis, intestinal fibrostenosis, scleroderma, pulmonary fibrosis (e.g., idiopathic pulmonary fibrosis) and primary sclerosing cholangitis.
26. The use of any of embodiments 22-25, wherein the sample comprises whole blood, plasma, serum, or tissue.
27. The use of embodiment 23, wherein assaying the sample from the subject for detecting the presence of the risk allele corresponding to the polymorphism provided in **Table 1** of step (b) comprises:
    a) contacting the sample with the one or more binding agents that specifically bind to at least 10 contiguous nucleobases that includes the risk allele provided in any one of SEQ ID NOS: 2001-2041, or 2057-2059; and
    b) determining whether the sample specifically binds to said one or more binding agents, wherein binding of the sample to the one or more binding agents indicates the presence of the polymorphism in the subject.

28. The use of embodiment 23, wherein assaying the sample from the subject for detecting the presence of the risk allele corresponding to the polymorphism provided in **Table 1** of step (b) comprises sequencing of the sample.
29. The use of embodiment 23, wherein assaying the sample from the subject for detecting the presence of the one or more polymorphisms of step (b) comprises quantifying the amount of DNA comprising the risk allele.
30. The use of embodiment 29, wherein the quantifying comprises PCR.
31. The use of embodiment 30, wherein the PCR comprises real-time PCR.
32. The use of embodiment 29, wherein the quantifying comprises hybridization.
33. A composition comprising one or more binding agents that specifically bind to a risk allele corresponding to a polymorphism provided in **Table 1**, wherein the one or more binding agents are selected to classify a sample as at least one of (i) a disease or non-disease or a disease state and (ii) a response or a non-response to an anti-TL1A therapy.
34. The composition of embodiment 33, wherein the one or more binding agents comprise oligonucleotides.
35. The composition of embodiment 34, wherein the oligonucleotides comprise RNA or DNA.
36. The composition of embodiment 34, wherein the one or more binding agents comprise aptamers, antibodies, peptide nucleic acids, or pyranosyl RNA.
37. A kit for detecting at least one of an inflammatory, a fibrostenotic, and a fibrotic, disease or condition in a subject, the kit comprising:
    a) at least one binding agent that specifically binds to at least 10 contiguous nucleic acid molecules provided in any one of SEQ ID NOS: 2001-2041, or 2057-2059 including a corresponding risk allele provided in **Table 1**, or their complement, wherein the at least one binding agent is selected to detect at least one of (i) a disease or non-disease state and (ii) a response or a non-response to an anti-TL1A therapy; and
    b) reagents for detecting binding of said at least one binding agent to a DNA sample from a subject.
38. The kit of embodiment 37, wherein the at least one binding agent comprises at least one oligonucleotide.
39. The kit of embodiment 37, wherein the at least one binding agent comprises at least one aptamer, antibody, peptide nucleic acid, or pyranosyl RNA.

40. The kit of embodiment 37-39, wherein the at least one binding agent is labelled with a detectable label.
41. The kit of embodiment 37-40, wherein the at least one binding agent is immobilized to a surface.
42. A system for generating a report that classifies a sample a disease or non-disease of a disease state, comprising:
    a) a computer system that:
        i. generates a molecular profile of a DNA sample based upon the presence of at least one polymorphism, or their complement; and
        ii. generates a report that classifies the sample based on said molecular profile; and
    b) a computer screen that displays said report.
43. The system of embodiment 42, wherein the presence of the at least one polymorphism is based on the result of an assay of said DNA sample, which result is entered into a database.
44. The system of embodiment 42-43, further comprising an input for said result.
45. The system of claim 42-44, wherein the at least one polymorphism is selected from **Table 1**.
46. The system of claim 42-45, wherein the at least one polymorphism comprises a non-reference allele.
47. The system of claim 46, wherein the at least one polymorphism is two polymorphisms.
48. The system of claim 46, wherein the at least one polymorphism is three polymorphisms.
49. Use of a composition comprising an inhibitor of TL1A for treating a subject, provided the subject is a carrier of a genotype comprising a polymorphism provided in **Table 1** or **Table 4**.
50. The use of embodiment 49, wherein the inhibitor of TL1A activity or expression is an anti-TL1A antibody.
51. The use of embodiment 50, wherein the anti-TL1A antibody is selected from **Table 20.**
52. The use of embodiment 50, wherein the anti-TL1A antibody comprises an amino acid sequence provided in **Tables 16-17**.
53. The use of embodiment 50, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody selected from **Table 20**.

54. The use of embodiment 50, wherein the anti-TL1A antibody binds to the same region of human TL1A as a reference antibody, the reference antibody comprising an amino acid sequence provided in **Tables 16-17**.
55. The use of embodiments 50-55, wherein the anti-TL1A antibody is a neutralizing TL1A antibody.
56. The use of embodiments 50-55, wherein the anti-TL1A antibody is an antagonist of TL1A.
57. The use of embodiments 49-56, wherein the genotype comprises at least two polymorphisms provided in **Table 1** or **Table 4**.
58. The use of embodiments 49-56, wherein the genotype comprises at least three polymorphisms provided in **Table 1** or **Table 4**.
59. The use of embodiments 49-56, wherein the genotype comprises at least four polymorphisms provided in **Table 1** or **Table 4**.
60. The use of embodiments 49-56, wherein the genotype comprises at least five polymorphisms provided in **Table 1** or **Table 4**.
61. The use of embodiments 49-56, wherein the genotype comprises at least six polymorphisms provided in **Table 1** or **Table 4**.
62. The use of embodiments 49-56, wherein the genotype comprises at least seven polymorphisms provided in **Table 1** or **Table 4**.
63. The use of embodiments 49-56, wherein the genotype comprises at least eight polymorphisms provided in **Table 1** or **Table 4**.
64. The method of use of embodiments 49-63, wherein the genotype comprises at least one polymorphism comprising a non-reference allele.
65. The computer system of embodiments 1-21, wherein said algorithm is configured to classify said sample as a positive therapeutic response to the anti-TL1A therapy with a positive predictive value of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.
66. The computer system of embodiments 1-21, wherein said algorithm is configured to classify said sample as a positive therapeutic response to the anti-TL1A therapy with a specificity of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.
67. The use of embodiments 22-32, wherein the report classifies the sample as a positive therapeutic response to the anti-TL1A therapy with a positive predictive value of at least

or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.

68. The use of embodiments 22-32, wherein the report classifies the sample as a positive therapeutic response to the anti-TL1A therapy with a specificity of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.
69. The system of embodiments 72-78, wherein the report that classifies the sample based on said molecular profile as positive for a therapeutic response to a treatment with an anti-TL1A therapy with a positive predictive value of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.
70. The system of embodiments 72-78, wherein the report that classifies the sample based on said molecular profile as positive for a therapeutic response to a treatment with an anti-TL1A therapy with a specificity of at least or about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94% 95%, 96%, 97%, 98%, 99%, or 100%.

Definitions

[0378] Unless defined otherwise, all terms of art, notations and other technical and scientific terms or terminology used herein are intended to have the same meaning as is commonly understood by one of ordinary skill in the art to which the claimed subject matter pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art.

[0379] Throughout this application, various embodiments may be presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the disclosure. Accordingly, the description of a range should be considered to have specifically disclosed all the possible subranges as well as individual numerical values within that range. For example, description of a range such as from 1 to 6 should be considered to have specifically disclosed subranges such as from 1 to 3, from 1 to 4, from 1 to 5, from 2 to 4, from 2 to 6, from 3 to 6 etc., as well as individual numbers within that range, for example, 1, 2, 3, 4, 5, and 6. This applies regardless of the breadth of the range.

[0380] As used in the specification and claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a sample" includes a plurality of samples, including mixtures thereof.

[0381] The terms "determining," "measuring," "evaluating," "assessing," "assaying," and "analyzing" are often used interchangeably herein to refer to forms of measurement. The terms include determining if an element is present or not (for example, detection). These terms can include quantitative, qualitative or quantitative and qualitative determinations. Assessing can be relative or absolute. "Detecting the presence of" can include determining the amount of something present in addition to determining whether it is present or absent depending on the context.

[0382] The term "*in vivo*" is used to describe an event that takes place in a subject's body.

[0383] The term "*ex vivo*" is used to describe an event that takes place outside of a subject's body. An *ex vivo* assay is not performed on a subject. Rather, it is performed upon a sample separate from a subject. An example of an *ex vivo* assay performed on a sample is an "*in vitro*" assay.

[0384] The term "*in vitro*" is used to describe an event that takes places contained in a container for holding laboratory reagent such that it is separated from the biological source from which the material is obtained. *In vitro* assays can encompass cell-based assays in which living or dead cells are employed. *In vitro* assays can also encompass a cell-free assay in which no intact cells are employed.

[0385] As used herein, the term "about" a number refers to that number plus or minus 10% of that number. The term "about" a range refers to that range minus 10% of its lowest value and plus 10% of its greatest value. For instance, an antibody variable region comprising about 80% identity to a reference variable region may comprise 72% to 88% identity to the reference variable region.

[0386] The terms "complementarity determining region," and "CDR," which are synonymous with "hypervariable region" or "HVR," are known in the art to refer to non-contiguous sequences of amino acids within antibody variable regions, which confer antigen specificity and/or binding affinity. In general, there are three CDRs in each heavy chain variable region (CDR-H1, CDR-H2, CDR-H3) and three CDRs in each light chain variable region (CDR-L1, CDR-L2, CDR-L3). "Framework regions" and "FR" are known in the art to refer to the non-CDR portions of the variable regions of the heavy and light chains. In general, there are four FRs in each full-length heavy chain variable region (FR-H1, FR-H2,

FR-H3, and FR-H4), and four FRs in each full-length light chain variable region (FR-L1, FR-L2, FR-L3, and FR-L4). The precise amino acid sequence boundaries of a given CDR or FR can be readily determined using any of a number of well-known schemes, including those described by Kabat et al. (1991), "Sequences of Proteins of Immunological Interest," 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD ("Kabat" numbering scheme), Al-Lazikani et al., (1997) *JMB* 273,927-948 ("Chothia" numbering scheme); MacCallum et al., J. *Mol. Biol.* 262:732-745 (1996), "Antibody-antigen interactions: Contact analysis and binding site topography," *J. Mol. Biol.* 262, 732-745." ("Contact" numbering scheme); Lefranc MP et al.,"IMGT unique numbering for immunoglobulin and T cell receptor variable domains and Ig superfamily V-like domains," Dev Comp *Immunol*, 2003 Jan;27(1):55-77 ("IMGT" numbering scheme); Honegger A and Plückthun A, "Yet another numbering scheme for immunoglobulin variable domains: an automatic modeling and analysis tool," *J Mol Biol*, 2001 Jun 8;309(3):657-70, ("Aho" numbering scheme); and Whitelegg NR and Rees AR, "WAM: an improved algorithm for modelling antibodies on the WEB," *Protein Eng.* 2000 Dec;13(12):819-24 ("AbM" numbering scheme. In certain embodiments, the CDRs of the antibodies described herein can be defined by a method selected from Kabat, Chothia, IMGT, Aho, AbM, or combinations thereof.

[0387] In some embodiments, an antibody that specifically binds to a protein indicates that the antibody reacts or associates more frequently, more rapidly, with greater duration, with greater affinity, or with some combination of the above to the protein than with alternative substances, including unrelated proteins.

[0388] In some embodiments, the terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The polymer may be linear or branched, it may comprise modified amino acids, and it may be interrupted by non-amino acids. The terms also encompass an amino acid polymer that has been modified naturally or by intervention; for example, disulfide bond formation, glycosylation, lipidation, acetylation, phosphorylation, or any other manipulation or modification, such as fusion with another polypeptide and/or conjugation, e.g., with a labeling component. Also included within the definition are, for example, polypeptides containing one or more analogs of an amino acid (for example, unnatural amino acids, etc.), as well as other modifications known in the art.

[0389] In some embodiments, a protein such as an antibody described herein comprises a hydrophobic amino acid. Non-limiting exemplary hydrophobic amino acids include glycine (Gly), proline (Pro), phenylalanine (Phe), alanine (Ala), isoleucine (Ile), leucine (Leu), and

valine (Val). In some embodiments, a protein such as an antibody described herein comprises a hydrophilic amino acid. Non-limiting exemplary hydrophilic amino acids include serine (Ser), threonine (Thr), aspartic acid (Asp), glutamic acid (Glu), cysteine (Cys), asparagine (Asn), glutamine (Gln), arginine (Arg), and histidine (His). In some embodiments, a protein such as an antibody described herein comprises an amphipathic amino acid. Non-limiting exemplary amphipathic amino acids include lysine (Lys), tryptophan (Trp), tyrosine (Tyr), and methionine (Met). In some embodiments, a protein such as an antibody described herein comprises an aliphatic amino acid. Non-limiting exemplary aliphatic amino acids include alanine (Ala), isoleucine (Ile), leucine (Leu) and valine (Val). In some embodiments, a protein such as an antibody described herein comprises an aromatic amino acid. Non-limiting exemplary aromatic amino acids include phenylalanine (Phe), tryptophan (Trp), and tyrosine (Tyr). In some embodiments, a protein such as an antibody described herein comprises an acidic amino acid. Non-limiting exemplary acidic amino acids include aspartic acid (Asp) and glutamic acid (Glu). In some embodiments, a protein such as an antibody described herein comprises a basic amino acid. Non-limiting exemplary basic amino acids include arginine (Arg), histidine (His), and lysine (Lys). In some embodiments, a protein such as an antibody described herein comprises a hydroxylic amino acid. Non-limiting exemplary hydroxylic amino acids include serine (Ser) and threonine (Thr). In some embodiments, a protein such as an antibody described herein comprises a sulfur-containing amino acid. Non-limiting exemplary sulfur-containing amino acids include cysteine (Cys) and methionine (Met). In some embodiments, a protein such as an antibody described herein comprises an amidic amino acid. Non-limiting exemplary amidic amino acids include asparagine (Asn) and glutamine (Gln).

[0390] As used herein, the terms “homologous,” “homology,” or “percent homology” when used herein to describe to an amino acid sequence or a nucleic acid sequence, relative to a reference sequence, can be determined using the formula described by Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87: 2264-2268, 1990, modified as in Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such a formula is incorporated into the basic local alignment search tool (BLAST) programs of Altschul et al. (J Mol Biol. 1990 Oct 5;215(3):403-10; Nucleic Acids Res. 1997 Sep 1;25(17):3389-402). Percent homology of sequences can be determined using the most recent version of BLAST, as of the filing date of this application. Percent identity of sequences can be determined using the most recent version of BLAST, as of the filing date of this application.

[0391] As used herein, the term "percent (%) identity", or "percent sequence identity," with respect to a reference polypeptide sequence is the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. As used herein, the term "percent (%) identity", or "percent sequence identity," with respect to a reference nucleic acid sequence is the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the reference nucleic acid sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent sequence identity can be achieved in various ways that are known for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Appropriate parameters for aligning sequences are able to be determined, including algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc., and the source code has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available from Genentech, Inc., South San Francisco, Calif., or may be compiled from the source code. The ALIGN-2 program should be compiled for use on a UNIX operating system, including digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0392] In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows: 100 times the fraction X/Y, where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program.

[0393] 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. An increase can be an absolute amount (*e.g.*, level of protein expression), or a rate of production (*e.g.*, rate of protein expression between two points in time).

[0394] 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.

[0395] In some embodiments, the terms "individual" or "subject" are used interchangeably and refer to any animal, including, but not limited to, humans, non-human primates, rodents, and domestic and game animals, which is to be the recipient of a particular treatment. Primates include chimpanzees, cynomolgus monkeys, spider monkeys, and macaques, e.g., Rhesus. Rodents include mice, rats, woodchucks, ferrets, rabbits and hamsters. Domestic and game animals include cows, horses, pigs, deer, bison, buffalo, feline species, e.g., domestic cat, canine species, e.g., dog, fox, wolf, avian species, e.g., chicken, emu, ostrich, and fish, e.g., trout, catfish and salmon. In various embodiments, a subject can

be one who has been previously diagnosed with or identified as suffering from or having a condition in need of treatment. In certain embodiments, the subject is a human. In various other embodiments, the subject previously diagnosed with or identified as suffering from or having a condition may or may not have undergone treatment for a condition. In yet other embodiments, a subject can also be one who has not been previously diagnosed as having a condition (i.e., a subject who exhibits one or more risk factors for a condition). A "subject in need" of treatment for a particular condition can be a subject having that condition, diagnosed as having that condition, or at risk of developing that condition. In some embodiments, the subject is a "patient," that has been diagnosed with a disease or condition described herein.

[0396] 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. A "genetic locus" referred to herein, is a particular location within a gene.

[0397] 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.

[0398] A "polymorphism" as used herein refers to an aberration in (*e.g.*, a mutation), or of (e.g., insertion/deletion), a nucleic acid sequence, as compared to the nucleic acid sequence in a reference population. In some embodiments, the polymorphism is common in the reference population. In some embodiments, the polymorphism is rare in the reference population. In some embodiments, the polymorphism is a single nucleotide polymorphism.

[0399] The term, "single nucleotide polymorphism" or SNP as disclosed herein, refers to a variation in a single nucleotide within a polynucleotide sequence. The term should not be interpreted as placing a restriction on a frequency of the SNP in a given population. The variation of an SNP may have multiple different forms. A single form of an SNP is referred to as an "allele." An SNP can be mono-, bi-, tri, or tetra-allelic. A 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. The SNP may be observed in at least 1% of a given population. 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 SNV is defined as the genomic position identified with [brackets] or an "N" in a sequence disclosed herein.

[0400] 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.

[0401] "Haplotype" as used herein, encompasses a group of one or more genotypes, which tend to be inherited together in a reference population. In some embodiments, a haplotype comprises particular polymorphism or another polymorphism in linkage disequilibrium (LD) therewith.

[0402] "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=Pab-PaPb), 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=Pab-PaPb), 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.

[0403] In some embodiments, "polynucleotide," or "nucleic acid," as used interchangeably herein, refer to polymers of nucleotides of any length, and include DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a polymer by DNA or RNA polymerase. A polynucleotide may comprise modified nucleotides, such as, but not limited to methylated nucleotides and their analogs or non-nucleotide components. Modifications to the nucleotide structure may be imparted before or after assembly of the polymer. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

[0404] 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 glucocorticosteriods, anti-TNF therapy, anti-a4-b7 therapy (vedolizumab), anti-IL12p40 therapy (ustekinumab), Thalidomide, and Cytoxin.

[0405] 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.

[0406] 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. In some cases, therapeutically effective amount of the drug

reduces the severity of symptoms of the disease or disorder. In some instances, the disease or disorder comprises inflammatory bowel disease (IBD), Crohn's disease (CD), or ulcerative colitis (UC). In some instances, the IBD, CD, and/or UC are severe or medically refractory forms of the IBD, CD, and/or UC. Non-limiting examples of symptoms of IBD, CD, and/or UC include, but are not limited to, diarrhea, fever, fatigue, abdominal pain, abdominal cramping, inflammation, ulceration, nausea, vomiting, bleeding, blood in stool, reduced appetite, and weight loss.

[0407] 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).

[0408] 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.

[0409] 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.

[0410] 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.

[0411] 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, gene expression product (*e.g.,* RNA or protein), or a cell-type (*e.g.,*immune cell).

[0412] 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 globasa 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.

[0413] 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.

[0414] The terms "non-response," or "loss-of-response," as used herein, refer to phenomena in which a subject or a patient does not respond to the induction of a standard treatment (*e.g.,* anti-TNF therapy), or experiences a loss of response to the standard treatment after a successful induction of the therapy. The induction of the standard treatment may

include 1, 2, 3, 4, or 5, doses of the therapy. A "successful induction" of the therapy may be an initial therapeutic response or benefit provided by the therapy. The loss of response may be characterized by a reappearance of symptoms consistent with a flare after a successful induction of the therapy.

[0415] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

EXAMPLES

[0416] The following examples are included for illustrative purposes only and are not intended to limit the scope of the invention.

Example 1: Overview of The Identification of Genotypes

[0417] Tumor Necrosis Factor (Ligand) Superfamily, Member 15 (*TNFSF15*) has been determined to be significantly associated with inflammatory bowel disease (IBD), including Crohn's disease (CD),by Genome Wide Association Studies (GWAS) (*e.g.*, cases versus controls).In addition, increased levels of TL1A (*e.g.,* RNA and protein) are associated with IBD, including CD. Therefore, therapeutic strategies targeting TNFSF15 (TL1A) expression or activity offer a promising approach for the treatment of IBD. Disclosed herein is the identification of polymorphisms that are associated with, and therefore predictive of, an increase in TNFSF15 (TL1A) expression in patients with IBD, including CD, using a machine learning approach.

[0418] A polygenic risk score (PRS) adapted to identify individuals at risk for having increased TNFSF15 (TL1A) was applied to a cohort of CD patients recruited at the Cedars-Sinai Medical Center. A machine learning algorithm (e.g., XGBoost) was used to identify combinations of polymorphisms associated with increased TNFSF15 (TL1A) expression or activity. The resulting 41 polymorphisms, and a possible combinations of polymorphisms, have optimal prediction precision across multiple iterations of training the machine learning algorithm, which was able to analyze large combinations of polymorphism interactions (*e.g.,* including non-linear interactions) in an efficient manner, which traditional GWAS methodologies cannot achieve. The resulting polymorphisms are useful for selecting a subject, who may or may not be diagnosed with IBD, who may exhibit a therapeutic response to an TNFSF15 (TL1A)-targeting therapeutic agent (*e.g.,* neutralizing anti-TL1A antibody).

Example 2: Calculation of TNFSF15 PRS

[0419] A polygenic risk score (PRS) based on polymorphisms within multiple genes of interest (*e.g.,* involved in the TL1A-mediated inflammatory pathways) and their associated

weights in each respective reference population was calculated. The PRS is referred to herein as the "TNFSF15 PRS." The polymorphisms were selected from multiple GWAS based on a defined distances from the transcription start and stop sites for the gene(s) of interest (*e.g.*, 250 kilobases upstream and downstream). Each GWAS was to define the individual weights for contribution of a polymorphism to the total score. The GWAS used include, but are not limited to, Jostins et *al.*, 2012. Nature. 491:119-124, Liu et *al.*, 2015. Nat Genet. 47:979-986, Ellinghaus et *al.*, 2016. Nat Genet. 48:510-518, Huang et *al.*, 2017. Nat Genet. 49:256-261, and de Lange et *al.*, 2017. Nat Genet. 48:256-261.

[0420] To confirm the relevance of inclusion of a polymorphism within the TNFSF15 PRS, the polymorphisms were cross-checked by (i) evidence of cis-QTL, where the SNP is directly associated with target gene expression in tissues and (ii) sensitivity analysis, where selected polymorphisms are removed from the TNFSF15 PRS and a regression analysis is run against disease susceptibility and subclinical phenotypes, thus highlighting relevant polymorphisms to disease risk. In some cases, the polymorphisms were subjected to sensitivity analysis, and in other cases, they were not. For example, in some cases, only those polymorphisms with questionable association to the pathway TNFSF15 PRS (*e.g.*, no eQTL or multiple genes within the loci) are subjected to sensitivity analysis.

[0421] Patients with Crohn's disease (CD) were recruited. The diagnosis of each patient was based on standard endoscopic, histologic, and radiographic features. Blood samples were collected from patients at the time of enrollment. Genotyping was performed using Immunochip (ICHIP) per manufacturer's protocol on all samples collected.

[0422] A TNFSF15 PRS was calculated for Caucasian patients within a Cedars-Sinai CD cohort from Example 1, based on the defined set of polymorphisms selected in this **Example 2**, which are provided in **Table 4**. An exemplary calculation of TNFSF15 PRS is outlined in Li et *al.*, 2018. Inflamm Bowel Dis. 12;24(11):2413-2422. The TNFSF15 PRS is calculated as the weighted sum of the number of risk alleles carried by each patient (in the Cedars-Sinai CD cohort) (0, 1, or 2) at each loci for the genes described in this **Example 2**, divided by a total number of genetic variants used in the model. The same calculations were performed for each individual belonging to a reference group, thereby generating a range of raw scores (observed range). The resulting TNFSF15 PRS is generated by comparing the score of each patient with the observed range observed in the reference group.

Table 4. *TNFSF15* Polygenic Risk Score (PRS) Polymorphisms							
rsID	**Illumina_id**	**Minor Allele**	**Minor Allele Frequency**	**Major Allele**	**Chromosome**	**Gene**	**Seq ID No.**
rs11221332	imm_11_127886184	A	0.232475	G	chr11	ETS1	20041
rs7134599	imm_12_66786342	A	0.381954	G	chr12	IFNG	20042
rs6062496	imm_20_61799543	G	0.406514	A	chr20	TNFRSF6B	20043
rs4246905	imm_9_116593070	A	0.270925	G	chr9	TNFSF15	2008
rs7468800	imm_9_116631826	A	0.124622	C	chr9	TNFSF15;TNFSF8	20044
rs1569328	rs1569328	A	0.14869	G	chr14	U2;FOS	20045
rs2284553	rs2284553	A	0.386244	G	chr21	IFNGR2	20046
rs6062504	rs6062504	A	0.27128	G	chr20	ZGPAT	20047
rs7556897	rs7556897	G	0.334936	A	chr2	SLC19A3;CCL20	20048

Example 3: XGBoost Machine Learning Algorithm Trained on Binary Classifiers based on TNFSF15 Polygenic Risk Score

[0423] A binary classifier to be used in the XGBoost machine learning platform for CD samples was created based on the distribution of the TNFSF15 PRS scores (calculated in **Example 2**) across the CD cohort. In this example, patient samples from the CD cohort were classified as 0 if their TNFSF15 PRS was ≤ 25th percentile of the TNFSF15 PRS CD distribution. Patient samples were classified as 1 if their TNFSF15 PRS was ≥ 75th percentile of the TNFSF15 PRS CD distribution.

[0424] Once the initial classifier of TNFSF15 SNPs was established, the XGBoost algorithm was optimized for the polymorphisms and implemented to generate an initial list of candidate polymorphisms. XGBoost is rooted in the gradient boosted decision trees, which in contrast to lasso and ridge regression methods, incorporates complex non-linear feature interactions into prediction models in a non-additive form. Exemplary optimization and implementation procedures are provided in Behravan et *al.* Sci Rep. 2018;8:13149. A total of ten iterations of 5-fold cross validation were used to obtain an initial list of candidate polymorphisms. These polymorphisms were further filtered/optimized using an adaptive iterative search procedure as outlined in Behravan *et al.* as well as support vector machines

(SVM) resulting in a final list of SNPs, which had high prediction precision (> 90%) for the TNFSF15 PRS binary classifier.

Example 4: XGBoost Machine Learning Algorithm Trained on Binary Classifiers based on TNFSF15 Protein Expression

[0425] Patients with Crohn's disease (CD) were recruited. The diagnosis of each patient was based on standard endoscopic, histologic, and radiographic features. Blood samples were collected from the patients . All patients were genotyped either by Illumina ImmunoArray or polymerase chain reaction (PCR) under standard hybridization conditions. Peripheral blood mononuclear cells (PBMCs) were isolated from the blood samples. The PMBCs were stimulated *in vitro* with immune complex. Supernatants were collected from unstimulated samples and from stimulated samples at 6, 18, 24, and 72 hours. Soluble TL1A protein in the supernatants was quantified using a plate-based ELISA using and monoclonal antibodies at all time points.

[0426] Binary classifiers to be used in the XGBoost machine learning platform for the samples were derived using TL1A protein expression levels at 6 hours. The classifier at 6 hours reflects absolute levels of TL1A protein expression at that time point. Additional binary classifiers were derived using the results of clustering of samples (k=2 and k=3 groups) based on TNFSF15 protein expression across 6, 18, 24, and 72-hour time points. The classifiers at the combination of time points (*e.g.*, 6, 18, 24, and 72) reflect a rate of production of TL1A between time points. The clustering was performed using the TMixClust Bioconductor package as described in Golumbeanu *et al.* ("Clustering time series gene expression data with TMixClust 2018). A set of predictive SNPs was obtained from each of the three XGBoost analyses of the three classifiers. The polymorphisms identified here were compared to the list of polymorphisms generated in **Example 3** to identify only those polymorphisms that overlap between the two analyses.

[0427] Determination of overlaps of SNPs was performed on the gene annotation (refGene annotation) of the generated SNPs and not on the actual ICHIP or dbSNP reference sequence identification numbers. Only polymorphisms with minor allele frequencies (MAF) ≥ 0.1 and the beta coefficients (from support vector machine (SVM) runs) with absolute values ≥ 0.1 were kept. This resulted in 129 polymorphisms remaining for further analysis. The 9 polymorphisms used in the TNFF15 PRS (**Table 4**) were also added to this list of SNPs, resulting in a total of 138 SNPs.

Example 5: Implementation of Market Basket Analysis to Determine Non-Linear Polymorphism Combination Rules Associated with CD

[0428] In order to further filter out SNPs not strongly associated with clinical phenotypes, a market basket analysis approach was used to determine combination rules for the polymorphisms associated with Crohn's Disease (CD) clinical phenotypes. An exemplary market basket analysis is described in Breuer et *al.* Int J Bipolar Disord. 2018; 6:24). The initial dataset on CD localization and CD characterization was obtained from 1,803 CD cohorts from Cedars-Sinai Medical Center. The RUDI (Rule Discoverer) program (dominant minor model), also described in Breuer *et al.*, was run on the 1,803 CD cohorts using the genotypes of the previously generated 138 SNPs (**Example 4**). The analysis resulted in 57 rules with significant associations with clinical phenotypes for Crohn's Disease. The clinical phenotypes used in the analysis were CD location (ileum, colon, and ilealcolon), CD characterization (non-stricturing/non-penetrating, stricturing, stricturing and internal penetrating, and isolated internal penetrating), and presence of perianal disease. The 57 association rules consisted of only 89 out of the 138 input polymorphisms from **Example 4**. Therefore, only these 89 polymorphisms were considered for further evaluation.

[0429] Finally, support vector machines (SVM) analysis based on the 3 binary classifiers described in **Example 3** and **Example 4** were re-applied to this list of 89 polymorphisms. Only XGBoost models (and their corresponding polymorphisms) with a prediction precision ≥ 0.70 were maintained. And further, only the polymorphisms from these models with an SVM coefficient ≥ 0.25 or an SVM coefficient ≤ -0.25 were kept. Applying these filters, a total of 41 polymorphisms were generated when analyzing all 3 classifiers. These polymorphisms and reference alleles are provided in **Table 1**. The nucleic acid sequences comprising the polymorphisms are provided in SEQ ID NOS: 1-41, or 57-59, and the position of the polymorphism within the nucleic acid sequence is indicated with a non-nucleobase letter (*e.g.*, V, R, S, and the like). The sequences provided are from build 151.

[0430] The polymorphisms identified in the analysis provided in the Examples above may be used to predict a positive therapeutic response in a subject or a patient to an inhibitor of TL1A activity or expression (*e.g.,* anti-TL1A antibody), either alone, or in combinations (*e.g.*, 2, 3, 4, 5, 6, 7, and so forth). The polymorphisms described herein may be used in a diagnostic or prognostic test to identify a subject suitable for treatment with an inhibitor of TL1A activity or expression to treat a disease or condition described herein in the subject. In some cases, the diagnostic is a companion diagnostic test, such as for example, a TL1A companion diagnostic test ("TL1A CDx").

[0431] In a non-limiting example, any combination of three polymorphisms, each selected from **Table 1**, may be used to predict a positive therapeutic response to an inhibitor of TL1A activity or expression. Exemplary three-polymorphism combinations include: imm_9_116608587, imm_11_127948309, and rs1892231; imm_9_116608587, imm_11_127948309, and rs9806914; imm_9_116608587, imm_11_127948309, and imm_21_44478192; imm_9_116608587, imm_11_127948309, and imm_21_44479552 imm_9_116608587, rs1892231, and rs9806914; imm_9_116608587, rs1892231, and imm_21_44478192; imm_9_116608587, rs1892231, and imm_21_44479552; imm_9_116608587, rs9806914, and imm_21_44478192; imm_9_116608587, rs9806914, and imm_21_44479552; imm_9_116608587, imm_21_44478192, and imm_21_44479552; imm_11_127948309, rs1892231, and rs9806914; imm_11_127948309, rs1892231, and imm_21_44478192; imm_11_127948309, rs1892231, and imm_21_44479552; imm_11_127948309, rs9806914, and imm_21_44478192; imm_11_127948309, rs9806914, and imm_21_44479552; imm_11_127948309, imm_21_44478192, and imm_21_44479552; rs1892231, rs9806914, and imm_21_44478192; rs1892231, rs9806914, and imm_21_44479552; rs1892231, imm_21_44478192, and imm_21_44479552; and rs9806914, imm_21_44478192, and imm_21_44479552.

[0432] **Table 5** provides a table with the position of each polymorphism provided in Table 1 within the human genome according to GRCh38.p13 Primary Assembly. The nucleic acid sequence flanking each polymorphism is identified with the relevant SEQ ID NO.

Table 5. GRCh38.p13 Primary Assembly Positions of Polymorphisms

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs11897732	2060	>NC_000002.12:43313747-43314246 Homo sapiens chromosome 2 SEQ=[G/A] >NC_000002.12:43314248-43314747 Homo sapiens chromosome 2
rs6740739	2061	>NC_000002.12:43628004-43628503 Homo sapiens chromosome 2 SEQ=[G/A] >NC_000002.12:43628505-43629004 Homo sapiens chromosome 2

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs17796285	2062	>NC_000008.11:11266446-11266945 Homo sapiens chromosome 8 SEQ=[G/A/C/T] >NC_000008.11:11266947-11267446 Homo sapiens chromosome 8
rs7935393	2063	>NC_000011.10:128572704-128573203 Homo sapiens chromosome 11 SEQ=[A/C] >NC_000011.10:128573205-128573704 Homo sapiens chromosome 11
rs12934476	2064	>NC_000016.10:11237152-11237651 Homo sapiens chromosome 16 SEQ=[A/G] >NC_000016.10:11237653-11238152 Homo sapiens chromosome 16
rs12457255	2065	>NC_000018.10:12759477-12759976 Homo sapiens chromosome 18 SEQ=[C/A] >NC_000018.10:12759978-12760477 Homo sapiens chromosome 18
rs2070557	2066	>NC_000021.9:44234741-44235240 Homo sapiens chromosome 21 SEQ=[A/T] >NC_000021.9:44235242-44235741 Homo sapiens chromosome 21
rs4246905	2067	>NC_000009.12:114790469-114790968 Homo sapiens chromosome 9 SEQ=[T/A/C] >NC_000009.12:114790970-114791469 Homo sapiens chromosome 9

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs10974900	2068	>NC_000009.12:4987458-4987957 Homo sapiens chromosome 9 SEQ=[C/T] >NC_000009.12:4987959-4988458 Homo sapiens chromosome 9
rs12434976	2069	>NC_000014.9:98185370-98185869 Homo sapiens chromosome 14 SEQ=[A/C] >NC_000014.9:98185871-98186370 Homo sapiens chromosome 14
rs16901748	2070	>NC_000005.10:11561609-11562108 Homo sapiens chromosome 5 SEQ=[G/T] >NC_000005.10:11562110-11562609 Homo sapiens chromosome 5
rs2815844	2071	>NC_000001.11:241083704-241084203 Homo sapiens chromosome 1 SEQ=[C/T] >NC_000001.11:241084205-241084704 Homo sapiens chromosome 1
rs889702	2072	>NC_000016.10:6088639-6089138 Homo sapiens chromosome 16 SEQ=[G/A] >NC_000016.10:6089140-6089639 Homo sapiens chromosome 16
rs2409750	2073	>NC_000008.11:11229685-11230184 Homo sapiens chromosome 8 SEQ=[A/C] >NC_000008.11:11230186-11230685 Homo sapiens chromosome 8

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs1541020	2074	>NC_000010.11:6122567-6123066 Homo sapiens chromosome 10 SEQ=[C/T] >NC_000010.11:6123068-6123567 Homo sapiens chromosome 10
rs4942248	2075	>NC_000013.11:43832169-43832668 Homo sapiens chromosome 13 SEQ=[T/A] >NC_000013.11:43832670-43833169 Homo sapiens chromosome 13
rs12934476	2076	>NC_000016.10:11237152-11237651 Homo sapiens chromosome 16 SEQ=[A/G] >NC_000016.10:11237653-11238152 Homo sapiens chromosome 16
rs12457255	2077	>NC_000018.10:12759477-12759976 Homo sapiens chromosome 18 SEQ=[C/A] >NC_000018.10:12759978-12760477 Homo sapiens chromosome 18
rs2297437	2078	>NC_000020.11:63673421-63673920 Homo sapiens chromosome 20 SEQ=[G/A] >NC_000020.11:63673922-63674421 Homo sapiens chromosome 20
rs41309367	2079	>NC_000020.11:63677701-63678200 Homo sapiens chromosome 20 SEQ=[C/T] >NC_000020.11:63678202-63678701 Homo sapiens chromosome 20

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs10733509	2080	>NC_000009.12:4307550-4308049 Homo sapiens chromosome 9 SEQ=[A/G] >NC_000009.12:4308051-4308550 Homo sapiens chromosome 9
rs10750376	2081	>NC_000011.10:127867534-127868033 Homo sapiens chromosome 11 SEQ=[C/T] >NC_000011.10:127868035-127868534 Homo sapiens chromosome 11
rs10932456	2082	>NC_000002.12:212988031-212988530 Homo sapiens chromosome 2 SEQ=[A/G] >NC_000002.12:212988532-212989031 Homo sapiens chromosome 2
rs1326860	2083	>NC_000001.11:193834579-193835078 Homo sapiens chromosome 1 SEQ=[A/G] >NC_000001.11:193835080-193835579 Homo sapiens chromosome 1
rs1528663	2084	>NC_000011.10:13945175-13945674 Homo sapiens chromosome 11 SEQ=[G/A] >NC_000011.10:13945676-13946175 Homo sapiens chromosome 11
rs1892231	2085	>NC_000014.9:98267730-98268229 Homo sapiens chromosome 14 SEQ=[A/C] >NC_000014.9:98268231-98268730 Homo sapiens chromosome 14

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs951279	2086	>NC_000001.11:208593050-208593549 Homo sapiens chromosome 1 SEQ=[A/G] >NC_000001.11:208593551-208594050 Homo sapiens chromosome 1
rs9806914	2087	>NC_000016.10:6097144-6097643 Homo sapiens chromosome 16 SEQ=[A/C/G/T] >NC_000016.10:6097645-6098144 Homo sapiens chromosome 16
rs7935393	2088	>NC_000011.10:128572704-128573203 Homo sapiens chromosome 11 SEQ=[A/C] >NC_000011.10:128573205-128573704 Homo sapiens chromosome 11
rs1690492	2089	>NC_000016.10:11224459-11224958 Homo sapiens chromosome 16 SEQ=[G/C] >NC_000016.10:11224960-11225459 Homo sapiens chromosome 16
rs420726	2090	>NC_000021.9:44239062-44239561 Homo sapiens chromosome 21 SEQ=[T/C] >NC_000021.9:44239563-44240062 Homo sapiens chromosome 21
rs7759385	2091	>NC_000006.12:106140395-106140894 Homo sapiens chromosome 6 SEQ=[T/A] >NC_000006.12:106140896-106141395 Homo sapiens chromosome 6

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs10974900	2092	>NC_000009.12:4987458-4987957 Homo sapiens chromosome 9 SEQ=[C/T] >NC_000009.12:4987959-4988458 Homo sapiens chromosome 9
rs1326860	2093	>NC_000001.11:193834579-193835078 Homo sapiens chromosome 1 SEQ=[A/G] >NC_000001.11:193835080-193835579 Homo sapiens chromosome 1
rs2548147	2094	>NC_000005.10:40151459-40151958 Homo sapiens chromosome 5 SEQ=[G/C] >NC_000005.10:40151960-40152459 Homo sapiens chromosome 5
rs2815844	2095	>NC_000001.11:241083704-241084203 Homo sapiens chromosome 1 SEQ=[C/T] >NC_000001.11:241084205-241084704 Homo sapiens chromosome 1
rs889702	2096	>NC_000016.10:6088639-6089138 Homo sapiens chromosome 16 SEQ=[G/A] >NC_000016.10:6089140-6089639 Homo sapiens chromosome 16
rs9806914	2097	>NC_000016.10:6097144-6097643 Homo sapiens chromosome 16 SEQ=[A/C/G/T] >NC_000016.10:6097645-6098144 Homo sapiens chromosome 16

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs6478109	2098	>NC_000009.12:114805986-114806485 Homo sapiens chromosome 9 SEQ=[A/G] >NC_000009.12:114806487-114806986 Homo sapiens chromosome 9
rs7278257	2099	>NC_000021.9:44233381-44233880 Homo sapiens chromosome 21 SEQ=[G/C] >NC_000021.9:44233882-44234381 Homo sapiens chromosome 21
rs11221332	2100	>NC_000011.10:128510579-128511078 Homo sapiens chromosome 11 SEQ=[C/A/T] >NC_000011.10:128511080-128511579 Homo sapiens chromosome 11
rs56124762	2101	>NC_000021.9:44238091-44238590 Homo sapiens chromosome 21 SEQ=[A/G] >NC_000021.9:44238592-44239091 Homo sapiens chromosome 21
rs2070558	2102	>NC_000021.9:44235275-44235774 Homo sapiens chromosome 21 SEQ=[G/A] >NC_000021.9:44235776-44236275 Homo sapiens chromosome 21
rs2070561	2103	>NC_000021.9:44237587-44238086 Homo sapiens chromosome 21 SEQ=[T/C] >NC_000021.9:44238088-44238587 Homo sapiens chromosome 21

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
rs7134599	2104	>NC_000012.12:68105795-68106294 Homo sapiens chromosome 12 SEQ=[G/A] >NC_000012.12:68106296-68106795 Homo sapiens chromosome 12
rs6062496	2105	>NC_000020.11:63697246-63697745 Homo sapiens chromosome 20 SEQ=[G/A] >NC_000020.11:63697747-63698246 Homo sapiens chromosome 20
rs7468800	2106	>NC_000009.12:114829225-114829724 Homo sapiens chromosome 9 SEQ=[C/A] >NC_000009.12:114829726-114830225 Homo sapiens chromosome 9
rs1569328	2107	>NC_000014.9:75274548-75275047 Homo sapiens chromosome 14 SEQ=[C/T] >NC_000014.9:75275049-75275548 Homo sapiens chromosome 14
rs2284553	2108	>NC_000021.9:33403889-33404388 Homo sapiens chromosome 21 SEQ=[A/G] >NC_000021.9:33404390-33404889 Homo sapiens chromosome 21
rs6062504	364157	>NC_000020.11:63717055-63717554 Homo sapiens chromosome 20 SEQ=[A/G/T] >NC_000020.11:63717556-63718055 Homo sapiens chromosome 20
rs7556897	364158	>NC_000002.12:227794896-227795395 Homo sapiens chromosome 2

dbSNP	SEQ ID NO:	SNP_SEQ_GRCh38.p13 Primary Assembly
		SEQ=[C/G/A/T] >NC_000002.12:227795397-227795896 Homo sapiens chromosome 2

Example 6. Validation of 3-SNP Models for TL1A Companion Diagnostic

[0433] The machine learning workflow identified several SNP model combinations for the development of the TL1A companion diagnostic (TL1A CDx). Previous analyses had identified 3-SNP combination models composed of variants associated with *TNFSF15 (rs6478109), ICOSLG(rs7278257, rs2070557), ETS1 (rs7935393),* and *RBFOX1 (rs9806914)* genes as well as variant *rs1892231*. These SNP models were identified via a Cedars Sinai Crohn's Disease cohort. In order to validate the findings, an external cohort of Crohn's Disease patients was identified and genotyped. Genotype and TL1A protein expression were obtained from the non-Cedars cohort in order to validate the 3- SNP models. A total of 712 Crohn's Disease individuals were genotyped while a 114 subset of the 712 samples were used to obtain TL1A protein expression via PBMC assays.

Genotyping and Imputation of Cohort

[0434] The initial data mining analyses was performed on a Cedars Sinai cohort using genotypes from the Illumina's ICHIP (Immunochip) platform. The validation cohort was genotyped using Illumina's GSA platform (24v2.0), which has substantial improvements over the Immunochip platform. Most of the SNPs identified in the models were not present on the GSA platform. Therefore, imputation of the GSA genotype data was initiated in order to obtain a larger panel of genotyped SNPs so the SNP models could be validated. Genotype imputation refers to the prediction of genotypes that are not directly assayed on a given platform. Different methodologies and significant improvements in algorithms have been developed for implementing genotype imputation. The quality of the genotype imputation was validated by selecting a random sample of 120 patients from our validation cohort to be genotyped for a small set of imputed SNPs. The overall agreement between imputed genotype and assay genotypes were evaluated using Cohen's Kappa statistic.

[0435] Validation cohort genotyped results were downloaded from Illumina and transformed into PED format (through Illumina's Genome Studio Workbench) so that they could be further processed using the PLINK software (v1.9). The genotyped data went

through a process of QC looking at factors such as heterozygosity, SNP missingness, MAF distributions, and relatedness of samples in order to prepare the genotype data for ancestry determination. Once genotyped data was QCed, the admixture and ancestry PCA plots were used to determine which samples were of European (EUR) ancestry to move forward with imputation. In order to perform imputation, ancestry needs to be taken into account, since genotype reference panels based on ancestry are used by imputation algorithms. For our imputation, the European Reference Panel: hrc.r1.1 for the reference panel was selected. All qc'd EUR ancestry genotyped samples were submitted to the Michigan Imputation Server for genotype imputation. The resulting imputed genotypes were downloaded and further processed for model validation.

[0436] In order to move forward with analyzing the imputed genotypes for the 3-SNP model validation, a random selection of 120 samples from the initial 470 samples were sent to Illumina for genotyping in order to compare the imputed genotype with the actual laboratory genotype results. The imputed genotypes were evaluated by looking at the level of agreement for the following SNPs: rs6478109, rs2070557, rs1892231, rs7935393.

[0437] The SNP rs6478109 was already on the GSA platform and this was used as a "control" to determine that the assay was in fact working appropriately. The levels of agreement (based on Cohen's Kappa) were high (based on the table below) and therefore it was decided to move forward with using the imputed genotype data for further analysis.

Table 6. Levels of Agreement Based On Cohen's Kappa

SNP	Rsq	Cohen's Kappa
rs6478109	0.998	1.00
rs2070557	0.978	0.98
rs1892231	0.989	1.00
rs7935393	0.980	1.00

Evaluation and Validation of 3-SNP Models

[0438] Next, the initial 3-SNP models were evaluated using the validation cohort. Similar to the analysis of the Cedars cohort TL1A protein expression data, the TL1A Expression (based on PBMC assay) from the validation cohort was clustered using the TL1A measurements at the 0, 3, 6, 24, and 72 hour time points. The clustering identified 3 cluster within the dataset, which are provided in FIG. 5A-5C. FIG. 5A shows cluster 1, FIG. 5B shows cluster 2, and FIG. 5C shows cluster 3.

[0439] The 3 clusters were collapsed into 2 clusters (high expression clusters) and (low expression clusters), which are shown in FIG. 6. The clusters above were collapsed down to

two clusters because there was substantial overlap between cluster 3 (FIG. 5C) above and cluster 1 (FIG. 6, left). The same level of overlap was seen for clusters 1 (FIG. 5A) and 2 (FIG. 5B) (based on the 3 clusters) and cluster 2 (FIG. 6, right).

[0440] The imputed genotype data were integrated from the validation cohort with the TL1A protein expression data in order to determine which models validated in the external validation cohort. This was done by looking at results of the TL1A CDx 3-SNP model. The 3-SNP models were evaluated in the context of the validation cohort and the TL1A expression clusters. "Positive" genotype hits were determined based on the association of a particular genotype and its ability to associate with the higher expressing TL1A cluster. Without being bound by any particular theory, high TL1A clusters (e.g., high expression of TL1A in CD patients, relative to baseline expression of TL1A in normal individuals) directly correlates with positive therapeutic responsiveness to an inhibitor of TL1A activity or expression; whereas low TL1A clusters (e.g., low TL1A expression in CD patients, relative to baseline expression of TL1A in normal individuals) directly correlates to non-responsiveness to an inhibitor of TL1A activity or expression.

[0441] Calculations of Positive Predictive Value (PPV) and Specificity were calculated for the 3-SNP models. Each model consists of 3 unique SNPs based off of the identified SNPs in our training cohort analysis (*TNFSF15 (rs6478109), ICOSLG(rs7278257, rs2070557), ETS1 (rs7935393),* and *RBFOX1 (rs9806914)* genes as well as variant *rs1892231)*. The PPV and Specificity for Models A-C are provided in Table 7. As shown in Table 7, Model A may be used to predict a positive therapeutic response to a treatment with an inhibitor of TL1A activity or expression with a PPV of at least or about 0.797 and a specificity of at least or about 0816 (when considering both training and validation cohorts combined). Model A was further explored due to its better performance compared to Models B and C (when considering both training and validation cohorts combined).

Table 7. Exemplary 3-SNP Models A-C

Model	Training Cohort		Validation Cohort		Combined		CD FREQ
	PPV	SPEC	PPV	SPEC	PPV	SPEC	
A	0.902	0.867	0.643	0.783	0.797	0.816	38.7
B	0.806	0.767	0.682	0.848	0.759	0.816	26.3
C	0.838	0.800	0.576	0.696	0.714	0.737	36.7

[0442] Other previously identified 3-SNP models were further evaluated due the fact that only Model A showed strong concordance of positive hit genotypes across the training and

validation cohorts. These additional SNP models (Models D-K) consisted of 3-SNP combinations of the following SNPs: *rs6478109, rs7935393, rs9806914, rs16901748, rs2070557, rs7278257, rs2297437, rs1892231*, as shown in Table 8.

Table 8. 3-SNP Models D-K

Model	Cohort 1		Cohort 2		Combined		CD FREQ
	PPV	SPEC	PPV	SPEC	PPV	SPEC	
D	0.815	0.833	0.750	0.848	0.782	0.842	18.6
E	0.848	0.833	0.606	0.717	0.727	0.763	31.2
F	0.909	0.933	0.667	0.870	0.800	0.895	18.3
G	0.917	0.933	0.609	0.804	0.766	0.855	22.6
H	0.923	0.967	0.727	0.935	0.833	0.947	12.9
I	0.941	0.967	0.733	0.913	0.844	0.934	17.2
J	0.923	0.967	0.727	0.935	0.833	0.947	12.9
K	0.844	0.833	0.731	0.848	0.793	0.842	23.9

[0443] As before, the PPV and Specificity for each model was evaluated in the context of positive and negative hits and their association with high and lower TL1A clusters. After evaluating the models across both training and validation cohorts, an additional model (Model K) was evaluated, which contained SNP, rs16901748 (CTNND2), which had not been utilized in our previous models (based on the initial training cohort).

ICOSLG Proxy SNP Selection

[0444] One of ICOSLG SNPs (rs7278257) was determined to be challenging to genotype given the SNP location within the genome. Therefore, candidate proxy SNPs to rs7278257 were identified. The proxy SNPs were identified via LDLink. A list of potential proxy SNPs for rs7278257 is shown below in Table 9.

Table 9. Proxy SNPs Utilized in Validation

RS Number	Coord	Alleles	MAF	Distance	Dprime	R2
rs7278257	chr21:45653764	(G/C)	0.2833	0	1	1
rs56124762	chr21:45658474	(A/G)	0.2763	4710	0.9849	0.9372
rs11558819	chr21:45656774	(C/T)	0.2873	3010	0.9705	0.9236
rs2070557	chr21:45655124	(A/T)	0.2972	1360	0.9651	0.8705
rs2070558	chr21:45655658	(G/A)	0.2952	1894	0.9602	0.87
rs2329718	chr21:45656199	(T/C)	0.2952	2435	0.9602	0.87
rs2070559	chr21:45657700	(C/G)	0.2982	3936	0.96	0.8573
rs2070560	chr21:45657848	(C/G)	0.2972	4084	0.9551	0.8526
rs2070561	chr21:45657970	(T/C)	0.2972	4206	0.9551	0.8526

[0445] Next, the SNPs provided in Table 9 were analyzed for relevant inflammatory bowel disease related clinical associations within the Cedars R/Shiny database. From the

SNPs above, the following SNPs had relevant clinical associations (examples include key phenotypes: CD vs. Ctrl, IBD vs. Ctrl,L1 B2a+B2b vs B1): rs2070561, rs56124762, rs2070558, rs11558819. CD v. Ctrl refers to cases of Crohn's disease versus cases of controls (individuals without Crohn's disease); IBD vs. Ctrl refers to cases of inflammatory bowel disease versus cases of controls (individuals without IBD); L1 refers to the ileum; B2a+B2b refers to stricturing and penetrating disease; B1 refers to non-stricturing and non-penetrating disease.

[0446] The TL1A companion diagnostic (CDx) described herein was validated in two independent CD and UC patient cohorts, the results of which are summarized in FIG. 10. The TL1A CDx captured approximately 32% of the IBD population and predicted with positive predictive value (PPV) of 86% whether the CD or the UC subjects were positive for a therapeutic response to TL1A ("CDx+"). Overall, the TL1A CDx had an approximately 4.6x greater probability of identifying patients predisposed to increased TL1A expression ("high producers") over IBD patients predisposed to lowered TL1A expression ("low producers"). Across two CD patient cohorts alone, the TL1A CDx predicted as high as 42% of the IBD patients to have increased TL1A expression.

Example 7. Validation in Japanese Cohort

[0447] An external cohort of Crohn's Disease patients of Japanese ancestry is identified and genotyped. Genotype and TL1A protein expression are obtained from second Japanese cohort in order to validate the 3-SNP models. A total of 800 Crohn's Disease individuals are genotyped while a 100 subset of the 800 samples are used to obtain TL1A protein expression via PBMC assays.

[0448] The initial 3-SNP models are evaluated using the Japanese validation cohort. Similar to the analysis of the validation cohort in Example 6, the TL1A Expression (based on PBMC assay) from the validation cohort is clustered using the TL1A measurements at the 0, 3, 6, 24, and 72 hour time points. The clustering identifies at least 2 clusters in the dataset: (i) high expression clusters and (ii) low expression clusters.

[0449] The imputed genotype data are integrated from the Japanese validation cohort with the TL1A protein expression data in order to determine which models validated in the Japanese validation cohort. This is done by looking at results of the TL1A CDx 3-SNP model. The 3-SNP models are evaluated in the context of the Japanese validation cohort and the TL1A expression clusters. "Positive" genotype hits are determined based on the association of a particular genotype and its ability to associate with the higher expressing TL1A cluster. Calculations of PPV and Specificity are calculated for the 3-SNP models. Each

model consists of 3 unique SNPs based off of the identified SNPs in the training cohort analysis (*TNFSF15 (rs6478109), ICOSLG(rs7278257, rs2070557), ETS1 (rs7935393),* and *RBFOX1 (rs9806914)* genes as well as variant *rs1892231)*. The 3-SNP models shown in Table 7 and Table 8 are explored in this validation. The PPV and SPEC values expected in the Japanese validation cohort for Models A-K are the same as those reported in Table 7 and op. Without being bound by any particular theory, validation of the 3-SNP models for the TL1A CDx is expected across all ancestral populations.

[0450] Candidate proxy SNPs to any one of the SNPs provided in Table 7 or Table 8 may be identified. The proxy SNPs are identified via LDLink using a reference population of Japanese ancestry. The proxy SNPs are further analyzed for relevant inflammatory bowel disease related clinical associations within the Cedars R/Shiny database in Japanese cohorts, such as for example, CD vs. Ctrl, IBD vs. Ctrl,L1 B2a+B2b vs B1).

Example 8: Design of humanized anti-TL1A antibodies

[0451] Two different strategies were employed to identify humanized variants that express well in mammalian cells, preserve TL1A binding, and display high monomeric content.

[0452] The first strategy utilized a previously humanized variant, termed ASX, that displays high monomeric content (98%) and expresses well (30 µg/mL in small-scale transient cultures) as a template for additional mutagenesis. However, ASX contains a significant number of murine framework residues, eight heavy chain residues and 7 light chain residues, that may pose an immunogenicity risk. The ASX heavy and light chain templates were used to systematically mutate murine framework residues to human residues corresponding to the most closely related human germline framework. The goal of this strategy was to reduce the total number of murine framework residues while preserving the favorable expression and solubility characteristics of ASX. Because ASX contained 15 murine framework residues there were 2^15 (32,768) distinct variants (restricting each position to either the murine or the human residue) that could be made and tested.

[0453] The second strategy utilized a previously humanized variant, termed c34, that expresses well (17 µg/mL in small-scale transient cultures) and contains CDRs optimized for binding within a fully human germline framework, as a template for additional mutagenesis. Large-scale expression of c34 unexpectedly resulted in a sub-optimal monomeric content (55-60%). The c34 heavy and light chain templates were used to systematically mutate certain framework residues to murine residues corresponding to the original murine antibody framework. The goal of this strategy was to improve the solubility of c34 (monomeric

content) through the introduction of as few murine framework residues as possible (minimizing potential immunogenicity risks) while preserving the favorable expression characteristics of c34.

[0454] For both strategies, the initial approach was to scan differing framework residues, one at a time, and express and characterize the variants. Thus, human framework residues were introduced into variant ASX where it differed from c34 and conversely, murine framework mutations were introduced into variant c34 where it differed from ASX. The initial scan identified certain framework and CDR residues that had minimal impact on the characteristics displayed by the template antibody while other mutations had a more dramatic impact, favorable in some cases and unfavorable in others. The information gained from the positional scan was subsequently used in an iterative and combinatorial fashion, to identify multiple variants with favorable characteristics. Importantly, by applying a stepwise, iterative and combinatorial approach the beneficial variants were identified without necessitating the expression and characterization of 32,768 distinct variants.

[0455] In certain cases, mutation of the first residue of the heavy chain from glutamine to aspartic acid or glutamic acid was evaluated, alone or in combination with other mutations.

[0456] In addition, for both strategies certain CDR residues were also mutated to determine the impact on expression and solubility. For example, a limited number of mutations in HCDR2, HCDR3 and LCDR3 were examined. Similar to the approach used with frameworks, the mutations were predominantly restricted to the original murine CDR residue or mutations that were previously identified as enhancing binding affinity.

[0457] Finally, for both strategies "shuffling" of heavy and light chains was used. Specifically, certain human light chains containing few murine framework residues and having a favorable impact on expression of antibody with higher monomeric content were identified early in the process and these were paired with various engineered heavy chains in order to accelerate the process of identifying suitable variants.

Table 10. Sequences of Certain Designed anti-TL1A Antibodies

Antibody	Heavy Chain Variable Region SEQ ID NO	Light Chain Variable Region SEQ ID NOS
A15	108	203
A29	108	205
A30	108	204
A31	136	205
A32	137	205
A33	137	202
A34	107	208
A35	138	208
A36	139	208
A37	140	208
A38	141	208
A39	142	208
A40	143	208
A41	115	208
A42	144	208
A43	145	208
A44	146	208
A45	120	208
A46	147	208
A47	148	208
A48	108	210
A49	108	211
A50	108	212
A51	108	213
A52	108	214
A53	146	208
A54	149	208
A55	109	208
A56	108	215
A57	150	202
A58	125	202
A59	117	202
A60	151	202
A61	152	202
A62	153	202
A63	154	202
A64	121	202
A65	128	202
A66	155	202
A67	122	202
A68	123	202
A69	156	202
A70	157	202

A71	158	202
A72	131	202
A73	157	205
A74	158	205
A75	131	205
A76	159	202
A77	160	202
A78	124	202
A79	107	208
A81	139	208
A82	140	208
A83	144	208
A85	136	209
A86	136	216
A87	136	217
A88	136	218
A89	136	219
A90	136	220
A91	133	202
A92	161	202
A93	162	202
A94	124	202
A95	131	205
A96	128	205
A97	121	202
A98	122	202
A99	123	202
A100	107	204
A101	140	204
A102	115	204
A103	120	204
A104	139	204
A105	143	204
A107	108	202
A108	156	205
A109	133	205
A110	125	205
A111	150	205
A112	117	205
A113	124	205
A114	121	205
A115	122	205
A116	123	205
A117	151	205
A118	153	205
A119	159	205
A120	154	205
A121	163	204

A122	113	204
A123	112	204
A124	164	204
A125	105	204
A126	114	204
A127	118	204
A128	111	204
A129	110	204
A130	121	205
A132	128	206
A133	121	206
A134	122	206
A135	133	206
A136	125	206
A137	121	207
A138	122	207
A139	110	207
A140	110	202
A141	111	207
A142	111	202
A143	136	202
A144	111	204
A145	133	201
A146	125	201
A147	117	201
A148	121	201
A149	122	201
A150	128	201
A151	124	201
A152	131	201
A153	133	205
A154	125	205
A155	121	205
A156	122	205
A157	104	204
A158	101	204
A159	119	204
A160	102	204
A161	165	204
A162	106	204
A163	166	204
A164	167	204
A165	139	205
A166	146	205
A167	120	205
A168	147	205
A169	126	205
A170	135	205

A171	168	205
A172	130	205
A173	127	205
A174	132	205
A175	126	201
A176	135	201
A177	168	201
A178	130	201
A179	127	201
A180	132	201
A181	107	202
A182	138	202
A183	140	202
A184	145	202
A185	147	202
A186	144	202
A187	120	202
A188	115	202
A189	146	202
A190	141	202
A191	142	202
A192	143	202
A193	109	205
A194	103	205
A195	169	205
A196	129	205
A197	116	205
A198	134	205
A199	109	201
A200	103	201
A201	169	201
A202	129	201
A203	116	201
A204	134	201
A205	109	202
A206	103	202
A207	169	202
A208	129	202
A209	116	202
A210	134	202
A211	108	201
A212	107	201
A213	106	201
A214	111	201
A215	110	201
A216	112	201
A217	101	201
A218	119	201

A219	104	201
A220	102	205
A221	105	201
A222	114	201
A223	103	202
A224	116	201
A500	301	303
A501	302	303

[0458] As used herein, reference to A(number), refers to an antibody of this table. For instance, A15 used herein refers to A15 in **Table 10**.

Example 9: Generation and characterization of humanized anti-tl1a antibodies

[0459] Humanized anti-TL1A antibodies designed in Example 1 were prepared and characterized.

Cloning of humanized antibodies

[0460] DNA encoding leader sequence and the heavy and light chain variable regions of humanized variants of interest was cloned into pFuse1-hIgG1-Fc1 (InvivoGen) and pFuse2-CLig-hk (InvivoGen), respectively. Two distinct humanized heavy chain templates, termed ASX-HC and c34-HC, and four distinct humanized light chain templates, termed ASX-LC, cH3-1, c34-LC, cXL3-13-LC and cXL3-15-LC were all cloned.

[0461] In order to introduce mutations into the templates, the QuickChange Site Directed Mutagenesis Kit (Agilent, cat. #200518) was used per manufacturer's directions. Briefly, mutagenesis was performed using miniprep double-stranded plasmid DNA, two synthetic oligonucleotides primers containing the desired mutation, PfuTurbo® DNA polymerase and a temperature cycler. Following temperature cycling, the product was treated with Dpn I. The nicked vector DNA containing the mutation(s) of interest was used to transform bacteria. Subsequently, colonies were picked, the DNA was sequenced to confirm mutagenesis and was subsequently used for transfection of mammalian FreeStyle 293-F cells.

Antibody expression

[0462] Small-scale (3 mL, 6-well) expression of variants in FreeStyle 293-F cells was performed in the following manner. One or two days prior to transfection cells were passaged so that the density would be >1 x 10^6 cells/mL on the day of the transfection. Typically, this meant passaging at 6-7 x 105 cells/mL one day prior or 4 x 105 cells/mL two days prior. Transfections were only performed with cell viability >90%. On the day of the transfection Opti-MEM media was warmed to 37°C and cells were resuspended to 1.1 x 106 cells/mL, using 3.3 x 106 cells per 3 mL transfection. A total of 3 ug DNA was used for each

transfection. Briefly, the transfections used heavy and light chain plasmid at a heavy chain:light chain ratio of 1:3. For 3 mL transfections, 4 uL 293fectin was added to 96 uL Opti-MEM, combined with 100 uL DNA mixture, and incubated at 25°C for 20-30 minutes. Subsequently, this mixture was added dropwise to 2.8 mL cells and the plate was transferred to an incubator and placed on a rotating platform at 175 rpm for up to 120 hours. After 96-120 hours, transfection supernatants were collected by centrifuging the transfected cells and supernatant at 1200 rpm for 5 min. The supernatant was transferred to a clean tube and centrifuged again at 3900 rpm for 10 min to remove any remaining cell debris. The supernatant was filtered through a 0.45 mm PES syringe filter and stored at 4°C until the next step.

Quantitation of antibody expression

[0463] Antibody expression was quantitated by ELISA. Briefly, a Corning Costar 3366 96-well round bottom high bind plate was coated with 50 mL anti-kappa (2 µg/mL) in PBS overnight at 4°C. The plate was washed 3x with PBS-0.05% Tween 20 (PBS-T) and was blocked with 100 µL 1% BSA/PBS for 1 h at 25°C. The block was removed, and culture supernatant diluted 5-fold was added and serially diluted 2-fold across the plate. Every plate also contained an IgG standard diluted serially 3-fold beginning at 1 ug/mL. Samples were incubated for 1 h at 25°C, the plate was washed three times with PBS-T, and 50 uL anti-Fc HRP secondary (Southern Biotech #2048-05), diluted 1:4000 in BSA/PBS was added for 1 h at 25°C. The plate was washed three times with PBS-T and developed for up to 15 min following the addition of 50 µL Ultra TMB ELISA substrate (Thermo #34028). The reaction was terminated by the addition of 50 µL 2 N H_2SO_4 and the A450 nm was measured. Antibody expression levels obtained from 3 mL scale transfections are shown in **Table 11**.

Table 11. Expression, Binding, and Analytical SEC Characterization of anti-TL1A Antibodies (ND, not determined)

Variant	Expression (ug/mL)	KD (pM)	% Monomer	Murine FR	HC Template	LC Template
15	21	ND	87	8	ASX	cH3-1
29	18	65	65	10	ASX	c34
30	29	77	90	8	ASX	cXL3-13
31	11	92	73	2	c34	c34
32	10	111	78	2 +D	c34	c34
33	21	81	54	0 +D	c34	c34
34	35	<50	97	14	ASX	ASX
35	36	72	91	14	ASX	ASX
36	40	<50	87	13	ASX	ASX

Variant	Expression (ug/mL)	KD (pM)	% Monomer	Murine FR	HC Template	LC Template
37	40	34	95	14	ASX	ASX
38	28	103	75	14	ASX	ASX
39	15	125	83	14	ASX	ASX
40	30	<50	87	13	ASX	ASX
41	20	16	96	14	ASX	ASX
42	30	<50	88	14	ASX	ASX
43	18	51	90	14	ASX	ASX
44	ND	ND	ND	13	ASX	ASX
45	15	85	90	13	ASX	ASX
46	27	63	72	13	ASX	ASX
47	18	82	78	12	ASX	ASX
48	22	76	92	14	ASX	ASX
49	26	92	65	13	ASX	ASX
50	33	19	94	14	ASX	ASX
51	16	<50	93	14	ASX	ASX
52	29	27	91	13	ASX	ASX
53	26	126	84	13	ASX	ASX
54	25	83	94	15 +D	ASX	ASX
55	22	91	99	15 +E	ASX	ASX
56	15	116	71	14	ASX	ASX
57	20	191	59	1	c34	c34
58	9	112	67	1	c34	c34
59	11	136	78	2	c34	c34
60	19	168	57	0	c34	c34
61	15	127	44	1	c34	c34
62	21	150	58	1	c34	c34
63	20	132	52	0	c34	c34
64	2	90	97	0	c34	c34
65	7	97	69	1	c34	c34
66	19	150	49	1	c34	c34
67	4	89	97	1	c34	c34
68	2	74	92	1	c34	c34
69	12	136	64	0 +E	c34	c34
70	15	149	54	1	c34	c34
71	18	150	55	2	c34	c34
72	13	159	61	3	c34	c34
73	8	128	71	3	c34	c34
74	10	141	70	4	c34	c34
75	8	259	95	5	c34	c34
76	19	ND	50	0	c34	c34
77	12	ND	50	2	c34	c34
78	3	ND	86	2	c34	c34
79	42	ND	98	14	ASX	ASX
81	31	ND	88	13	ASX	ASX
82	26	ND	92	14	ASX	ASX
83	29	ND	74	14	ASX	ASX

Variant	Expression (ug/mL)	KD (pM)	% Monomer	Murine FR	HC Template	LC Template
85	25	130	49	1	c34	c34
86	26	129	55	1	c34	c34
87	26	121	52	1	c34	c34
88	9	81	63	2	c34	c34
89	31	117	55	1	c34	c34
90	19	107	53	1	c34	c34
91	14	132	63	1	c34	c34
92	20	121	49	1	c34	c34
93	12	117	63	2	c34	c34
94	5	81	91	2	c34	c34
95	13	105	92	5	c34	c34
96	7	95	99	3	c34	c34
97	2	71	97	0	c34	c34
98	7	140	98	1	c34	c34
99	3	102	95	1	c34	c34
100	39	84	84	7	ASX	cXL3-13
101	23	96	81	7	ASX	cXL3-13
102	19	104	75	7	ASX	cXL3-13
103	11	107	90	6	ASX	cXL3-13
104	26	108	70	6	ASX	cXL3-13
105	23	110	58	6	ASX	cXL3-13
107	55	71	85	8	ASX	c34
108	9	55	83	2 +E	c34	c34
109	9	50	96	3	c34	c34
110	7	56	95	3	c34	c34
111	17	68	61	3	c34	c34
112	6	54	93	4	c34	c34
113	2	50	99	4	c34	c34
114	1	51	99	2	c34	c34
115	3	58	99	3	c34	c34
116	1	53	99	3	c34	c34
117	16	94	80	2	c34	c34
118	21	83	70	3	c34	c34
119	15	87	77	2	c34	c34
120	12	85	64	2	c34	c34
121	24	106	77	6	ASX	cXL3-13
122	22	112	85	6	ASX	cXL3-13
123	18	104	76	5	ASX	cXL3-13
124	21	91	83	6	ASX	cXL3-13
125	10	116	98	6	ASX	cXL3-13
126	4	123	99	5	ASX	cXL3-13
127	8	70	94	6	ASX	cXL3-13
128	17	111	84	4	ASX	cXL3-13
129	17	99	92	5	ASX	cXL3-13
130	1	75	99	2	c34	c34
132	6	62	99	2	c34	cXL3-13

Variant	Expression (ug/mL)	KD (pM)	% Monomer	Murine FR	HC Template	LC Template
133	1	58	99	1	c34	cXL3-13
134	3	55	99	2	c34	cXL3-13
135	7	56	74	2	c34	cXL3-13
136	6	53	84	2	c34	cXL3-13
137	2	50	96	0	c34	cXL3-15
138	5	69	99	1	c34	cXL3-15
139	35	74	78	5	ASX	cXL3-15
140	26	73	75	5	ASX	c34
141	27	108	81	4	ASX	cXL3-15
142	25	126	68	4	ASX	c34
143	16	85	57	0	c34	c34
144	ND	ND	ND	4	ASX	cXL3-13
145	20	70	78	2	c34	c34
146	25	65	84	2	c34	c34
147	26	63	87	3	c34	c34
148	2	46	98	1	c34	c34
149	7	48	99	2	c34	c34
150	15	59	83	2	c34	c34
151	5	57	96	3	c34	c34
152	36	58	73	4	c34	c34
153	9	49	97	3	c34	c34
154	8	66	92	3	c34	c34
155	1	67	99	2	c34	c34
156	2	94	99	3	c34	c34
157	6	69	93	4	ASX	cXL3-13
158	6	66	91	3	ASX	cXL3-13
159	4	69	99	4	ASX	cXL3-13
160	7	94	99	4	ASX	cXL3-13
161	11	72	59	4	ASX	cXL3-13
162	9	75	79	3	ASX	cXL3-13
163	22	51	60	4	ASX	cXL3-13
164	23	58	61	4	ASX	cXL3-13
165	19	59	53	8	ASX	c34
166	13	57	76	8	ASX	c34
167	9	42	96	8	ASX	c34
168	16	62	85	8	ASX	c34
169	8	47	90	3	c34	c34
170	9	49	93	3	c34	c34
171	13	50	80	5	c34	c34
172	7	40	96	3	c34	c34
173	4	40	99	4	c34	c34
174	4	43	98	4	c34	c34
175	31	45	86	2	c34	c34
176	18	48	80	2	c34	c34
177	35	52	67	4	c34	c34
178	18	43	85	2	c34	c34

Variant	Expression (ug/mL)	KD (pM)	% Monomer	Murine FR	HC Template	LC Template
179	16	79	93	3	c34	c34
180	17	58	94	3	c34	c34
181	46	60	87	7	ASX	c34
182	39	67	74	7	ASX	c34
183	38	65	82	7	ASX	c34
184	30	61	73	7	ASX	c34
185	30	56	66	6	ASX	c34
186	38	67	66	7	ASX	c34
187	27	56	72	6	ASX	c34
188	31	63	87	7	ASX	c34
189	44	76	71	6	ASX	c34
190	32	57	69	7	ASX	c34
191	21	57	80	7	ASX	c34
192	27	55	70	6	ASX	c34
193	16	55	68	10 +E	ASX	c34
194	16	51	87	9 +E	ASX	c34
195	12	56	82	5 +E	c34	c34
196	7	54	97	3 +E	c34	c34
197	7	54	97	3 +E	c34	c34
198	9	53	95	3 +E	c34	c34
199	28	50	93	9 +E	ASX	c34
200	24	52	99	8 +E	ASX	c34
201	25	58	82	4 +E	c34	c34
202	13	59	87	2 +E	c34	c34
203	18	62	89	2 +E	c34	c34
204	11	53	84	2 +E	c34	c34
205	27	55	86	8 +E	ASX	c34
206	20	50	98	7 +E	ASX	c34
207	ND	ND	ND	3 +E	c34	c34
208	ND	ND	ND	1 +E	c34	c34
209	14	58	66	1 +E	c34	c34
210	15	70	61	1 +E	c34	c34
211	42	58	96	9	ASX	c34
212	33	50	99	8	ASX	c34
213	29	49	99	4	ASX	c34
214	27	51	97	5	ASX	c34
215	20	48	77	6	ASX	c34
216	24	49	97	6	ASX	c34
217	15	43	99	4	ASX	c34
218	13	51	96	5	ASX	c34
219	21	50	99	5	ASX	c34
220	18	50	99	6	ASX	c34
221	23	51	98	7	ASX	c34
222	29	60	96	6	ASX	c34
223	19	62	98	7 +E	ASX	c34
224	15	76	92	2 +E	c34	c34

Antibody binding to human TL1A

[0464] Antibody binding to human TL1A (Fitzgerald #30R-AT070) was quantitated by ELISA. Briefly, a Corning Costar 3366 96-well round bottom high bind plate was coated with 50 µL TL1A (1 µg/mL) in PBS overnight at 4°C. The plate was washed 3x with PBS-0.05% Tween 20 (PBS-T) and was blocked with 100 µL 1% BSA/PBS for 1 h at 25°C. The block was removed, and culture supernatant diluted 5-fold was added and serially diluted 2-fold across the plate. Samples were incubated for 1 h at 25°C, the plate was washed three times with PBS-T, and 50 µL anti-Fc HRP secondary, diluted 1:4000 in BSA/PBS was added for 1 h at 25°C. The plate was washed three times with PBS-T and developed for up to 15 min following the addition of 50 µL Ultra TMB ELISA substrate. The reaction was terminated by the addition of 50 µL 2 N H_2SO_4 and the A450 nm was measured. The antibody affinities, as determined by ELISA titration against human TL1A using unpurified culture supernatants, is shown in **Table 11**.

Purification of antibodies

[0465] Antibodies were purified from culture supernatants in a single step using Dynabeads Protein A (ThermoFisher Scientific, cat. #10002D). First, culture supernatants were concentrated per manufacturer's instructions using an Amicon Ultra-4 Centrifugal Filter Unit (30,000 MWCO; Millipore Sigma, cat. #C7719). The Dynabeads were resuspended by gentle vortexing and 100 uL were transferred to an Eppendorf tube. Using a magnet to retain the beads, the storage buffer was removed, and the beads were washed with 0.5 mL of 20 mM sodium phosphate, 150 mM NaCl, pH 7.4 (EB, Equilibration Buffer). A total of up to 24 ug of IgG from culture supernatant was added to the beads and mixed gently until the beads were resuspended. When necessary, antibody supernatants were diluted with EB. The tubes were placed sideways on a shaking platform and mixed for 10 min at 25°C at 500 rpm. Subsequently, the beads were collected at the bottom of the tube using a microfuge at 10,000 rpm for 30 sec. Using a magnet to retain the beads, the supernatant was removed. The beads were washed once with 0.5 mL of 20 mM sodium phosphate, 500 mM NaCl, pH 7.4 followed by another wash with 50 mM sodium phosphate, pH 6.0. The beads were collected at the bottom of the tube using a microfuge at 10,000 rpm for 30 sec. Purified antibody was eluted from the beads using 20 uL 50 mM sodium acetate, pH 3.5 with gentle mixing for 2 min at 25°C. Using a magnet to retain the beads, the eluate was transferred to a fresh tube containing 1.1 uL 1 M Tris, pH 8.5 to neutralize the pH of the sample. This sample was then centrifuged at 10,000 rpm for 2 min and transferred to a fresh tube to ensure removal of residual Dynabeads. The concentration of the purified sample was determined using a DeNovix DS-

11 Spectrophotometer/Fluorometer, buffer blank, and a mass extinction coefficient of 13.70 at 280 nm for a 1% IgG solution.

Size exclusion chromatography

[0466] The antibodies were analyzed by size exclusion chromatography (SEC) to determine percent monomer and identify any large molecular weight aggregate contaminant species. A total volume of 15 µL of protein A purified antibodies at a concentration of 0.1 – 1 µg/µL were analyzed using a Waters SEC column (Acquity UPLC BEH SEC, 200 Å, 1.7 µm, 4.6 x 150 mm) on a Shimadzu UPLC instrument at a flow rate of 0.2 mL/min and a column oven temperature of 30°C. Standard PBS was used as the mobile phase and absorbance at 280 nm was used to monitor protein elution. For some antibody clones tested that demonstrated non-symmetrical elution profiles, PBS buffer supplemented with 350 mM NaCl at pH 6.0 was utilized to reduced non-specific interactions with the column matrix. The percent main peak (monomer) value was calculated using the Shimadzu software. Representative sample profiles are shown in **FIGS. 7A-7C.** The monomeric content of purified antibody variants is shown in **Table 11**.

Example 10: Abrogation of effector function

[0467] In certain cases, it might be beneficial to reduce the potential effector function of the antibodies. Multiple strategies to diminish effector function have been described, including point mutations to ablate FcγR and C1q binding, cross-subclass Fc designs to eliminate FcγR and C1q binding, and glycoengineering to ablate FcγR and C1q binding. Representative examples are highlighted in **Table 12**.

Table 12. Representative Aproaches to Abrogating Effector Function

Mutation(s)	Effect
E233P	Decreases binding to FcγRI, II, III
S228P, L235E SPLE in IgG4	Decreases binding to FcγRI
L235E	Decreases binding to FcγRs
L234A, L235A	Decreases binding to FcγRI, II, III
L234A, L235A, G237A	Decreases binding to FcγRI, II, III, C1q
L234A, L235A, P329G	Decreases binding to FcγRI, II, III, C1q
L234F, L235E, P331S	Decreases binding to FcγRI, II, III, C1q
L234A, L235E, G237A	Decreases binding to FcγRI, II, III, C1q
L234A, L235E, G237A, P331S	Decreases binding to FcγRI, II, III, C1q
L234A, L235A, G237A, P238S, H268A, A330S, P331S (IgG1σ)	Decreases binding to FcγRI, IIa, IIb, IIIa
L234A, L235A, P329A	Decreases binding to FcγRI, II, III, C1q
G236R, L328R	Decreases binding to FcγRI, II, III
G237A	Decreases binding to FcγRII
F241A	Decreases binding to C1q

V264A	Decreases binding to C1q
D265A	Decreases binding to FcγRI, II, III
D265A, N297A	Decreases binding to FcγRI, II, III, C1q
D265A, N297G	Decreases binding to FcγRI, II, III, C1q
D270A	Decreases binding to C1q
N297A, G, D, Q	Elimination of N-linked glycosylation Decreases binding to FcγRI, II, III, C1q
P329A, G, R	Decreases binding to C1q
A330L	Decreases binding to C1q
P331A, S	Diminished C1q binding
IgG2	Decreases binding to FcγRs
IgG4	Decreases binding to FcγRs; Does not activate complement system
S228P	Prevent IgG4 Fab arm exchange
S228P, F234A, L235A (IgG4)	Decreases binding to FcγRI, IIa, IIIa
IgG2-IgG4 cross-subclass (IgG2/G4)	Decreases binding to FcγRI, II, III, C1q
IgG2-IgG3 cross-subclass	Decreases binding to FcγRs; Decreases binding to C1q
H268Q, V309L, A330S, P331S (IgG2m4)	Decreases binding to FcγRI, II, III, C1q
V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2 σ)	Decreases binding to FcγRI, IIa, IIb, IIIa, C1q
High mannose glycosylation	Decreases binding to C1q

[0468] In order to express antibodies with abrogated effector function, the light chain variable regions of the antibodies disclosed in Example 2 and **Table 10** are cloned with a kappa light chain constant region, while the heavy chain variable regions are cloned with a modified IgG1 heavy chain backbone, or a modified IgG2 backbone, or a modified IgG4 backbone, or an unmodified IgG2 or IgG4 backbone, such as those disclosed in **Table 3** or elsewhere.

[0469] The impact of the various Fc engineering approaches on CDC activity can be assessed using C1q binding and C3 fixation assays. Purified antibodies are diluted in PBS and serial dilutions are plated on a microtiter plate for 12-18h at 4°C. The plates are blocked with 5% gelatin/PBS containing 1% (v/v) Tween-20 for 1h at 25°C. Subsequently, the plates are incubated with 10% (v/v) human sera in PBS and C1q binding is detected using 1:500 dilution of HRP-conjugated rabbit anti-C1q (Bioss Inc.) in PBS containing 1% (v/v) Tween-20. To test C3 fixation, a 1:1000 dilution of rabbit anti C3 (abcam) is used followed by a 1:2000 dilution of HRP-conjugated chicken anti-rabbit IgG (abcam). The plates are developed as described for antibody quantitation assays in Example 1. EC50 values are calculated by fitting the data to a log (agonist) vs. response-variable slope (four parameter) model using GraphPad Prism (Sunnyvale, CA).

[0470] Additionally, the variants may be characterized for the binding of isolated C1q. MaxiSorp 384-well plates (Thermo Scientific, Nunc) are coated with serially diluted antibodies in 50 mM carbonate buffer, pH 9.6 (coat buffer), for 12-18h at 4°C. Plates are washed with phosphate buffered saline (PBS) containing 0.05% polysorbate 20, pH 7.4 and blocked with PBS containing 0.5% BSA, 0.05% polysorbate 20, 15 ppm Proclin and 10% Blocker Casein (ThermoScientific), pH 7.4. After 1-hour incubation at 25°C, plates are washed. Human C1q (Quidel, San Diego, CA) in the same buffer is added and incubated for 1.5 hour. Bound C1q is detected by adding 20 ng/mL biotinylated mouse anti-mouse C1q (Hycult biotech; cross reacting with human C1q) for 1.5 hour followed by horseradish peroxidase (HRP)-conjugated streptavidin (GE Healthcare Life Sciences) for 1 hour. To check for coating efficiency, some coated wells receive buffer only for the first two incubation steps and receive goat anti-human Fab'2-HRP when the wells used for measuring C1q binding received streptavidin-HRP. Plates are washed after each incubation step. Peroxidase activity is detected with substrate 3, 3′, 5, 5′-tetramethyl benzidine (TMB) (Kirkegaard & Perry Laboratories). The reaction is stopped with 1M phosphoric acid and absorbance is measured at 450 nm. Dose-response binding curves are fitted with a four-parameter model and EC50 values are calculated using GraphPad Prism (Sunnyvale, CA).

[0471] The impact of the various Fc engineering approaches on ADCC activity is assessed using soluble FcγR receptor binding ELISAs. Soluble human FcγRI, FcγRIIb and FcγRIII (binding affinity to both the F158 and V158 polymorphic forms of FcγRIII is assessed) are expressed as recombinant fusion proteins with Gly-His6-glutathione-S-transferase (GST) at the C-terminus of the extracellular domain of the receptor. MaxiSorp 384-well plates are coated with 1 μg/ml human FcγR in coat buffer. Plates are washed and blocked with PBS containing 0.5% BSA, 15 ppm Proclin, pH 7.4. After a 1 h incubation, plates are washed and 3-fold serial dilution of antibodies in PBS containing 0.5% BSA, 0.05% polysorbate 20, 15 ppm Proclin, pH 7.4 is added to the plates and incubated for 2 h. For enhanced binding sensitivity due to avidity, immune complexes are formed using anti-human antibody. Bound antibody is detected with HRP-conjugated goat anti-human kappa (Southern Biotech) using Ultra TMB substrate as described in Example 1. The reaction is terminated and the plate is read as described above. The dose-dependent binding curve of the wild type antibody (no Fc modifications) is fitted with GraphPad Prism (Sunnyvale, CA) four parameter curve fitting program. The relative affinity of the variant vs. the wild type is estimated by dividing the equivalent ng/ml wild type concentration at the appropriate concentration.

[0472] In addition, the variants are tested directly in Fc effector bioassays (Promega) following manufacturer's directions. These assays include FcγRIIa-H ADCP Bioassay (Promega cat #G9901), ADCC Reporter Bioassays, FcγRIIIa F Variant (Promega, cat #G9798), ADCC Reporter Bioassays, FcγRIIIa V Variant (Promega, cat. #G7015). The variants are tested both as monomeric Ig and as small immune complexes (ICs) by using an anti-hu Ig antibody to form small ICs.

[0473] A Europium based ADCC assay is performed. Briefly, peripheral blood lymphocytes (PBLs) are isolated by Ficoll Paque Plus gradient centrifugation. The PBLs are collected, washed with RPMI1640, 10% FCS and resuspended in cell culture medium. The cells are diluted to 2.5 x 10^6 cells/ml. Target cells are labelled with BADTA (2,2':6',2''-terpyridine-6,6''-dicarboxylic acid acetoxymethylester): Cells are harvested by adding Accutase (Millipore), washed once and diluted to 1 x 10^6 cells/ml. Next, 2.5 uL BADTA is added per 1 x 10^6 cells and incubated for 35 min at 37°C with 5% CO_2. After labelling the cells are diluted with 10 ml culture medium, centrifuged at 200 x g for 10 min and supernatant aspirated. This step is repeated 3X with culture medium/2 mM Probenicid and the sample is diluted to 1 x 10^5 cells/ml, centrifuged at 300 x g for 5 min, supernatant taken off and 50 uL pipetted into the wells intended for the background controls. The final ratio of effector (PBL) to target cells is 25:1.

[0474] Controls include: (1) Background: the 50 uL aliquot, diluted with 100 uL medium, (2) Spontaneous lysis: 50 uL of the labelled target cell suspension plus 100 uL culture medium, incubated 2 h at 37°C, (3) Maximal lysis: 50 uL/well of the labelled target cell suspension plus 100 uL Triton X-100 (0.5% in PBS) incubated 2 h at 37°C, (4) Lysis control without antibodies: 50 uL/well of the labelled target cell suspension and 50 uL culture medium plus 50 uL of effector cells incubated 2 h at 37°C, (5) Lysis control without effector cells: 50 uL/well of the labelled target cell suspension; add 50 uL culture medium plus antibody at highest concentration used and incubate 2 h at 37°C.
At the end of the incubation period the 96 well plate is centrifuged at 100 rpm. 20 uL of each supernatant is transferred into an OptiPlate HTRF-96 (Packard) and 200 uL Europium solution is added and incubated for 15 min on a shaker. Fluorescence is measured as for time resolved fluorescence and spontaneous release and specific release are calculated.

[0475] A CDC assay is performed. Briefly, target cells are washed and diluted to 1 x 10^5 cells/ml and 100 uL/well (10^4 cells) are added to a 96-well flat bottom microtiter plate. A titration curve of the test antibody is created using serial dilutions, beginning at 1 ug/mL. Antibody is added to the plate, mixed gently, and is then placed at 37°C/5% CO2 incubator

for 30 min. Next, 25 uL freshly dissolved baby rabbit complement (Cedarlane CL3441, 1 ml lyophilized, dilute freshly in 4 ml double distilled water) is added, mixed gently, and the plate is incubated at 37°C/5% CO2 incubator for 30 min. After the incubation period 50 uL supernatant is taken off and 100 uL Cell Titer Glo. reagent (Promega Corp.) is added to the remaining 100 uL supernatant. The plate is placed on an orbital shaker for 2 min, 100 uL/well is transferred into a black luminescence microtiter plate (Costar) and luminescence is measured.

Controls included: (1) medium control (target cells plus 50 uL medium), (2) maximal lysis control (target cells plus 50 uL 0.5% Triton X-100), (3) complement control (target cells plus 25 uL medium plus 25 uL complement).

Example 11: Characterization Of Potency And Species Selectivity In Whole Blood Assay

[0476] The relative potency of a panel of candidate antibodies was first assessed by determining the inhibition of interferon gamma release in human blood using the antibodies at 1 and 10 nM. All of the antibodies displayed potent activity, with A219 appearing to be one of the most potent candidates (**Table 13**).

Table 13.

Clone	% Inhibition at 1 nM Ig	% Inhibition at 10 nM Ig
A147	51.3	72.4
A212	46.8	71.2
A213	48.6	69.8
A217	46.0	72.2
A219	59.8	75.2
A220	36.9	63.2

[0477] Next, three of the variants were characterized for inhibition of interferon gamma release in human blood using multiple human blood donors and testing the antibodies across a broader range of concentrations (0.01 – 100 nM). Representative inhibition profiles of variants A212, A213 and A219 are shown in **FIG 8**. The mean IC50 values for these variants, and a control antibody termed 1D1, for the inhibition of interferon gamma release from multiple human donors is shown in **Table 14**.

Table 14.

Clone	Mean	SD
A212	51.3	72.4
A213	46.8	71.2
A219	48.6	69.8
1D1	46.0	72.2

Example 12: In Vivo Assessment Of Anti-Tl1a Efficacy

[0478] The efficacy of anti-TL1A antibodies in animal models of colitis is performed. Anti-TL1A antibodies are tested in rodent models of acute colitis induced by intrarectal administration of di- or tri-nitrobenzenesulfonic acid (D/TNBS) or oxazolone, and chronic colitis induced by administration of DSS in drinking water or transfer of $CD45RB^{hi}$ T cells. DNBS and oxazolone induce localized ulceration and inflammation. DSS administration induces robust generalized inflammation of the intestinal tract characterized by erosive lesions and inflammatory infiltrate. Symptoms of all these models usually include diarrhea, occult blood, weight loss and occasionally rectal prolapse. In a prophylactic model, antibody treatment begins at the start of administration of the colitis-inducing compound. In a therapeutic model, antibody treatment begins several days after commencement of induction. The effect of the treatment on weight, stool consistency and occult blood, as well as microscopic effects on epithelial integrity and degree of inflammatory infiltrate is determined. Daily clinical scoring is performed based on stool consistency and presence of occult blood giving a disease activity index (DAI) score.

Example 13: Phase I Clinical Trial

[0479] A phase 1 clinical trial is performed to evaluate the safety, tolerability, pharmacokinetics and pharmacodynamics of an anti-TL1A antibody from Table 20 on subjects having Crohn's disease (CD).

[0480] **Single ascending dose (SAD) arms:** Subjects in each group (subjects are grouped based on the presence of a genotype comprising at least one, and preferably three, polymorphism(s) selected from **Table 1** and subjects without the presence of the genotype) receive either a single dose of the antibody or a placebo. Exemplary doses are 1, 3, 10, 30, 100, 300, 600 and 800 mg of antibody. Safety monitoring and PK assessments are performed for a predetermined time. Based on evaluation of the PK data, and if the antibody is deemed to be well tolerated, dose escalation occurs, either within the same groups or a further group of healthy subjects. Dose escalation continues until the maximum dose has been attained unless predefined maximum exposure is reached or intolerable side effects become apparent.

[0481] **Multiple ascending dose (MAD) arms:** Subjects in each group (subjects are grouped based on the same criteria as above) receive multiple doses of the antibody or a placebo. The dose levels and dosing intervals are selected as those that are predicted to be safe from the SAD data. Dose levels and dosing frequency are chosen to achieve therapeutic drug levels within the systemic circulation that are maintained at steady state for several days

to allow appropriate safety parameters to be monitored. Samples are collected and analyzed to determination PK profiles.

[0482] **Inclusion Criteria:** Healthy subjects of non-childbearing potential between the ages of 18 and 55 years. Healthy is defined as no clinically relevant abnormalities identified by a detailed medical history, full physical examination, including blood pressure and pulse rate measurement, 12 lead ECG and clinical laboratory tests. Female subjects of non-childbearing potential must meet at least one of the following criteria: (1) achieved postmenopausal status, defined as: cessation of regular menses for at least 12 consecutive months with no alternative pathological or physiological cause; and have a serum follicle stimulating hormone (FSH) level within the laboratory's reference range for postmenopausal females; (2) have undergone a documented hysterectomy and/or bilateral oophorectomy; (3) have medically confirmed ovarian failure. All other female subjects (including females with tubal ligations and females that do NOT have a documented hysterectomy, bilateral oophorectomy and/or ovarian failure) will be considered to be of childbearing potential. Body Mass Index (BMI) of 17.5 to 30.5 kg/m2; and a total body weight >50 kg (110 lbs). Evidence of a personally signed and dated informed consent document indicating that the subject (or a legal representative) has been informed of all pertinent aspects of the study.

[0483] Two groups of CD patients are selected: patients having the genotype described herein, and patients without the genotype. For example, the genotype may comprise rs6478109, rs56124762, and rs1892231; rs6478109, rs56124762, and rs16901748; rs6478109, rs1892231, and rs16901748; rs56124762, rs1892231, and rs16901748; rs6478109, rs2070558, and rs1892231; rs6478109, rs2070558, and rs16901748; rs6478109, rs1892231, and rs16901748; rs2070558, rs1892231, and rs16901748; rs6478109, rs2070561, and rs1892231; rs6478109, rs2070561 , and rs16901748; rs6478109, rs1892231, and rs16901748; rs2070561, rs1892231, and rs16901748; rs6478109, rs7935393, and rs1892231; rs6478109, rs7935393, and rs9806914; rs6478109, rs7935393, and rs7278257; rs6478109, rs7935393, and rs2070557; rs6478109, rs1892231, and rs9806914; rs6478109, rs1892231, and rs7278257; rs6478109, rs1892231, and rs2070557; rs6478109, rs9806914, and rs7278257; rs6478109, rs9806914, and rs2070557; rs6478109, rs7278257, and rs2070557; rs7935393, rs1892231, and rs9806914; rs7935393, rs1892231, and rs7278257; rs7935393, rs1892231, and rs2070557; rs7935393, rs9806914, and rs7278257; rs7935393, rs9806914, and rs2070557; rs7935393, rs7278257, and rs2070557; rs1892231, rs9806914, and rs7278257; rs1892231, rs9806914, and rs2070557; rs1892231, rs7278257, and rs2070557; or rs9806914, rs7278257, and rs2070557.

[0484] **Exclusion Criteria:** Evidence or history of clinically significant hematological, renal, endocrine, pulmonary, gastrointestinal, cardiovascular, hepatic, psychiatric, neurologic, or allergic disease (including drug allergies, but excluding untreated, asymptomatic, seasonal allergies at time of dosing). Subjects with a history of or current positive results for any of the following serological tests: Hepatitis B surface antigen (HBsAg), Hepatitis B core antibody (HBcAb), anti-Hepatitis C antibody (HCV Ab) or human immunodeficiency virus (HIV). Subjects with a history of allergic or anaphylactic reaction to a therapeutic drug. Treatment with an investigational drug within 30 days (or as determined by the local requirement, whichever is longer) or 5 half-lives or 180 days for biologics preceding the first dose of study medication. Pregnant females; breastfeeding females; and females of childbearing potential.

[0485] **Primary Outcome Measures:** Incidence of dose limiting or intolerability treatment related adverse events (AEs) [Time Frame: 12 weeks]. Incidence, severity and causal relationship of treatment emergent AEs (TEAEs) and withdrawals due to treatment emergent adverse events [Time Frame: 12 weeks]. Incidence and magnitude of abnormal laboratory findings [Time Frame: 12 weeks]. Abnormal and clinically relevant changes in vital signs, blood pressure (BP) and electrocardiogram (ECG) parameters [Time Frame: 12 weeks].

[0486] **Secondary Outcome Measures:** Single Ascending Dose: Maximum Observed Plasma Concentration (Cmax) [Time Frame: 12 weeks]. Single Ascending Dose: Time to Reach Maximum Observed Plasma Concentration (Tmax) [Time Frame: 12 weeks]. Single Ascending Dose: Area under the plasma concentration-time profile from time zero to 14 days (AUC14 days) [Time Frame: 12 weeks]. Single Ascending Dose: Area under the plasma concentration-time profile from time zero extrapolated to infinite time (AUCinf) [Time Frame: 12 weeks]. Single Ascending Dose: Area under the plasma concentration-time profile from time zero to the time of last quantifiable concentration (AUClast) [Time Frame: 12 weeks]. Single Ascending Dose: Dose normalized maximum plasma concentration (Cmax[dn]) [Time Frame: 12 weeks]. Single Ascending Dose: Dose normalized area under the plasma concentration-time profile from time zero extrapolated to infinite time (AUCinf[dn]) [Time Frame: 12 weeks]. Single Ascending Dose: Dose normalized area under the plasma concentration-time profile from time zero to the time of last quantifiable concentration (AUClast[dn]) [Time Frame: 12 weeks]. Single Ascending Dose: Plasma Decay Half-Life (t1/2) [Time Frame: 12 weeks]. Plasma decay half-life is the time measured for the plasma concentration to decrease by one half. Single Ascending Dose: Mean residence time (MRT) [Time Frame: 12 weeks]. Single Ascending Dose: Volume of

Distribution at Steady State (Vss) [Time Frame: 6 weeks]. Volume of distribution is defined as the theoretical volume in which the total amount of drug would need to be uniformly distributed to produce the desired blood concentration of a drug. Steady state volume of distribution (Vss) is the apparent volume of distribution at steady-state. Single Ascending Dose: Systemic Clearance (CL) [Time Frame: 6]. CL is a quantitative measure of the rate at which a drug substance is removed from the body.

[0487] Multiple Ascending Dose First Dose: Maximum Observed Plasma Concentration (Cmax) [Time Frame: 12 weeks]. Multiple Ascending Dose First Dose: Time to Reach Maximum Observed Plasma Concentration (Tmax) [Time Frame: 12 weeks]. Multiple Ascending Dose First Dose: Area under the plasma concentration-time profile from time zero to time τ, the dosing interval where τ=2 weeks (AUCτ) [Time Frame: 12 weeks]. Multiple Ascending Dose First Dose: Dose normalized maximum plasma concentration (Cmax[dn]) [Time Frame: 12 weeks]. Multiple Ascending Dose First Dose: Dose normalized Area under the plasma concentration-time profile from time zero to time τ, the dosing interval where τ=2 weeks (AUCτ [dn]) [Time Frame: 12 weeks]. Plasma Decay Half-Life (t1/2) [Time Frame: 12 weeks]. Plasma decay half-life is the time measured for the plasma concentration to decrease by one half. Multiple Ascending Dose First Dose: Mean residence time (MRT) [Time Frame: 12 weeks]. Apparent Volume of Distribution (Vz/F) [Time Frame: 12 weeks]. Volume of distribution is defined as the theoretical volume in which the total amount of drug would need to be uniformly distributed to produce the desired plasma concentration of a drug. Apparent volume of distribution after oral dose (Vz/F) is influenced by the fraction absorbed. Multiple Ascending Dose First Dose: Volume of Distribution at Steady State (Vss) [Time Frame: 12 weeks]. Volume of distribution is defined as the theoretical volume in which the total amount of drug would need to be uniformly distributed to produce the desired blood concentration of a drug. Steady state volume of distribution (Vss) is the apparent volume of distribution at steady-state. Multiple Ascending Dose First Dose: Apparent Oral Clearance (CL/F) [Time Frame: 12 weeks]. Clearance of a drug is a measure of the rate at which a drug is metabolized or eliminated by normal biological processes. Clearance obtained after oral dose (apparent oral clearance) is influenced by the fraction of the dose absorbed. Clearance is estimated from population pharmacokinetic (PK) modeling. Drug clearance is a quantitative measure of the rate at which a drug substance is removed from the blood. Multiple Ascending Dose First Dose: Systemic Clearance (CL) [Time Frame: 12 weeks]. CL is a quantitative measure of the rate at which a drug substance is removed from the body.

[0488] Multiple Ascending Dose Multiple Dose: Maximum Observed Plasma Concentration (Cmax) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Time to Reach Maximum Observed Plasma Concentration (Tmax) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Area under the plasma concentration-time profile from time zero to time τ, the dosing interval where τ=2 weeks (AUCτ) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Dose normalized maximum plasma concentration (Cmax[dn]) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Dose normalized Area under the plasma concentration-time profile from time zero to time τ, the dosing interval where τ=2 weeks (AUCτ [dn]) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Plasma Decay Half-Life (t1/2) [Time Frame: 12 weeks]. Plasma decay half-life is the time measured for the plasma concentration to decrease by one half. Multiple Ascending Dose Multiple Dose: Apparent Volume of Distribution (Vz/F) [Time Frame: 12 weeks]. Volume of distribution is defined as the theoretical volume in which the total amount of drug would need to be uniformly distributed to produce the desired plasma concentration of a drug. Apparent volume of distribution after oral dose (Vz/F) is influenced by the fraction absorbed. Multiple Ascending Dose Multiple Dose: Volume of Distribution at Steady State (Vss) [Time Frame: 12 weeks]. Volume of distribution is defined as the theoretical volume in which the total amount of drug would need to be uniformly distributed to produce the desired blood concentration of a drug. Steady state volume of distribution (Vss) is the apparent volume of distribution at steady-state.

[0489] Multiple Ascending Dose Multiple Dose: Apparent Oral Clearance (CL/F) [Time Frame: 12 weeks]. Clearance of a drug is a measure of the rate at which a drug is metabolized or eliminated by normal biological processes. Clearance obtained after oral dose (apparent oral clearance) is influenced by the fraction of the dose absorbed. Clearance was estimated from population pharmacokinetic (PK) modeling. Drug clearance is a quantitative measure of the rate at which a drug substance is removed from the blood. Multiple Ascending Dose Multiple Dose: Systemic Clearance (CL) [Time Frame: 12 weeks]. CL is a quantitative measure of the rate at which a drug substance is removed from the body. Multiple Ascending Dose Multiple Dose: Minimum Observed Plasma Trough Concentration (Cmin) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Average concentration at steady state (Cav) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Observed accumulation ratio (Rac) [Time Frame: 12 weeks]. Multiple Ascending Dose Multiple Dose: Peak to trough fluctuation (PTF) [Time Frame: 12 weeks]. Multiple Ascending Dose Additional Parameter: estimate of bioavailability (F) for subcutaneous

administration at the corresponding intravenous dose [Time Frame: 12 weeks]. Immunogenicity for both Single Ascending Dose and Multiple Ascending Dose: Development of anti-drug antibodies (ADA) [Time Frame: 12 weeks].

Example 14: Phase 1B Clinical Trial

[0490] A phase 1b open label clinical trial is performed to evaluate efficacy of an anti-TL1A antibody on subjects having CD.

[0491] **Arms:** 10 patients positive for genotypes comprising at least one, but preferably three, polymorphism(s) provided in **Table 1** are administered the antibody. 10 patients negative for the genotype are administered the antibody. 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.

[0492] For example, the genotypes may comprise rs6478109, rs56124762, and rs1892231; rs6478109, rs56124762, and rs16901748; rs6478109, rs1892231, and rs16901748; rs56124762, rs1892231, and rs16901748; rs6478109, rs2070558, and rs1892231; rs6478109, rs2070558, and rs16901748; rs6478109, rs1892231, and rs16901748; rs2070558, rs1892231, and rs16901748; rs6478109, rs2070561, and rs1892231; rs6478109, rs2070561, and rs16901748; rs6478109, rs1892231, and rs16901748; rs2070561, rs1892231, and rs16901748; rs6478109, rs7935393, and rs1892231; rs6478109, rs7935393, and rs9806914; rs6478109, rs7935393, and rs7278257; rs6478109, rs7935393, and rs2070557; rs6478109, rs1892231, and rs9806914; rs6478109, rs1892231, and rs7278257; rs6478109, rs1892231, and rs2070557; rs6478109, rs9806914, and rs7278257; rs6478109, rs9806914, and rs2070557; rs6478109, rs7278257, and rs2070557; rs7935393, rs1892231, and rs9806914; rs7935393, rs1892231, and rs7278257; rs7935393, rs1892231, and rs2070557; rs7935393, rs9806914, and rs7278257; rs7935393, rs9806914, and rs2070557; rs7935393, rs7278257, and rs2070557; rs1892231, rs9806914, and rs7278257; rs1892231, rs9806914, and rs2070557; rs1892231, rs7278257, and rs2070557; or rs9806914, rs7278257, and rs2070557.

[0493] **Inclusion Criteria:** Two groups of patients are selected: subject with the genotype described herein, and patients without the genotype.

[0494] **Primary Outcome Measures:** Simple Endoscopic Score for Crohn's Disease (SESCD), Crohn's Disease Activity Index (CDAI), and Patient Reported Outcome (PRO). If risk either positive group shows 50% reduction from baseline, a Phase 2a clinical trial is performed.

[0495] **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 15: Phase 2A Clinical Trial

[0496] A phase 2a clinical trial is performed to evaluate the efficacy of an anti-TL1A antibody in patients with CD. Optionally, the patients are positive for a genotype comprising at least one, but preferably three, polymorphism(s) provided in **Table 1**.

[0497] **Arms:** 40 patients per arm (antibody and placebo arms) are treated with antibody 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 a 40-50% delta between placebo and treated group in primary outcome (50% reduction from baseline in SESCD, CDAI, and PRO).

[0498] **Primary Outcome Measures:** Simple Endoscopic Score for Crohn's Disease (SESCD), Crohn's Disease Activity Index (CDAI), and Patient Reported Outcome (PRO).

[0499] **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 16: Treating Crohn's Disease (CD) in a Subject

[0500] CD is treated in a subject, by first, determining the genotypes of the subject. Optionally, the subject is, or is susceptible to, non-response to the induction of certain therapies such as anti-TNF, steroids, or immunomodulators, or loses response to such therapies after a period of time. 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 of a genotype comprising at least one, but preferably three or four, polymorphism(s) provided in **Table 1.**

[0501] At three polymorphisms comprising rs6478109, rs56124762, and rs1892231; rs6478109, rs56124762, and rs16901748; rs6478109, rs1892231, and rs16901748; rs56124762, rs1892231, and rs16901748; rs6478109, rs2070558, and rs1892231; rs6478109, rs2070558, and rs16901748; rs6478109, rs1892231, and rs16901748; rs2070558, rs1892231, and rs16901748; rs6478109, rs2070561, and rs1892231; rs6478109, rs2070561 , and rs16901748; rs6478109, rs1892231, and rs16901748; rs2070561, rs1892231, and rs16901748; rs6478109, rs7935393, and rs1892231; rs6478109, rs7935393, and rs9806914;

rs6478109, rs7935393, and rs7278257; rs6478109, rs7935393, and rs2070557; rs6478109, rs1892231, and rs9806914; rs6478109, rs1892231, and rs7278257; rs6478109, rs1892231, and rs2070557; rs6478109, rs9806914, and rs7278257; rs6478109, rs9806914, and rs2070557; rs6478109, rs7278257, and rs2070557; rs7935393, rs1892231, and rs9806914; rs7935393, rs1892231, and rs7278257; rs7935393, rs1892231, and rs2070557; rs7935393, rs9806914, and rs7278257; rs7935393, rs9806914, and rs2070557; rs7935393, rs7278257, and rs2070557; rs1892231, rs9806914, and rs7278257; rs1892231, rs9806914, and rs2070557; rs1892231, rs7278257, and rs2070557; or rs9806914, rs7278257, and rs2070557, or any of the above combinations in which a polymorphism is substituted with a proxy polymorphism, are detected in the sample by Illumina ImmunoArray or polymerase chain reaction (PCR) under standard hybridization conditions. Proxy polymorphisms are identified using linkage disequilibrium with a D'1 value of at least 0.8, or an r^2 value of at least 0.85. In some cases, the proxy polymorphism is additionally selected based on an independent association between the polymorphism and a relevant clinical phenotype of CD (e.g., stricturing and penetrating disease) In this example, one or more primer pairs described herein and/or nucleic acid probes comprising nucleic acid sequences capable of hybridizing the nucleic acid sequences, or their reverse compliments, provided in SEQ ID NOS: 2001-2041, or 2057-2059, are used.

[0502] A TNFSF15 profile is generated that correlates the presence or absence of the genotypes with a positive, negative or indeterminate result for a therapeutic response to treatment with an inhibitor of TL1A activity or expression with a positive predictive value and specificity of at least or about 70%.

[0503] The TNFSF15 profile of the subject is positive. Based on the TNFSF15 profile of the CD patient, a doctor determines that the subject is suitable for treatment with the inhibitor of TL1A activity or expression.. A therapeutically effective amount of an inhibitor of TL1A activity or expression is administered to the subject with the positive TNFSF15 profile. The inhibitor of TL1A activity or expression may comprise an anti-TL1A antibody. The anti-TL1A antibody may be an antibody listed in Table 20. The anti-TL1A antibody may be a neutralizing anti-TL1A antibody.

Table 15. CDR Amino Acid Sequences

SEQ ID NO	Description	Sequence
1	P HCDR1	GFDIQDTYMH
601	P HCDR1	DTYMH
602	P HCDR1	KYDIN
603	P HCDR1	GFEIQDTYMH
604	P HCDR1	GFDPQDTYMH
605	P HCDR1	GFDVQDTYMH
606	P HCDR1	GFDIGDTYMH
607	P HCDR1	GFDISDTYMH
608	P HCDR1	GFDIVDTYMH
609	P HCDR1	GFDIQDAYMH
610	P HCDR1	GFDIQDSYMH
611	P HCDR1	GFDIQDTFMH
612	P HCDR1	GFDIQDTYIH
613	P HCDR1	GFDLQDTYMH
614	P HCDR1	GFDIQDTYLH
615	P HCDR1	GFDIGDTFIH
616	P HCDR1	GFDIGDTFMH
617	P HCDR1	GFDIGDTYIH
618	P HCDR1	GFDIQDTFIH
619	P HCDR1	GFDIQDTFMH
620	P HCDR1	GFDIQDTYIH
621	P HCDR1	GFDISDTFIH
622	P HCDR1	GFDISDTFMH
623	P HCDR1	GFDISDTYIH
624	P HCDR1	GFDISDTYMH
625	P HCDR1	GFDIVDTFIH
626	P HCDR1	GFDIVDTFMH
627	P HCDR1	GFDIVDTYIH
628	P HCDR1	GFDPGDTFIH
629	P HCDR1	GFDPGDTFMH
630	P HCDR1	GFDPGDTYIH
631	P HCDR1	GFDPGDTYMH
632	P HCDR1	GFDPQDTFIH
633	P HCDR1	GFDPQDTFMH
634	P HCDR1	GFDPQDTYIH
635	P HCDR1	GFDPQDTYMH
636	P HCDR1	GFDPSDTFIH
637	P HCDR1	GFDPSDTFMH
638	P HCDR1	GFDPSDTYIH
639	P HCDR1	GFDPSDTYMH
640	P HCDR1	GFDPVDTFIH
641	P HCDR1	GFDPVDTFMH
642	P HCDR1	GFDPVDTYIH
643	P HCDR1	GFDPVDTYMH

644	P HCDR1	GFDVGDTFIH
645	P HCDR1	GFDVGDTFMH
646	P HCDR1	GFDVGDTYIH
647	P HCDR1	GFDVGDTYMH
648	P HCDR1	GFDVQDTFIH
649	P HCDR1	GFDVQDTFMH
650	P HCDR1	GFDVQDTYIH
651	P HCDR1	GFDVSDTFIH
652	P HCDR1	GFDVSDTFMH
653	P HCDR1	GFDVSDTYIH
654	P HCDR1	GFDVSDTYMH
655	P HCDR1	GFDVVDTFIH
656	P HCDR1	GFDVVDTFMH
657	P HCDR1	GFDVVDTYIH
658	P HCDR1	GFDVVDTYMH
659	P HCDR1	GFEIGDTFIH
660	P HCDR1	GFEIGDTFMH
661	P HCDR1	GFEIGDTYIH
662	P HCDR1	GFEIGDTYMH
663	P HCDR1	GFEIQDTFIH
664	P HCDR1	GFEIQDTFMH
665	P HCDR1	GFEIQDTYIH
666	P HCDR1	GFEIQDTYMH
667	P HCDR1	GFEISDTFIH
668	P HCDR1	GFEISDTFMH
669	P HCDR1	GFEISDTYIH
670	P HCDR1	GFEISDTYMH
671	P HCDR1	GFEIVDTFIH
672	P HCDR1	GFEIVDTFMH
673	P HCDR1	GFEIVDTYIH
674	P HCDR1	GFEIVDTYMH
675	P HCDR1	GFEPGDTFIH
676	P HCDR1	GFEPGDTFMH
677	P HCDR1	GFEPGDTYIH
678	P HCDR1	GFEPGDTYMH
679	P HCDR1	GFEPQDTFIH
680	P HCDR1	GFEPQDTFMH
681	P HCDR1	GFEPQDTYIH
682	P HCDR1	GFEPQDTYMH
683	P HCDR1	GFEPSDTFIH
684	P HCDR1	GFEPSDTFMH
685	P HCDR1	GFEPSDTYIH
686	P HCDR1	GFEPSDTYMH
687	P HCDR1	GFEPVDTFIH
688	P HCDR1	GFEPVDTFMH
689	P HCDR1	GFEPVDTYIH
690	P HCDR1	GFEPVDTYMH
691	P HCDR1	GFEVGDTFIH

692	P HCDR1	GFEVGDTFMH
693	P HCDR1	GFEVGDTYIH
694	P HCDR1	GFEVGDTYMH
695	P HCDR1	GFEVQDTFIH
696	P HCDR1	GFEVQDTFMH
697	P HCDR1	GFEVQDTYIH
698	P HCDR1	GFEVQDTYMH
699	P HCDR1	GFEVSDTFIH
700	P HCDR1	GFEVSDTFMH
701	P HCDR1	GFEVSDTYIH
702	P HCDR1	GFEVSDTYMH
703	P HCDR1	GFEVVDTFIH
704	P HCDR1	GFEVVDTFMH
705	P HCDR1	GFEVVDTYIH
706	P HCDR1	GFEVVDTYMH
707	P HCDR1	$GFX_1X_2X_3DX_4X_5X_6H$ X1 = D or E X2 = I, L, P, or V X3 = G, Q, S, or V X4 = A, S, T X5 = F or Y X6 = I, L, or M
708	P HCDR1	$GFX_1X_2X_3DTX_4X_5H$ X_1 = D, OR E X_2 = I, P, OR V X_3 = G, Q, S, OR V X_4 = F, OR Y X_5 = I, OR M
709	M1 HCDR1	GFTFSSYW
710	M2 HCDR1	GGSFTGFY
711	M3 HCDR1	GY(X1)F(X2)(X3)YGIS; X1 = P, S, D, Q, N; X2 = T, R; X3 = N, T, Y, H
712	M3 HCDR1	GYDFTYYGIS
713	M4 HCDR1	SRSYYWG
714	M5 HCDR1	TSNMGVV
715	M6 HCDR1	LYGMN
716	M6 HCDR1	NYGMN
717	M7 HCDR1	GYTFTSSWMH
718	M8 HCDR1	GYTFTSYDIN
719	M9 HCDR1	SYFWS
720	M10 HCDR1	GYYWN
721	M11 HCDR1	GFTFSTYG
722	M12 HCDR1	TYGMS
2	P HCDR2	RIDPASGHTKYDPKFQV
3	P HCDR2	RIEPASGHIKYDPKFQG
4	P HCDR2	RIDPASGHIKYDPKFQG
5	P HCDR2	RIEPASGHIKYDPKFQV
723	P HCDR2	WIFPGDGRTDYNEKFKG

724	P HCDR2	RLDPASGHTK
725	P HCDR2	RIEPASGHTK
726	P HCDR2	RIDPESGHTK
727	P HCDR2	RIDPASGHTK
728	P HCDR2	RIDPAGGHTK
729	P HCDR2	RIDPASAHTK
730	P HCDR2	RIDPASGHIK
731	P HCDR2	RIDPASGHLK
732	P HCDR2	RIDPASGHVK
733	P HCDR2	YDPKFQV
734	P HCDR2	IDPKFQV
735	P HCDR2	LDPKFQV
736	P HCDR2	MDPKFQV
737	P HCDR2	SDPKFQV
738	P HCDR2	TDPKFQV
739	P HCDR2	VDPKFQV
740	P HCDR2	YIPKFQV
741	P HCDR2	YNPKFQV
742	P HCDR2	YRPKFQV
743	P HCDR2	YSPKFQV
744	P HCDR2	YDPKFRV
745	P HCDR2	YDPKFQA
746	P HCDR2	YDPKFQD
747	P HCDR2	YDPKFQE
748	P HCDR2	YDPKFQG
749	P HCDR2	YDPKFQH
750	P HCDR2	YDPKFQK
751	P HCDR2	YDPKFQL
752	P HCDR2	YDPKFQM
753	P HCDR2	YDPKFQN
754	P HCDR2	YDPKFQP
755	P HCDR2	YDPKFQR
756	P HCDR2	YDPKFQS
757	P HCDR2	YDPKFQT
758	P HCDR2	RIEPASGHIKYDPKFQG
759	P HCDR2	RIEPASGHIKYSPKFQG
760	P HCDR2	RIEPASGHVKYSPKFQV
761	P HCDR2	RIEPASGHVKYDPKFQT
762	P HCDR2	RIDPASGHIKYDPKFQK
763	P HCDR2	RIDPASGHVKIDPKFQV
764	P HCDR2	RIDPASGHLKYDPKFQV
765	P HCDR2	RIDPASGHLKYDPKFQR
766	P HCDR2	RIDPASGHLKYDPKFQN
767	P HCDR2	RIEPASGHLKYDPKFQE
768	P HCDR2	PASGH
769	P HCDR2	RIDPASGHTKYDPKFQV
770	P HCDR2	RIDPASGHLKYDPKFQG
771	P HCDR2	RIDPASGHTKYDPKFQG

772	P HCDR2	RIDPASGHSKYDPKFQV
773	P HCDR2	RIDPASGHYKYDPKFQV
774	P HCDR2	$RX_1X_2PX_3X_4X_5HX_6KX_7X_8PKFX_9X_{10}$ X1 = I or L X2 = D or E X3 = A or E X4 = G or S X5 = A or G X6 = I, L, T, or V X7 = I, L, M, S, T, V, or Y X8 = D, I, N, R, or S X9 = Q or R X10 = A, D, E, G, H, K, L, M, N, P, R, S, T, or V
775	M1 HCDR2	IKEDGSEK
776	M2 HCDR2	INHRGNT
777	M3 HCDR2	WIS(X1)YNG(X2)(X3)(X4) YA(X5)(X6)(X7)QG; X1 = T, P, S, A; X2 = N, G, V, K, A; X3 = T, K; X4 = H, N; X5 = Q, R; X6 = K, M; X7 = L, H
778	M3 HCDR2	WISTYNGNTHYARMLQG
779	M4 HCDR2	SIYYNGRTYYNPSLKS
780	M5 HCDR2	HILWDDREYSNPALKS
781	M6 HCDR2	WINTYTGEPTYADDFKG
782	M7 HCDR2	IHPNSGGT
783	M8 HCDR2	WLNPNSGXTG; X = N, Y
784	M9 HCDR2	YIYYSGNTKYNPSLKS
785	M10 HCDR2	EINHAGNTNYNPSLKS
786	M11 HCDR2	ISGTGRTT
787	M12 HCDR2	WMNTYSGVTTYADDFKG
6	P HCDR3	SGGLPDV
7	P HCDR3	ARSGGLPDV
8	P HCDR3	SGGLPDW
9	P HCDR3	ARSGGLPDW
788	P HCDR3	YGPAMDY
789	P HCDR3	LGGLPDV
790	P HCDR3	SAGLPDV
791	P HCDR3	SGGAPDV
792	P HCDR3	SGGMPDV
793	P HCDR3	SGGLPEV
794	P HCDR3	SGGLPDK
795	P HCDR3	SGGLPDM
796	P HCDR3	SGGLPDQ
797	P HCDR3	SGGLPDR
798	P HCDR3	SGGLPDS
799	P HCDR3	SGGLPDT
800	P HCDR3	SGGLPDH
801	P HCDR3	SGGLPDF
802	P HCDR3	SGGSPDV
803	P HCDR3	ARSGGLPDM

804	P HCDR3	ARSGGLPDK
805	P HCDR3	SGGLPD
806	P HCDR3	ARSGGLPDF
807	P HCDR3	ARSGGLPDL
808	P HCDR3	SGGLPDE
809	P HCDR3	SGGLPDI
810	P HCDR3	SGGLPDK
811	P HCDR3	SGGLPDL
812	P HCDR3	SGGLPDM
813	P HCDR3	SGGLPDQ
814	P HCDR3	SGGLPDT
815	P HCDR3	SGGLPDW
816	P HCDR3	SGGLPDY
817	P HCDR3	SGGMPDE
818	P HCDR3	SGGMPDI
819	P HCDR3	SGGMPDK
820	P HCDR3	SGGMPDL
821	P HCDR3	SGGMPDM
822	P HCDR3	SGGMPDQ
823	P HCDR3	SGGMPDT
824	P HCDR3	SGGMPDV
825	P HCDR3	SGGMPDW
826	P HCDR3	SGGMPDY
827	P HCDR3	$X_1X_2GX_3PX_4X_5$ X1 = L or S X2 = A or G X3 = A, L, or M X4 = D or E X5 = K, M, Q, R, S, T, V, or W
828	P HCDR3	$SGGX_1PDX_2$ X_1 = L, OR M X_2 = E, I, K, L, M, Q, T, V, W, OR Y
829	M1 HCDR3	AREDYDSYYKYGMDV
830	M2 HCDR3	ASPFYDFWSGSDY
831	M3 HCDR3	ENYYGSG(X1)(X2)R GGMD(X3); X1 = S, A; X2 = Y, P; X3 = V, A, G
832	M3 HCDR3	ENYYGSGAYRGGMDV
833	M4 HCDR3	EDYGDYGAFDI
834	M5 HCDR3	MSRNYYGSSYVMDY
835	M6 HCDR3	DTAMDYAMAY
836	M6 HCDR3	DYGKYGDYYAMDY
837	M7 HCDR3	ARGDYYGYVSWFAY
838	M8 HCDR3	EVPETAAFEY
839	M9 HCDR3	ETGSYYGFDY
840	M10 HCDR3	GYCRSTTCYFDY
841	M11 HCDR3	TKERGDYYYGVFDY
842	M12 HCDR3	EGYVFDDYYATDY
10	P LCDR1	RASSSVSYMY

843	P LCDR1	RSSQTIVHSNGDTYLD
844	P LCDR1	GASSSVSYMY
845	P LCDR1	WASSSVSYMY
846	P LCDR1	RASSSVIYMY
847	P LCDR1	RASSSVSFMY
848	P LCDR1	RASSSVSYLY
849	P LCDR1	RASSSVSYMR
850	P LCDR1	GASSSVSYMY
851	P LCDR1	ASSSVSYMY
852	P LCDR1	X_1ASSSV$X_2X_3X_4X_5$ X1 = G, R, or W X2 = I or S X3 = F or Y X4 = L or M X5 = R or Y
853	M1 LCDR1	QSILYSSNNKNY
854	M2 LCDR1	QSLVHSDGNTY
855	M3 LCDR1	RASQSVSSYLA
856	M4 LCDR1	RASQGISSALA
857	M5 LCDR1	SASSSVNYMH
858	M6 LCDR1	KSSQNIVHSDGNTYLE
859	M6 LCDR1	RSSQSIVHSNGNTYLD
860	M7 LCDR1	QNINVL
861	M8 LCDR1	TSSSSDIGA(X1) (X2)GV(X3); X1 = G, A; X2 = L, S, Q; X3 = H, L
862	M9 LCDR1	RASQSINNYLN
863	M10 LCDR1	RASQSVRSSYLA
864	M11 LCDR1	QTISSW
865	M12 LCDR1	RSSQNIVHSDGNTYLE
11	P LCDR2	ATSNLAS
866	P LCDR2	KVSNRFS
867	P LCDR2	AKSNLAS
868	P LCDR2	ATPNLAS
869	P LCDR2	ATENLAS
870	P LCDR2	ATSLLAS
871	P LCDR2	ATSPLAS
872	P LCDR2	ATSNLTS
873	P LCDR2	A$X_1X_2X_3$LX_4S X1 = K or T X2 = E, P, or S X3 = L, N, or P X4 = A or T
874	M1 LCDR2	WAS
875	M2 LCDR2	KIS
876	M3 LCDR2	DASNRAT
877	M4 LCDR2	DASSLES
878	M5 LCDR2	STSNLAS

879	M6 LCDR2	KVSNRFS
880	M7 LCDR2	KAS
881	M8 LCDR2	GYYNRPS
882	M9 LCDR2	AASSLQS
883	M10 LCDR2	GASSRAT
884	M11 LCDR2	AAS
885	M12 LCDR2	KVSNRFS
12	P LCDR3	QQWEGNPRT
13	P LCDR3	QQWKGNPRT
14	P LCDR3	QQWSGNPRT
15	P LCDR3	QQWSRNPRT
886	P LCDR3	FQGSHVPYT
887	P LCDR3	HQWSGNPRT
888	P LCDR3	NQWSGNPRT
889	P LCDR3	SQWSGNPRT
890	P LCDR3	QQSSGNPRT
891	P LCDR3	QQWDGNPRT
892	P LCDR3	QQWHGNPRT
893	P LCDR3	QQWNGNPRT
894	P LCDR3	QQWQGNPRT
895	P LCDR3	QQWVGNPRT
896	P LCDR3	QQWSANPRT
897	P LCDR3	QQWSDNPRT
898	P LCDR3	QQWSQNPRT
899	P LCDR3	QQWSSNPRT
900	P LCDR3	QQWSGNPRS
901	P LCDR3	QQFSGNPRT
902	P LCDR3	QQHSGNPRT
903	P LCDR3	QQISGNPRT
904	P LCDR3	QQPSGNPRT
905	P LCDR3	QQRSGNPRT
906	P LCDR3	QQYSGNPRT
907	P LCDR3	QQWSGHPRT
908	P LCDR3	QQWSGLPRT
909	P LCDR3	QQWSGQPRT
910	P LCDR3	QQWSGSPRT
911	P LCDR3	QQWSGTPRT
912	P LCDR3	QQWSGMPRT
913	P LCDR3	QQWSGFPRT
914	P LCDR3	QQWSGKPRT
915	P LCDR3	QQWSGRPRT
916	P LCDR3	QQWSGDPRT
917	P LCDR3	QQWAGNPRT
918	P LCDR3	QQWYGNPRT
919	P LCDR3	QQWFGNPRT
920	P LCDR3	QQWQGNPRT
921	P LCDR3	GNPRT
922	P LCDR3	SQWSGNPRT

923	P LCDR3	QQWSGNPRS
924	P LCDR3	QQWSGTPRT
925	P LCDR3	QQWSGDPRT
926	P LCDR3	QQWSGFPRT
927	P LCDR3	QQWSGKPRT
928	P LCDR3	QQWSGRPRT
929	P LCDR3	QQWSGSPRT
930	P LCDR3	QQWDADPRT
931	P LCDR3	QQWDAFPRT
932	P LCDR3	QQWDAKPRT
933	P LCDR3	QQWDANPRT
934	P LCDR3	QQWDARPRT
935	P LCDR3	QQWDASPRT
936	P LCDR3	QQWDATPRT
937	P LCDR3	QQWDGDPRT
938	P LCDR3	QQWDGFPRT
939	P LCDR3	QQWDGKPRT
940	P LCDR3	QQWDGNPRT
941	P LCDR3	QQWDGRPRT
942	P LCDR3	QQWDGSPRT
943	P LCDR3	QQWDGTPRT
944	P LCDR3	QQWEADPRT
945	P LCDR3	QQWEAFPRT
946	P LCDR3	QQWEAKPRT
947	P LCDR3	QQWEANPRT
948	P LCDR3	QQWEARPRT
949	P LCDR3	QQWEASPRT
950	P LCDR3	QQWEATPRT
951	P LCDR3	QQWEGDPRT
952	P LCDR3	QQWEGFPRT
953	P LCDR3	QQWEGKPRT
954	P LCDR3	QQWEGRPRT
955	P LCDR3	QQWEGSPRT
956	P LCDR3	QQWEGTPRT
957	P LCDR3	QQWHADPRT
958	P LCDR3	QQWHAFPRT
959	P LCDR3	QQWHAKPRT
960	P LCDR3	QQWHANPRT
961	P LCDR3	QQWHARPRT
962	P LCDR3	QQWHASPRT
963	P LCDR3	QQWHATPRT
964	P LCDR3	QQWHGDPRT
965	P LCDR3	QQWHGFPRT
966	P LCDR3	QQWHGKPRT
967	P LCDR3	QQWHGNPRT
968	P LCDR3	QQWHGRPRT
969	P LCDR3	QQWHGSPRT
970	P LCDR3	QQWHGTPRT

971	P LCDR3	QQWNADPRT
972	P LCDR3	QQWNAFPRT
973	P LCDR3	QQWNAKPRT
974	P LCDR3	QQWNANPRT
975	P LCDR3	QQWNARPRT
976	P LCDR3	QQWNASPRT
977	P LCDR3	QQWNATPRT
978	P LCDR3	QQWNGDPRT
979	P LCDR3	QQWNGFPRT
980	P LCDR3	QQWNGKPRT
981	P LCDR3	QQWNGNPRT
982	P LCDR3	QQWNGRPRT
983	P LCDR3	QQWNGSPRT
984	P LCDR3	QQWNGTPRT
985	P LCDR3	QQWQADPRT
986	P LCDR3	QQWQAFPRT
987	P LCDR3	QQWQAKPRT
988	P LCDR3	QQWQANPRT
989	P LCDR3	QQWQARPRT
990	P LCDR3	QQWQASPRT
991	P LCDR3	QQWQATPRT
992	P LCDR3	QQWQGDPRT
993	P LCDR3	QQWQGFPRT
994	P LCDR3	QQWQGKPRT
995	P LCDR3	QQWQGRPRT
996	P LCDR3	QQWQGSPRT
997	P LCDR3	QQWQGTPRT
998	P LCDR3	QQWSADPRT
999	P LCDR3	QQWSAFPRT
1000	P LCDR3	QQWSAKPRT
1001	P LCDR3	QQWSANPRT
1002	P LCDR3	QQWSARPRT
1003	P LCDR3	QQWSASPRT
1004	P LCDR3	QQWSATPRT
1005	P LCDR3	NQWDAFPRT
1006	P LCDR3	NQWDAKPRT
1007	P LCDR3	NQWDANPRT
1008	P LCDR3	NQWDARPRT
1009	P LCDR3	NQWDASPRT
1010	P LCDR3	NQWDATPRT
1011	P LCDR3	NQWDGDPRT
1012	P LCDR3	NQWDGFPRT
1013	P LCDR3	NQWDGKPRT
1014	P LCDR3	NQWDGNPRT
1015	P LCDR3	NQWDGRPRT
1016	P LCDR3	NQWDGSPRT
1017	P LCDR3	NQWDGTPRT
1018	P LCDR3	NQWEADPRT

1019	P LCDR3	NQWEAFPRT
1020	P LCDR3	NQWEAKPRT
1021	P LCDR3	NQWEANPRT
1022	P LCDR3	NQWEARPRT
1023	P LCDR3	NQWEASPRT
1024	P LCDR3	NQWEATPRT
1025	P LCDR3	NQWEGDPRT
1026	P LCDR3	NQWEGFPRT
1027	P LCDR3	NQWEGKPRT
1028	P LCDR3	NQWEGNPRT
1029	P LCDR3	NQWEGRPRT
1030	P LCDR3	NQWEGSPRT
1031	P LCDR3	NQWEGTPRT
1032	P LCDR3	NQWHADPRT
1033	P LCDR3	NQWHAFPRT
1034	P LCDR3	NQWHAKPRT
1035	P LCDR3	NQWHANPRT
1036	P LCDR3	NQWHARPRT
1037	P LCDR3	NQWHASPRT
1038	P LCDR3	NQWHATPRT
1039	P LCDR3	NQWHGDPRT
1040	P LCDR3	NQWHGFPRT
1041	P LCDR3	NQWHGKPRT
1042	P LCDR3	NQWHGNPRT
1043	P LCDR3	NQWHGRPRT
1044	P LCDR3	NQWHGSPRT
1045	P LCDR3	NQWHGTPRT
1046	P LCDR3	NQWNADPRT
1047	P LCDR3	NQWNAFPRT
1048	P LCDR3	NQWNAKPRT
1049	P LCDR3	NQWNANPRT
1050	P LCDR3	NQWNARPRT
1051	P LCDR3	NQWNASPRT
1052	P LCDR3	NQWNATPRT
1053	P LCDR3	NQWNGDPRT
1054	P LCDR3	NQWNGFPRT
1055	P LCDR3	NQWNGKPRT
1056	P LCDR3	NQWNGNPRT
1057	P LCDR3	NQWNGRPRT
1058	P LCDR3	NQWNGSPRT
1059	P LCDR3	NQWNGTPRT
1060	P LCDR3	NQWQADPRT
1061	P LCDR3	NQWQAFPRT
1062	P LCDR3	NQWQAKPRT
1063	P LCDR3	NQWQANPRT
1064	P LCDR3	NQWQARPRT
1065	P LCDR3	NQWQASPRT
1066	P LCDR3	NQWQATPRT

1067	P LCDR3	NQWQGDPRT
1068	P LCDR3	NQWQGFPRT
1069	P LCDR3	NQWQGKPRT
1070	P LCDR3	NQWQGNPRT
1071	P LCDR3	NQWQGRPRT
1072	P LCDR3	NQWQGSPRT
1073	P LCDR3	NQWQGTPRT
1074	P LCDR3	NQWSADPRT
1075	P LCDR3	NQWSAFPRT
1076	P LCDR3	NQWSAKPRT
1077	P LCDR3	NQWSANPRT
1078	P LCDR3	NQWSARPRT
1079	P LCDR3	NQWSASPRT
1080	P LCDR3	NQWSATPRT
1081	P LCDR3	NQWSGDPRT
1082	P LCDR3	NQWSGFPRT
1083	P LCDR3	NQWSGKPRT
1084	P LCDR3	NQWSGNPRT
1085	P LCDR3	NQWSGRPRT
1086	P LCDR3	NQWSGSPRT
1087	P LCDR3	NQWSGTPRT
1088	P LCDR3	X_1QW$X_2X_3X_4$PRT X_1 = Q, OR N X_2 = D, E, H, N, Q, OR S X_3 = A, OR G X_4 = D, F, K, N, R, S, OR T
1089	P LCDR3	X_1Q$X_2X_3X_4X_5$PRX_6 X1 = H, N, Q, or S X2 = F, H, I, P, R, S, W, or Y X3 = D, E, H, N, Q, S, or V X4 = A, D, G, Q, or S X5 = D, F, H, K, L, M, N, Q, R, S, or T X6 = T or S
1090	M1 LCDR3	QQYYSTPFT
1091	M2 LCDR3	MQATQFPLT
1092	M3 LCDR3	QQRSNWPWT
1093	M4 LCDR3	QQFNSYPLT
1094	M5 LCDR3	HQWNNYGT
1095	M6 LCDR3	FQGSHVPLT
1096	M7 LCDR3	QQGQSYPYT
1097	M8 LCDR3	QSXDGTLSAL; X = Y, W, F
1098	M9 LCDR3	QQSYSTPRT
1099	M10 LCDR3	QQYGSSPT
1100	M11 LCDR3	QQYHRSWT
1101	M12 LCDR3	FQGSHVPLT

Table 16. Heavy Chain Variable Region (VH) Amino Acid Sequences

SEQ ID NO	Description	Sequence
101	217 VH, 158 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
102	220 VH, 160 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
103	223 VH, 200 VH, 194 VL, 206 VH	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
104	219 VH, 157 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITRDTSTSTV YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
105	221 VH, 125 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRATITRDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
106	213 VH, 162 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITTDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
107	212 VH, 100 VH, 181 VH, 34 VH, 79 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
108	107 VH, 211 VH, 15 VH, 30 VH, 29 VH, 48 VH, 49 VH, 50 VH, 51 VH, 52 VH, 56 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
109	205 VH, 199 VH, 55 VH, 193 VH	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
110	129 VH, 139 VH, 140 VH, 215 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
111	214 VH, 128 VH, 141 VH, 142 VH, 144 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITRDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
112	216 VH, 123 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWIGRIDPASGHTKYDPKFQVRVTITRDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
113	122 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITRDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
114	222 VH, 126 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITRDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS

115	188 VH, 41 VH, 102 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRVTITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
116	203 VH, 197 VH, 209 VH, 224 VH	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
117	147 VH, 112 VH, 59 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
118	127 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
119	159 VH, 218 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITRDTSTSTA YMELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
120	103 VH, 45 VH, 167 VH, 187 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRVTITRDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
121	64 VH, 148 VH, 97 VH, 114 VH, 130 VH, 133 VH, 137 VH, 155 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQVRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
122	67 VH, 138 VH, 115 VH, 149 VH, 134 VH, 98 VH, 156 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQVRATMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
123	68 VH, 99 VH, 116 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQVRVTITRDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
124	94 VH, 113 VH, 151 VH, 78 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQVRATITRDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
125	110 VH, 58 VH, 136 VH, 146 VH, 154 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
126	169 VH, 175 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ APGQGLEWMGRIDPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
127	173 VH, 179 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ APGQGLEWMGRIEPASGHIKYDPKFQGRATMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
128	96 VH, 132 VH, 65 VH, 150 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRATMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
129	196 VH, 202 VH, 208 VH	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRATMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS

130	172 VH, 178 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHIKYDPKFQGRATMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
131	75 VH, 72 VH, 95 VH, 152 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRATITTDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
132	174 VH, 180 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRATMTRDTSTSTA YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
133	109 VH, 91 VH, 135 VH, 145 VH, 153 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTA YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
134	198 VH, 204 VH, 210 VH	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTA YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
135	170 VH, 176 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHIKYDPKFQGRVTMTRDTSTSTA YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
136	31 VH, 85 VH, 86 VH, 87 VH, 88 VH, 89 VH, 90 VH, 143 VH, clone 34 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
137	32 VH, 33 VH	DVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
138	35 VH, 182 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ APGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
139	36 VH, 81 VH, 104 VH, 165 VH,	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
140	37 VH, 82 VH, 101 VH, 183 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWMGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
141	38 VH, 190 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTVY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
142	39 VH, 191 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY MELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
143	40 VH, 105 VH, 192 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
144	42 VH, 83 VH, 186 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATMTTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
145	43 VH, 184 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITRDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS

146	44 VH, 53 VH, 166 VH, 189 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRVTMTTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
147	46 VH, 168 VH, 185 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATMTRDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
148	47 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRVTMTRDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
149	54 VH	DVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
150	57 VH, 111 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
151	60 VH, 117 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
152	61 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWIGRIEPASGHIKYDPKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
153	62 VH, 118 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWIGRIDPASGHIKYDPKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
154	63 VH, 120 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHVKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
155	66 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTITRDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
156	69 VH, 108 VH	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
157	70 VH, 73 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTTDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
158	71 VH, 74 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTITTDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
159	76 VH, 119 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHTKYDPKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
160	77 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRATITRDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
161	92 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTV YLELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS

162	93 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRVTMTRDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
163	121 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
164	124 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWIGRIDPASGHTKYDPKFQVRVTITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
165	161 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITTDTSTSTVY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
166	163 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTITTDTSTSTAY MELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
167	164 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTTDTSTSTA YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
168	171 VH, 177 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHIKYDPKFQGRATITTDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
169	195 VH, 201 VH, 207 VH	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHIKYDPKFQGRATITTDTSTSTVY MELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
1200	5C3D11 VH	EVQLQQSGAELVKPGASVKLSCTASGFDIQDTYMHWVKQ RPEQGLEWIGRIDPASGHTKYDPKFQVKATITTDTSSNTAY LQLSSLTSEDTAVYYCSRSGGLPDVWGAGTTVTVSS
1201	9E12E5 VH	QVHLQQSGPELVKPGASVKLSCKASGYTFTKYDINWVRQR PEQGLEWIGWIFPGDGRTDYNEKFKGKATLTTDKSSSTAY MEVSRLTSEDSAVYFCARYGPAMDYWGQGTSVTVAS
1202	AS12824 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDICDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITTDTSTSTAY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
1203	AS12823 VH	QVQLVQSGAEVKKPGASVKLSCKASGFDICDTYMHWVRQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATMTTDTSTSTVY LELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
1204	AS12819 VH	QVQLVQSGAEVVKPGASVKLSCKASGFDICDTYMHWVRQ RPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTTDTSTSTV YLELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
1205	AS12816 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDICDTYMHWVKQ RPGQGLEWIGRIDPASGHTKYDPKFQVRATITRDTSTSTAY LELSSLRSEDTAVYYCSRSGGLPDVWGQGTTVTVSS
1206	AS12825 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDICDTYMHWVKQ APGQGLEWMGRIDPASGHTKYDPKFQVRATMTTDTSTSTA YLELSSLRSEDTAVYYCSRSGGLPDVWGQGTTVTVSS
1207	12835 VH	QVQLVQSGAEVKKPGASVKLSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHTKYDPKFQVRVTMTTDTSTSTV YMELSSLRSEDTAVYYCSRSGGLPDVWGQGTTVTVSS

1208	18-7 VH	QVQLVQSGAEVKKPGASVKLSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCSRSGGLPDVWGQGTTVTVSS
1209	21-3 VH, L8 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
1210	21-3 V102K VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGLPDKWGQGTTVTVSS
1211	21-3 V102M VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGLPDMWGQGTTVTVSS
1212	21-3 V102Q VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGLPDQWGQGTTVTVSS
1213	21-3 V102W VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
1214	21-3 CDRv VH	QVQLVQSGAEVKKPGASVKVSCKASGF$X_1X_2X_3$DTX_4X_5HWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGX_6PDX_7WGQGTTVTVSS X_1 = D or E X_2 = I, P, or V X_3 = G, Q, S, or V X_4 = F or Y X_5 = I or M X_6 = L or M X_7 = E, I, K, L, M, Q, T, V, W, or Y
1215	21-3 CDRv VH	QVQLVQSGAEVKKPGASVKVSCKASGF$X_1X_2X_3$DTX_4X_5HWVRQAPGQGLEWMGRIDPASGHTKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCSRSGGX_6PDX_7WGQGTTVTVSS X_1 = D or E X_2 = I, P, or V X_3 = G, Q, S, or V X_4 = F or Y X_5 = I or M X_6 = L or M X_7 = E, I, K, L, M, Q, T, V, W, or Y
1216	Clone 2 VH, clone 52 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIEPASGHIKYSPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
1217	Clone 46 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWMGRIEPASGHVKYSPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS

1218	Clone 47 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHVKYDPKFQTRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDWWGQGTTVTVSS
1219	Clone 14 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHiKYDPKFQkRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDMWGQGTTVTVSS
1220	Clone 16L VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHvKiDPKFQVRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDMWGQGTTVTVSS
1221	Clone 17L VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHLKYDPKFQVRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDMWGQGTTVTVSS
1222	Clone 17L-1 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHLKYDPKFQRRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDMWGQGTTVTVSS
1223	Clone 23 VH, clone A1 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHLKYDPKFQNRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDKWGQGTTVTVSS
1224	Clone 53 VH, clone E1 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIEPASGHLKYDPKFQERVTMTRDTSTSTV YMELSSLRSEDTAVYYCARSGGLPDKWGQGTTVTVSS
1225	Clone 3-17L V-A VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHLKYDPKFQGRVTITRDTSASTA YMELSSLRSEDTAVYYCARSGGLPDMWGQGTTVTVSS
1226	Clone 3-17L VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHLKYDPKFQGRVTITRDTSASTV YMELSSLRSEDTAVYYCARSGGLPDMWGQGTTVTVSS
1227	Clone L8mod VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHTKYDPKFQGRATITTDTSASTA YLQLSSLRSEDTAVYYCARSGGLPDVWGQGTTVTVSS
1228	Clone X-V VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHTKYDPKFQVRATITTDTSASTA YLQLSSLRSEDTAVYYCARSGGLPDFWGQGTTVTVSS
1229	Clone X VH, clone XL3-6 VH, clone XL3-10 VH, clone XL3-15 VH, clone L3-13 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHTKYDPKFQGRATITTDTSASTA YLQLSSLRSEDTAVYYCARSGGLPDFWGQGTTVTVSS
1230	Clone H3-1 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHTKYDPKFQGRATITTDTSASTA YLQLSSLRSEDTAVYYCARSGGLPDLWGQGTTVTVSS
1231	Clone H2-2 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHSKYDPKFQVRATITTDTSASTA YLQLSSLRSEDTAVYYCARSGGLPDFWGQGTTVTVSS
1232	Clone H2-5 VH	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQ APGQGLEWMGRIDPASGHYKYDPKFQVRATITTDTSASTA YLQLSSLRSEDTAVYYCARSGGLPDFWGQGTTVTVSS
1233	M1 VH	EVQLVESGGGLVQPGGSLRLSCAVSGFTFSSYWMSWVRQA PGKGLEWVANIKEDGSEKNYVDSVKGRFTLSSDNAKNSLY

		LQMNSLRAEDTAVYYCAREDYDSYYKYGMDVWGQGTAV IVSS
1234	M2 VH	QVQLQQWGAGLLKPSETLSLTCAVYGGSFTGFYWSWIRQP PGKGLEWIGEINHRGNTNYNPSLKSRVTMSVDTSKNQFSLN MISVTAADTAMYFCASPFYDFWSGSDYWGQGTLVTVSS
1235	M3 VH	QVQLVQSGAEVKKPGASVKVSCKASGYDFTYYGISWVRQ APGQGLEWMGWISTYNGNTHYARMLQGRVTMTTDTSTRT AYMELRSLRSDDTAVYYCARENYYGSGAYRGGMDVWGQ GTTVTVSS
1236	M3 VH + constant	QVQLVQSGAEVKKPGASVKVSCKASGYDFTYYGISWVRQ APGQGLEWMGWISTYNGNTHYARMLQGRVTMTTDTSTRT AYMELRSLRSDDTAVYYCARENYYGSGAYRGGMDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE AAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH NHYTQKSLSLSPG
1237	M4 VH	QLQLQESGPGLVKPSETLSLTCTVSGGSISSRSYYWGWIRQP PGKGLEWIGSIYYNGRTYYNPSLKSRVTISVDTSKNQFSLKL SSVTAADTAVYYCAREDYGDYGAFDIWGQGTMVTVSS
1238	M5 VH	QVTLKESGPALVKPTQTLTLTCTFSGFSLSTSNMGVVWIRQ PPGKALEWLAHILWDDREYSNPALKSRLTISKDTSKNQVVL TMTNMDPVDTATYYCARMSRNYYGSSYVMDYWGQGTLV TVSS
1239	M6 VH	QVQLVQSGSELKKPGASVKVSCKASGYTFTLYGMNWVRQ APGQGLEWMGWINTYTGEPTYADDFKGRFVFSLDTSVSTA YLQISSLKAEDTAVYYCAR DTAMDYAMAYWGQGTLVTVSS
1240	M6 VH	QVQLVQSGSELKKPGASVKVSCKASGYTFTLYGMNWVKQ APGKGLKWMGWINTYTGEPTYADDFKGRFVFSLDTSVSTA YLQISSLKAEDTAVYFCAR DTAMDYAMAYWGQGTLVTVSS
1241	M6 VH	QVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMNWVRQ APGQGLEWMGWINTYTGEPTYADDFKGRFVFSLDTSVSTA YLQISSLKAEDTAVYYCAR DYGKYGDYYAMDYWGQGTLVTVSS
1242	M6 VH	QVQLVQSGSELKKPGASVKVSCKASGYTFTNYGMNWVRQ APGKGLKWMGWINTYTGEPTYADDFKGRFVFSLDTSVSTA YLQISSLKAEDTAVYFCAR DYGKYGDYYAMDYWGQGTLVTVSS
1243	M7 VH	QVQLQQPGSVLVRPGASVKVSCKASGYTFTSSWMHWAKQ RPGQGLEWIGEIHPNSGGTNYNEKFKGKATVDTSSSTAYV DLSSLTSEDSAVYYCARGDYYGYVSWFAYWGQGTLVTVS S
1244	M7 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSWMHWARQ APGQGLEWIGEIHPNSGGTNYAQKFQGRATLTVDTSSSTAY

		MELSRLRSDDTAVYYCARGDYYGYVSWFAYWGQGTLVT VSS
1245	M7 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSWMHWARQ APGQGLEWIGEIHPNSGGTNYAQKFQGRATMTVDTSISTAY MELSRLRSDDTAVYYCARGDYYGYVSWFAYWGQGTLVT VSS
1246	M7 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSWMHWARQ APGQGLEWIGEIHPNSGGTNYAQKFQGRVTMTVDTSISTAY MELSRLRSDDTAVYYCARGDYYGYVSWFAYWGQGTLVT VSS
1247	M7 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSSWMHWARQ APGQGLEWMGEIHPNSGGTNYAQKFQGRVTMTVDTSISTA YMELSRLRSDDTAVYYCARGDYYGYVSWFAYWGQGTLV TVSS
1248	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGNTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1249	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGNTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1250	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGYTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1251	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGNTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1252	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGNTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1253	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGNTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1254	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGNTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1255	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGYTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS
1256	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQ APGQGLEWMGWLNPNSGYTGYAQKFQGRVTMTADRSTS TAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTV SS

1257	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWLNPNSGYTGYAQKFQGRVTMTADRSTSTAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTVSS
1258	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWLNPNSGYTGYAQKFQGRVTMTADRSTSTAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTVSS
1259	M8 VH	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQAPGQGLEWMGWLNPNSGYTGYAQKFQGRVTMTADRSTSTAYMELSSLRSEDTAVYYCAREVPETAAFEYWGQGTLVTVSS
1260	M9 VH	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRQPPGKGLEWIGYIYYSGNTKYNPSLKSRVTISIDTSKNQFSLKLSSVTAADTAVYYCARETGSYYGFDYWGQGTLVTVSS
1261	M10 VH	QVQLQQWGAGLLKPSETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEWIGEINHAGNTNYNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYYCARGYCRSTTCYFDYWGQGTLVTVSS
1262	M11 VH	EVQLLESGGGLVQPGKSLRLSCAVSGFTFSTYGMNWVRQAPGKGLEWVSSISGTGRTTYHADSVQGRFTVSRDNSKNILYLQMNSLRADDTAVYFCTKERGDYYYGVFDYWGQGTLVTVSS
1263	M12 VH	QIQLVQSGPELKKPGETVKISCKASGYTFTTYGMSWVKQAPGKGLKWMGWMNTYSGVTTYADDFKGRFAFSLETSASTAYMQIDNLKNEDTATYFCAREGYVFDDYYATDYWGQGTSVTVSS
301	Variable Heavy 1	**X1**VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WV**X2**Q**X3**PGQGLEW**X4**G[HCDR2]R**X5**T**X6**T**X7**DTSTST**X8**Y**X9**ELSSLRSEDTAVYYCAR[HCDR3]WGQGTTVTVSS wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V In some cases, X1 = Q or E In some cases, X2 = R or K In some cases, X3 = A or R In some cases, X4 = M or I In some cases, X5 = V or A In some cases, X6 = M or I In some cases, X7 = R or T In some cases, X8 = V or A In some cases, X9 = M or L
302	Variable Heavy 2	**X1**VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WV**X2**Q**X3**PGQGLEW**X4**G[HCDR2]R**X5**T**X6**T**X7**DTSTST**X8**Y**X9**ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V

		In some cases, X1 = Q or E In some cases, X2 = R or K In some cases, X3 = A or R In some cases, X4 = M or I In some cases, X5 = V or A In some cases, X6 = M or I In some cases, X7 = R or T In some cases, X8 = V or A In some cases, X9 = M or L
1301	Variable Heavy 3	X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QRP GQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRS EDTAVYYCAR[HCDR3]WGQGTTVTVSS wherein each of X1, X2, X4, X5, X6, X7, X8, X9, X10, and X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V In some cases, X1 = Q or E In some cases, X2 = R or K In some cases, X4 = M or I In some cases, X5 = V or A In some cases, X6 = M or I In some cases, X7 = R or T In some cases, X8 = V or A In some cases, X9 = M or L
1302	Variable Heavy 4	X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QRP GQGLEWX4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRS EDTAVYYC[HCDR3]WGQGTTVTVSS wherein each of X1, X2, X4, X5, X6, X7, X8, X9, X10, and X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V In some cases, X1 = Q or E In some cases, X2 = R or K In some cases, X4 = M or I In some cases, X5 = V or A In some cases, X6 = M or I In some cases, X7 = R or T In some cases, X8 = V or A In some cases, X9 = M or L

Table 17. Light Chain Variable Region (VL) Amino Acid Sequences

SEQ ID NO	Description	Sequence
201	217 VL, 219 VL, 221 VL, 200 VL, 213 VL, 212 VL, 211 VL, 199 VL, 214 VL, 216 VL, 222 VL, 203 VL, 147 VL, 218 VL, 179 VL, 148 VL, 149 VL, 151 VL, 180 VL, 175 VL, 178 VL, 145 VL, 146 VL, 150 VL, 152 VL, 176 VL, 177 VL, 201 VL, 202 VL, 204 VL, 215 VL, 224 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQ KPGQAPRPLIYATSNLASGIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYCQQWEGNPRTFGGGTKLEIK
202	223 VL, 107 VL, 205 VL, 181 VL, 188 VL, 64 VL, 67 VL, 68 VL, 94 VL, 33 VL, 57 VL, 58 VL, 59 VL, 60 VL, 61 VL, 62 VL, 63 VL, 65 VL, 66 VL, 69 VL, 70 VL, 71 VL, 72 VL, 76 VL, 77 VL, 78 VL, 91 VL, 92 VL, 93 VL, 97 VL, 98 VL, 99 VL, 140 VL, 142 VL, 143 VL, 182 VL, 183 VL, 184 VL, 185 VL, 186 VL, 187 VL, 189 VL, 190 VL, 191 VL, 192 VL, 206 VL, 207 VL, 208 VL, 209 VL, 210 VL, 18-7 S93E VL, clone 34 VL, clone 2 VL, clone 46 VL, clone	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQ KPGQAPRLLIYATSNLASGIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYCQQWEGNPRTFGGGTKLEIK

	47 VL, clone 23 VL, clone 53	
203	15 VL, 18-7, L8, clone L8mod VL, clone X-V VL, clone X VL, clone H3-1 VL, clone H2-2 VL, clone H2-5 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQ KPGQAPRLLIYATSNLASGIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYCQQWSGNPRTFGGGTKLEIK
204	30 VL, 100 VL, 129 VL, 122 VL, 127 VL, 126 VL, 160 VL, 157 VL, 159 VL, 158 VL, 125 VL, 103 VL, 101 VL, 102 VL, 104 VL, 105 VL, 121 VL, 123 VL, 124 VL, 128 VL, 144 VL, 161 VL, 162 VL, 163 VL, 164 VL, clone L3-13 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQ KPGQAPRLLIYATSNLASGIPDRFSGSGSGTDFTLTIS RLEPEDFAVYYCQQWKGNPRTFGGGTKLEIK
205	110 VL, 197 VL, 112 VL, 169 VL, 173 VL, 115 VL, 113 VL, 96 VL, 196 VL, 172 VL, 75 VL, 174 VL, 109 VL, 198 VL, 170 VL, 29 VL, 31 VL, 32 VL, 73 VL, 74 VL, 95 VL, 108 VL, 111 VL, 114 VL, 116 VL, 117 VL, 118 VL, 119 VL, 120 VL, 130 VL, 153 VL, 154 VL, 155 VL, 156 VL, 165 VL, 166 VL, 167 VL, 168 VL, 171 VL, 193 VL, 194 VL, 195 VL, 220 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRPWIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWEGNPRTFGGGTKLEIK
206	134 VL, 132 VL, 133 VL, 135 VL, 136 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRPLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWKGNPRTFGGGTKLEIK

207	138 VL, 137 VL, 139 VL, 141 VL, clone XL3-15 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWSRNPRTFGGGTKLEIK
208	34 VL, 35 VL, 36 VL, 37 VL, 38 VL, 39 VL, 40 VL, 41 VL, 42 VL, 43 VL, 44 VL, 45 VL, 46 VL, 47 VL, 53 VL, 54 VL, 55 VL, 79 VL, 81 VL, 82 VL, 83 VL, AS12824 VL	EIVLTQSPGTLSASPGERATMSCRASSSVSYMYWYQQKPG QAPRPWIYATSNLASGVPDRFSGSGSGTDYTLTISRVEPEDF AVYYCQQWSGNPRTFGGGTKLEIK
209	85 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGVPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWEGNPRTFGGGTKLEIK
210	48 VL	EIVLTQSPGTLSASPGERATLSCRASSSVSYMYWYQQKPGQ APRPWIYATSNLASGVPDRFSGSGSGTDYTLTISRVEPEDFA VYYCQQWSGNPRTFGGGTKLEIK
211	49 VL	EIVLTQSPGTLSASPGERATMSCRASSSVSYMYWYQQKPG QAPRLLIYATSNLASGVPDRFSGSGSGTDYTLTISRVEPEDF AVYYCQQWSGNPRTFGGGTKLEIK
212	50 VL	EIVLTQSPGTLSASPGERATMSCRASSSVSYMYWYQQKPG QAPRPWIYATSNLASGVPDRFSGSGSGTDFTLTISRVEPEDF AVYYCQQWSGNPRTFGGGTKLEIK
213	51 VL	EIVLTQSPGTLSASPGERATMSCRASSSVSYMYWYQQKPG QAPRPWIYATSNLASGVPDRFSGSGSGTDYTLTISRLEPEDF AVYYCQQWSGNPRTFGGGTKLEIK
214	52 VL	EIVLTQSPGTLSASPGERATMSCRASSSVSYMYWYQQKPG QAPRPWIYATSNLASGVPDRFSGSGSGTDFTLTISRLEPEDF AVYYCQQWSGNPRTFGGGTKLEIK
215	56 VL	EIVLTQSPGTLSASPGERATMSCRASSSVSYMYWYQQKPG QAPRPWIYATSNLASGIPDRFSGSGSGTDYTLTISRVEPEDF AVYYCQQWSGNPRTFGGGTKLEIK
216	86 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDYTLTISRLEPEDFAV YYCQQWEGNPRTFGGGTKLEIK
217	87 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRVEPEDFAV YYCQQWEGNPRTFGGGTKLEIK
218	88 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDYTLTISRVEPEDFAV YYCQQWEGNPRTFGGGTKLEIK
219	89 VL	EIVLTQSPGTLSASPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWEGNPRTFGGGTKLEIK
220	90 VL	EIVLTQSPGTMSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWEGNPRTFGGGTKLEIK

1264	5C3D11 VL	QIVLSQSPAILSASPGEKVTMTCRASSSVSYMYWYQQKPGS SPKPWIYATSNLASGVPDRFSGSGSGTSYSLTISRVEAEDAA TYYCQQWSGNPRTFGGGTKLEIK
1265	9E12E5 VL	MKLPVRLLVLMFWIPASSSDVLMTQTPLSLPVSLGDQASIS CRSSQTIVHSNGDTYLDWFLQKPGQSPKLLIYKVSNRFSGV PDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFG GGTKLEIK
1266	AS12823 VL	EIVLTQSPGTLSLSPGERATMSCRASSSVSYMYWYQQKPGQ APRPWIYATSNLASGIPDRFSGSGSGTDFTLTISRVEPEDFAV YYCQQWSGNPRTFGGGTKLEIK
1267	AS12819 VL	EIVLTQSPGTLSLSPGERVTMSCRASSSVSYMYWYQQKPGQ APRPWIYATSNLASGVPDRFSGSGSGTDFTLTISRVEPEDFA VYYCQQWSGNPRTFGGGTKVEIK
1268	AS12816 VL	EIVLTQSPGTLSASPGERVTLSCRASSSVSYMYWYQQKPGQ APRPWIYATSNLASGVPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQWSGNPRTFGGGTKLEIK
1269	AS12825 VL	EIVLTQSPGTLSASPGERVTMSCRASSSVSYMYWYQQKPG QAPRLLIYATSNLASGVPDRFSGSGSGTDFTLTISRVEPEDF AVYYCQQWSGNPRTFGGGTKLEIK
1270	12835 VL	EIVLTQSPGTLSLSPGERVTMSCRASSSVSYMYWYQQKPGQ APRPWIYATSNLASGVPDRFSGSGSGTDYTLTISRLEPEDFA VYYCQQWSGNPRTFGGGTKLEIK
1271	21-3 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGVPDRFSGSGSGTDYTLTISRLEPEDFA VYYCQQWSGNPRTFGGGTKLEIK
1272	18-7 S92D VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWDGNPRTFGGGTKLEIK
1273	18-7 S92H VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWHGNPRTFGGGTKLEIK
1274	18-7 S92N VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWNGNPRTFGGGTKLEIK
1275	18-7 S92Q VL, clone 14 VL, clone 16L VL, clone 17L VL, clone 17L-1 VL, clone 3-17L V-A VL, clone 3-17L VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWQGNPRTFGGGTKLEIK
1276	18-7 CDRv VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCX_1QW$X_2X_3X_4$PRTFGGGTKLEIK X_1 = Q or N X_2 = D, E, H, N, Q, or S X_3 = A or G X_4 = D, F, K, N, R, S, or T

1277	Clone 52 VL, clone A1 VL, clone E1 VL	EIVLTQSPGTLSLSPGERATLSCGASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWEGNPRTFGGGTKLEIK
1278	Clone XL3-6 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCSQWSGNPRTFGGGTKLEIK
1279	Clone XL3-10 VL	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQ APRLLIYATSNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAV YYCQQWSGNPRSFGGGTKLEIK
1280	M1 VL	DIVMTQSPDSLAVSLGERATINCKSSQSILYSSNNKNYLAW YQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISS LQAEDVS VYYCQQYYSTPFTFGPGTKVDIK
1281	M2 VL	DIMLTQTPLTSPVTLGQPASISCKSSQSLVHSDGNTYLSWLQ QRPGQPPRLLFYKISNRFSGVPDRFSGSGAGTDFTLKISRVE AEDVGVYYCMQATQFPLTFGGGTKVEIK
1282	M3 VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPG QAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQRSNWPWTFGQGTKVEIK
1283	M3 VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPG QAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFA VYYCQQRSNWPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSFNRGEC
1284	M4 VL	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGK APKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQFNSYPLTFGGGTKVEIK
1285	M5 VL	DIQLTQSPSFLSASVGDRVTITCSASSSVNYMHWYQQKPGK APKLLIYSTSNLASGVPSRFSGSGSGTEFTLTISSLQPEDFAT YYCHQWNNYGTFGQGTKVEIKR
1286	M6 VL	DVVMTQSPLSLPVTLGQPASISCKSSQNIVHSDGNTYLEWF QQRPGQSPRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCFQGSHVPLTFGGGTKVEIKR
1287	M6 VL	DVVMTQSPLSLPVTLGQPASISCKSSQNIVHSDGNTYLEWF QQRPGQSPRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCFQGSHVPLTFGQGTKVEIKR
1288	M6 VL	DVVMTQTPLSLPVTPGEPASISCKSSQNIVHSDGNTYLEWY LQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDLGVYYCFQGSHVPLTFGGGTKVEIKR
1289	M6 VL	DVVMTQTPLSLPVSLGDQASISCKSSQNIVHSDGNTYLEWY LQKPGQSPKVLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDLGVYYCFQGSHVPLTFGGGTKVEIKR
1290	M6 VL	DVVMTQSPLSLPVTLGQPASISCRSSQSIVHSNGNTYLDWF QQRPGQSPRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCFQGSHVPLTFGGGTKVEIKR
1291	M6 VL	DVVMTQSPLSLPVTLGQPASISCRSSQSIVHSNGNTYLDWF QQRPGQSPRRLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCFQGSHVPLTFGQGTKVEIKR

1292	M6 VL	DVVMTQTPLSLPVTPGEPASISCRSSQSIVHSNGNTYLDWY LQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDLGVYYCFQGSHVPLTFGGGTKVEIKR
1293	M6 VL	DVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLDWY LQKPGQSPKVLIYKVSNRFSGVPDRFSGSGSGTDFTLKINRV EAEDLGVYFCFQGSHVPLTFGGGTKLEIKR
1294	M7 VL	DIQMNQSPSSLSASLGDTITITCHASQNINVLLSWYQQKPGN IPKLLIYKASNLHTGVPSRFSGSGSGTGFTFTISSLQPEDIATY YCQQGQSYPYTFGGGTKLEIK
1295	M7 VL	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPG KAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIA TYYCQQYDNLPYTFGQGTKLEIK
1296	M7 VL	DIQMTQSPSSLSASVGDRVTITCQASQNINVLLNWYQQKPG KAPKLLIYKASNLHTGVPSRFSGSGSGTDFTFTISSLQPEDIA TYYCQQ GQSYPYTFGQGTKLEIK
1297	M7 VL	DIQMNQSPSSLSASVGDRVTITCQASQNINVLLSWYQQKPG KAPKLLIYKASNLHTGVPSRFSGSGSGTDFTFTISSLQPEDIA TYYCQQ GQSYPYTFGQGTKLEIK
1298	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAXXGVXWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSXDGTLSALFGGGTKLTVLG
1299	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGLGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSWDGTLSALFGGGTKLTVLG
1300	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGLGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSYDGTLSALFGGGTKLTVLG
1304	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAALGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSWDGTLSALFGGGTKLTVLG
1305	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGSGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSWDGTLSALFGGGTKLTVLG
1306	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGQGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSWDGTLSALFGGGTKLTVLG
1307	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGLGVLWYQQLP GTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPED EGDYYCQSWDGTLSALFGGGTKLTVLG
1308	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGLGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSWDGTLSALFGGGTKLTVLG
1309	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGSGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSWDGTLSALFGGGTKLTVLG
1310	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGQGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSWDGTLSALFGGGTKLTVLG

1311	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGLGVLWYQQLP GTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPED EGDYYCQSWDGTLSALFGGGTKLTVLG
1312	M8 VL	QSVLTQPPSVSGAPGQRVTISCTSSSSDIGAGLGVHWYQQL PGTAPKLLIEGYYNRPSGVPDRFSGSKSGTSASLTITGLLPE DEGDYYCQSFDGTLSALFGGGTKLTVLG
1313	M9 VL	DIQMTQSPSSLSASVGDRVTITCRASQSINNYLNWYQQRPG KAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPGDFA TYYCQQSYSTPRTFGQGTKLEIK
1314	M10 VL	EIVLTQSPGTLSLSPGERATLSCRASQSVRSSYLAWYQQKP GQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDF AVYYCQQYGSSPTFGQGTRLEIK
1315	M11 VL	DIQMTQSPSTLSASVGDRVTITCRASQTISSWLAWYQQTPE KAPKLLIYAASNLQSGVPSRFSGSGSGTEFTLTISSLQPDDFA TYYCQQYHRSWTFGQGTKVEIT
1316	M12 VL	DVLMTQTPLSLPVSLGDQASISCRSSQNIVHSDGNTYLEWY LQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDLGIYYCFQGSHVPLTFGAGTKLELK
303	Variable Light	EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPR**X 10X11**IY[LCDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYY C[LCDR3]FGGGTKLEIK wherein each of X10 and X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V In some cases, X10 = L or P In some cases, X11 = L or W

Table 18A. Additional Sequences

SEQ ID NO	Description	Sequence
304	219 HC FR1, 212 HC FR1	QVQLVQSGAEVKKPGASVKVSCKAS
305	219 HC FR2	WVKQRPGQGLEWMG
313	212 HC FR2	WVRQRPGQGLEWIG
1317	HC FR2	WVRQAPGQGLEWMG
306	219 HC FR3a	RVTITRDTSTSTVYLELSSLRSEDTAVYYCAR
307	219 HC FR3b	RVTITRDTSTSTVYLELSSLRSEDTAVYYC
314	212 HC FR3a	RATITTDTSTSTAYLELSSLRSEDTAVYYCAR
315	212 HC FR3b	RATITTDTSTSTAYLELSSLRSEDTAVYYC
1318	HC FR3	RVTMTRDTSTSTVYMELSSLRSEDTAVYYC
1319	HC FR3	RATITTDTSASTAYLQLSSLRSEDTAVYYC
1320	HC FR3	RVTITRDTSASTVYMELSSLRSEDTAVYYC
1321	HC FR3	RVTITRDTSASTAYMELSSLRSEDTAVYYC
1322	HC FR3	RVTMTRDTSTSTVYMELSSLRSEDTAVYYCSR
1323	HC FR3	RVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
308	219 HC FR4, 212 HC FR4	WGQGTTVTVSS
309	219 LC FR1, 212 LC FR1	EIVLTQSPGTLSLSPGERATLSC
310	219 LC FR2, 212 LC FR2	WYQQKPGQAPRPLIY
1324	LC FR2	WYQQKPGQAPRLLIY
311	219 LC FR3, 212 LC FR3	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC
1325	LC FR3	GVPDRFSGSGSGTDYTLTISRLEPEDFAVYYC
312	219 LC FR4, 212 LC FR4	FGGGTKLEIK
316	IGHV1-46*02	QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVR QAPGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTST VYMELSSLRSEDTAVYYCAR
317	IGKV3-20*01	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPG QAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA VYYCQQYGSSP
319	Light Chain Constant	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQW KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC

Table 18B: Additional sequences

SEQ ID NO	Sequence
3001	GFDIQDTYMH
3002	RIDPASGHTKYDPKFQV
3003	RIEPASGHIKYDPKFQG
3005	RIEPASGHIKYDPKFQV
3006	SGGLPDV
3008	SGGLPDW
3010	RASSSVSYMY
3011	ATSNLAS
3012	QQWEGNPRT
3013	QQWKGNPRT
3116	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3121	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQVRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3122	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQVRATMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3123	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQVRVTITRDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3124	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQVRATITRDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3125	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3128	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRATMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3129	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRATMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3131	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRATITTDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3133	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTAYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3134	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTAYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS

3136	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIDPASGHIKYDPKFQGRVTMTRDTSTSTAYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3137	DVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3138	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQAPGQGLEWI GRIDPASGHTKYDPKFQVRATITTDTSTSTAYLELSSLRSEDTAVYYCARS GGLPDVWGQGTTVTVSS
3139	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWI GRIDPASGHTKYDPKFQVRATITTDTSTSTAYLELSSLRSEDTAVYYCARS GGLPDVWGQGTTVTVSS
3151	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIDPASGHIKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3152	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWI GRIEPASGHIKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR SGGLPDWWGQGTTVTVSS
3153	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEWI GRIDPASGHIKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR SGGLPDWWGQGTTVTVSS
3154	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHVKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3155	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTITRDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3156	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3157	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTTDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3158	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTITTDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3159	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHTKYDPKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYC ARSGGLPDWWGQGTTVTVSS
3160	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRATITRDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3161	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTVYLELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3162	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRVTMTRDTSTSTAYLELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS

3168	QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIDPASGHIKYDPKFQGRATITTDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3169	EVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVRQAPGQGLEW MGRIEPASGHIKYDPKFQGRATITTDTSTSTVYMELSSLRSEDTAVYYCA RSGGLPDWWGQGTTVTVSS
3202	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYATS NLASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3204	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYATS NLASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWKGNPRTFGGGT KLEIK
3205	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRPWIYAT SNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3206	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRPLIYATS NLASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWKGNPRTFGGGT KLEIK
3207	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYATS NLASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWSRNPRTFGGGTK LEIK
3208	EIVLTQSPGTLSASPGERATMSCRASSSVSYMYWYQQKPGQAPRPWIYA TSNLASGVPDRFSGSGSGTDYTLTISRVEPEDFAVYYCQQWSGNPRTFGG GTKLEIK
3209	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYATS NLASGVPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3216	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYATS NLASGIPDRFSGSGSGTDYTLTISRLEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3217	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYATS NLASGIPDRFSGSGSGTDFTLTISRVEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3218	EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYATS NLASGIPDRFSGSGSGTDYTLTISRVEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3219	EIVLTQSPGTLSASPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYAT SNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3220	EIVLTQSPGTMSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRLLIYAT SNLASGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWEGNPRTFGGGT KLEIK
3319	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT KSFNRGEC
3320	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN

	GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Table 19. Fc and Constant Regions

SEQ ID NO: 320 IgG1 Constant ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 321 IgG1 Constant ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 322 IgG1 Constant ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 323 Fc1 (L235E) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 324 Fc2 (L235E) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 325 Fc3 (L235E) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 326 Fc4 (L234A, L235A)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 327 Fc5 (L234A, L235A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 328 Fc6 (L234A, L235A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 329 Fc7 (L234A, L235A, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 330 Fc8 (L234A, L235A, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 331 Fc9 (L234A, L235A, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 332 Fc10 (L234A, L235A, P329G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 333 Fc11 (L234A, L235A, P329G)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 334 Fc12 (L234A, L235A, P329G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALGAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 335 Fc13 (L234F, L235E, P331S) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 336 Fc14 (L234F, L235E, P331S) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 337 Fc15 (L234F, L235E, P331S) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 338 Fc16 (L234A, L235E, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 339 Fc17 (L234A, L235E, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 340 Fc18 (L234A, L235E, G237A)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 341 Fc19 (L234A, L235E, G237A, P331S) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 342 Fc20 (L234A, L235E, G237A, P331S) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 343 Fc21 (L234A, L235E, G237A, P331S) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 344 Fc22 (L234A, L235A, P329A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 345 Fc23 (L234A, L235A, P329A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 346 Fc24 (L234A, L235A, P329A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 347 Fc25 (D265A)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 348 Fc26 (D265A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 349 Fc27 (D265A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 350 Fc28 (N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 351 Fc29 (N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 352 Fc30 (N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 353 Fc31 (D265A, N297A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 354 Fc32 (D265A, N297A)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 355 Fc33 (D265A, N297A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 356 Fc34 (D265A, N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 357 Fc35 (D265A, N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 358 Fc36 (D265A, N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 359 Fc37 (L235A, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 360 Fc38 (L235A, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 361 Fc39 (L235A, G237A)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 362 Fc40 (IgG4) ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAP EFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
SEQ ID NO: 401 (L234A, L235A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 402 (L235E) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEL**E**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 403 (L234A, L235A, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPE**AA**G**A**PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 404 (L234A, L235E, G237A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPE**A**E**G**A**P**SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 405 (L234A, L235A, P329A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL**A**APIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 406 (L234A, L235A, P329G)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL**A**APIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 407 (P329A) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL**A**APIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 408 (L234E, L235F, P331S) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPE**EF**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA**S**IEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 409 (D265A, N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV**A**VSHEDPEVKFNWYVDGVEV HNAKTKPREEQY**G**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 410 (N297G) ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQY**G**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 411 (S228P) ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCP**P**CPAP EFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
SEQ ID NO: 412 (S228P, L235E) ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCP**P**CPAP EF**E**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
SEQ ID NO: 413 (S228P, F234A, L235A)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCP**P**CPAP E**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQ PREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
SEQ ID NO: 501 (L234A, L235A) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 502 (L235E) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPEL**E**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 503 (L234A, L235A, G237A) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPE**AA**G**A**PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 504 (L234A, L235E, G237A) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPE**AE**G**A**PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 505 (L234A, L235A, P329A) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS

GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL**A**A PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 506 (L234A, L235A, P329G) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL**A**A PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 507 (P329A) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL**A**A PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 508 (L234E, L235F, P331S) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPE**EF**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA **S**IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 509 (D265A, N297G) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV**A**VSHEDPEVKFNW YVDGVEVHNAKTKPREEQY**G**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 510 (N297G) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS

GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQY**G**STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
SEQ ID NO: 511 (S228P) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP PCP**P**CPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKT ISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG K
SEQ ID NO: 512 (S228P, L235E) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP PCP**P**CPAPEF**E**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKT ISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG K
SEQ ID NO: 513 (S228P, F234A, L235A) QVQLVQSGAEVKKPGASVKVSCKASGFDIQDTYMHWVKQRPGQGLEWMGRIDP ASGHTKYDPKFQVRVTITRDTSTSTVYLELSSLRSEDTAVYYCARSGGLPDVWGQ GTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP PCP**P**CPAPE**AA**GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKT ISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG K
SEQ ID NO: 514 EIVLTQSPGTLSLSPGERATLSCRASSSVSYMYWYQQKPGQAPRPLIYATSNLASGI PDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWEGNPRTFGGGTKLEIKRTVAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 515 G2 constant domain ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAP PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQP REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPML DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Table 20. Select Antibodies

Antibody	Heavy Chain CDR SEQ ID NOS (CDR1, CDR2, CDR3)	Light Chain CDR SEQ ID NOS (CDR1, CDR2, CDR3)
A	1, 2, 6	10, 11, 12
B	1, 3, 8	10, 11, 12
C	1, 4, 8	10, 11, 12
D	1, 2, 6	10, 11, 13
E	1, 2, 6	10, 11, 14
F	1, 5, 8	10, 11, 12
G	1, 5, 8	10, 11, 13
H	1, 3, 8	10, 11, 13
A2	1, 2, 7	10, 11, 12
B2	1, 3, 9	10, 11, 12
C2	1, 4, 9	10, 11, 12
D2	1, 2, 7	10, 11, 13
E2	1, 2, 7	10, 11, 14
F2	1, 5, 9	10, 11, 12
G2	1, 5, 9	10, 11, 13
H2	1, 3, 9	10, 11, 13
I	1, 5, 8	10, 11, 15
I2	1, 5, 9	10, 11, 15

Table 21. Select Antibodies – Variable Regions

Antibody	Heavy Chain Variable Region SEQ ID NO	Light Chain Variable Region SEQ ID NOS
15	108	203
30	108	204
64	121	202
67	122	202
68	123	202
75	131	205
94	124	202
96	128	205
100	107	204
103	120	204
107	108	202
109	133	205
110	125	205
112	117	205
113	124	205
115	122	205
122	113	204
125	105	204
126	114	204
127	118	204
129	110	204
132	128	206
134	122	206
138	122	204
147	117	201
148	121	201
149	122	201
151	124	201
157	104	204
158	101	204
159	119	204
160	102	204
169	126	205
170	135	205
172	130	205
173	127	205
174	132	205
175	126	201
178	130	201
179	127	201
180	132	201
181	107	202
188	115	202

196	129	205
197	116	205
198	134	205
199	109	201
200	103	201
203	116	201
205	109	202
211	108	201
212	107	201
213	106	201
214	111	201
216	112	201
217	101	201
218	119	201
219	104	201
220	102	201
221	105	201
222	114	201
223	103	202
500	301	303
501	302	303

Example 17: Design of humanized anti-TL1A antibodies with reduced cell-mediated cytotoxicity.

[0504] As provided and described herein, Fc variants (e.g. SEQ ID NOs: 401-413) were designed to diminish effector function and subsequently tested for the ability to (i) effectively be purified/manufactured (**Table 22**), (ii) reduce antibody-dependent cell-mediated cytotoxicity (ADCC), and (iii) reduce complement-dependent cytotoxicity. Test articles tested comprise heavy chain SEQ ID NOs: 501-513, comprising Fc regions that comprises SEQ ID NOs: 401-413, respectively. Heavy chains used were paired with a light chain comprising SEQ ID NO: 514. ELISA titration profiles and EC50s were generated against recombinant TL1A antigen ("EC50", **Table 23**). Interestingly, Fc mutations did affect purity, as measured by monomer content, for select mutations/Fc variants (**Table 22**, wild-type IgG1 control).

Reduction of CDC activity

[0505] Test articles were evaluated for CDC activity, compared to negative control Human IgG4 isotype control, on TL1A-expressing HEK293 target cells. Rituxan (anti-CD20) was used as a positive technical control on CD20-expressing Raji cell. All test articles were used at a final top concentration of 10 μg/mL followed by a five-fold dilution series (7 points total), in addition to a no treatment control, in triplicate. Cells were incubated with test

articles for 15 minutes at 37 C, then treated with human complement, at a final concentration of 25%, for 3 hours at 37 C, 5% CO2. Following incubation, cells were washed and resuspended in Propidium Iodide (P.I.) at a final concentration of 5 μg/mL prior to flow cytometry analysis. Total cells were examined by flow cytometry during sample acquisition. Data were plotted on an XY chart, graphing percentage P.I. positive cells against the log of the concentration and fit to a non-linear regression curve. Cell cytotoxicity in the presence of all test articles was not distinguishable from cell cytotoxicity in the presence of isotype control (**Table 23**). CDC bioactivity was observed on Raji target cells with Rituxan treatment.

Reduction of CDC activity

[0506] An antibody-dependent cell-mediated cytotoxicity (ADCC) reporter assay was performed for the characterization of test articles and IgG4 Isotype control on HEK 293 TL1A cells. A reporter cell line engineered to express human Fc-gamma-RIIIa V158 (high affinity) served as effector cells.

[0507] Prometheus test articles were evaluated with a top concentration of 10 ug/mL (log dilution for 7 points total, in addition to no test article control). Treatment conditions were tested in triplicate, effector and target cells were co-cultured for 6 hours at 37 C with 5% CO2. Raji target cells were used as a positive control, with Rituxan treatment at a top concentration of 10 ug/mL, 7-point log dilution series, and no treatment control. Test article 502 treatment resulted in dose-dependent increase in luciferase reporter gene activity, and 5044 treatment resulted in increase of reporter activity at the highest tested concentration. The rest of the test articles did not induce reporter activity (**Table 23**).

Table 22.

Class	Fc SEQ ID NO	Heavy Chain SEQ ID NO	mg/mL	mg	Purity	
					SDS-PAGE	SEC-HPLC
IgG1, protein variants	401	501	2.65	10.60	95%	90%
	402	502	1.15	12.65	95%	92%
	403	503	3.22	10.62	90%	89%
	404	504	1.61	11.27	95%	92%
	405	505	3.43	10.29	95%	91%
	406	506	1.51	15.10	95%	93%
	407	507	2.85	11.40	95%	92%
	408	508	1.55	10.85	95%	92%
IgG1, glycan knock-out	409	509	2.33	9.32	90%	90%
	410	510	1.36	12.24	95%	92%
IgG4	411	511	1.78	19.58	95%	82%
	412	512	2.33	18.64	90%	81%

	413	513	5.08	15.24	95%	90%
Control	-	-	3.70	5.55	95%	97%

Table 23.

Class	Fc SEQ ID NO	Heavy Chain SEQ ID NO	EC50 (nM)	ADCC	CDC
IgG1, protein variants	401	501	0.222	ND	ND
	402	502	0.215	100 ng/mL	ND
	403	503	0.188	ND	ND
	404	504	0.220	10 ug/mL	ND
	405	505	0.346	ND	ND
	406	506	0.347	ND	ND
	407	507	0.329	ND	ND
	408	508	0.330	ND	ND
IgG1, glycan knock-out	409	509	0.340	ND	ND
	410	510	0.293	ND	ND
IgG4	411	511	0.299	ND	ND
	412	512	0.324	ND	ND
	413	513	0.252	ND	ND

Example 18: Biophysical Properties Of Anti-Tl1a Antibodies At High Concentrations

[0508] The data for A219 anti-TL1A antibody properties in solution were analyzed together using a chemometric method termed partial least squares (PLS). Detailed descriptions of PLS modeling have been published in, for example, Katz, M. H. *Multivariate Analysis: A Practice Guide for Clinicians*. Cambridge University Press, New York, pp. 158-162 (1999); Stahle, L., Wold, K., Multivariate data analysis and experimental design in biomedical research. *Prog. Med. Chem.* 1988, 25: 291-338; Wold S. PLS-regression: a basic tool of chemometrics. *Chemom. Intell. Lab. Syst.* 2001, 58: 109-130; and Martens, H.; Martens, M. *Multivariate Analysis of Quality: An Introduction*, Wiley and Sons, Chichester, UK (2001).

[0509] **FIGS. 9A-9C** demonstrate viscosity as a function of antibody concentration and pH. Antibody concentration ranged from greater than about 125 mg/mL to greater than about 170 mg/mL. pH ranged from less than 5.0 to about 7.5. Concentration dependence is evident, with very low viscosities (e.g. as indicated by a viscosity less than 5 mPa-s or 7mPa-s). The viscosity was measured using an m-VROC™ viscometer by Rheosense with an A10 chip. The shear rates employed were about 1820 s-1. The viscometer was temperature controlled using a ThermoCube thermoelectric chiller and the samples were delivered using a Hamilton 100 µL syringe (81060). The accuracy of the instrument was verified using neat Isopropyl alcohol and measured at 25°C. Furthermore, across the concentration range tested, the

percent increase in the HMW fraction as measured by size exclusion chromatography ranged from 0% to a 1.3% increase. HMW as used herein refers to high molecular weight antibody fraction, e.g., aggregated protein, and which excludes monomeric antibody.

The foregoing description of various embodiments known to the applicant at this time of filing the application has been presented and is intended for the purposes of illustration and description. The present description is not intended to be exhaustive nor limited to the precise form disclosed and many modifications and variations are possible in the light of the above teachings. The embodiments described serve to explain principles and practical applications, and to enable others skilled in the art to utilize the various embodiments, optionally with various modifications, as are suited to the particular use contemplated. Therefore, it is intended that the disclosure not be limited to the particular embodiments disclosed.

Table 24. Additional Sequences

SEQ ID	Sequence
2001	CATTCTGCAG CAGGGACAGA AGCCTGGGAA GTTGAGTCCA CGAAGAGGGT TCTCGGACTC CCTTCCCTAA GCGAGTGACT GATGTTTCCT GACTCTGGCC CTGGTTGTGC CGTGAGGCCA CAGTGAGGGC AGCTGGAGAG CTCAGGATCT GCCACCTTAG CACACATGGG ATGTTAGGCA CTTCTCGCTA TGCCTCAGTT TCTGTGGTCT CATGAAGGAA CATTAGTACT TTCTTCATTA ATGCACATAA AATGCTTGGC AGTGCTTGGC ATAGAGATAG ATGCTCAATA AATGTTGGCC ACTATTATTA TAGCCCCCTA CAAACAAGGA GGATGAGATT GAAAACAATG TTTCCTAAAA ATGAGGGTAT AATGGGCATC CTATCCATAT TTCAGGGGTA GGAAAACAGC CTTCTGAGAT CATTTATATG AAGGGTATGG ATGGACAAAT CCTTATCAGC CTAAAATATT CCTATCTATG ATTGCTATGT CATTTCTTTA **R** GATTAATCAA TCCTCTTCAT GAGTCATATT TCAATATATT ACACATACAC ATAATTATAA AAGAACCAAG TTGCATAAAA TTTATAAAAT GGAGACTAGG AAAGGAAAAA CCCGCTCATA AAACCCAACA AGAGAGCTTA AAATGAAAGT CTGAAAGTGC AGGTAGGTAT TTGTTTAAAT ACTTGGTAAA AGAAAATGTT CAATTCAGTA GCTGTGACAG ACACAATTTT AAGGGGTGTG GGCATAAGAG AAACAGAAAG TCCATCTGTC AAAGGGGTAA ATATTTAGTC AAGTCTTAGA TAGTATTTCT GTAAACAGAA ATTTCAATGG AAAATTTCCA ACCTGAGAGC AAATAATTTA AGATGGGTTT AATATAAGAA TTAAAGCTCT CGTCTCCATG TCGCTGCCCA GCCTGAGACC CAGCCCTCTG AGTCCTTGTG GCAGTTCGGC TTTTTCTTTC TTGTTCCCTC AACTACAACT GGACACTATA ATTTTCTTTC

SEQ ID	Sequence
2002	GACTATTAAC CAATCATGAA AAACATTTTC AAATAATACT TAATGACAAG GAAAATGCTC ACAATAATAT GTTAACTATA AAAGCCTGAT AAAAGTAAGA ATTCAGCATA ATCCCATATT TTAAGGGAAA TAAGTATATG TACAGAAAAA AGACTGAAAG ACAACAAAAT GTAAAATTGT TTATGAAGAC TGCCTGTGGT TTATTTAGGT TATCTTTGTT CTTTCTATCT TTTTATATTT TCCAGTAAAA ATGAGTTTAT ATTGCTGTAG AATCAGGAAA CAAAATATTG TGATGCAAAT ATGGCTATGG GACTCTTAAG AAAAAGGTTT TTATATTGAT TTGAGTATAT AACAGAGTAA CATAGCACTA AAGTTCAAAG TACAAGGCCA CCATATGAAT TTGATTAAGT AAAGGAAAAG AATTATTGAA AACAAGGATG CAAGTAATTA CTTTTTCATT TGGATTGTTT GTTCAAAATG TTGCTGCCAA GTTATCTCAC **R** TTATTTCAGC TAAGCTCAGA GAGACCCCAA CCTCCTGAGT TCAGCATGTC ATTGGCTGTT CTGTTCCTAC ACATTGCCCT CTTGCATTTT TTCATTTCCC TGGCTTCAAC TGCCTAGTCC TCCTAACCTT AACTCTTGGG ATTGACCTGC TGTGTATCTC CTATTTTTCA AAAAAATGCT TTATGCAAGT TTCTAATACC CACCAAATAC ACTAGTATTG TACTTCATTC GGTACAGTGC AATCAAACAC AGGTTGAGTA TTCTTTATCT AAAGTGCTTG GGACTGGAGG TGTTGCAGGT TTGGGAATTT TTTGGATTTT GGAATATATG CATATACATA ATGAGATATC TTGGGGATGT GACCCAAGTC TAAACATGAA ATTCACTTAT GTTTCACATA TACCTTATAC ACATAGCCTG AAGGTTAATT TTATACAGTA TTTTAATTTA ATAAGATATT TAAAATAACT TATGCAATAT TTCAAATGCA TGAAACAAAG

SEQ ID	Sequence
2003	GAGGTGCATT CCTCGAGAGA AGATTGACAG TTGCTTTTGC AGGTACTGGA TATATTAGCA ATCCAGAATA TCTTTTTTTG TTTTTGTTTT CTTGTTGTTG TTGTTTTAAA GACAGGGTCT TGCTCTGTCA TCCAGGCTGG AATGCAGTGG CACAATCATA GCTCACTGCA ACCATGGATT CCTGAGCTCA AGCAATCCTC CTGCCTCAGC CTCCTGAGTA GCTGGGACTA GAGCTGCACA CCACCACACC TAGCTAATTT TTAAAACTTT TTTATAGAGA TGGGGTTGCC CCGGCTGATC TTGAACTCCT GGGCTCAAGT GTTTCCCCTG CCTCAGCCTC CCAAAGTGCT GGGATTACAG GCATGAACCA CCACATCCAG TACAGGATGT CTTTAAATTA TGTTATCAGT TTGGTGTTTC CAGAATTCTT GGAGAGTAGA AATTCTGTCC CTAAACTTGT GTGATGGTAA AATACAAATT CTTAAACATG TTTTTCTCCC **V** TTTACTCAGA GGCAAAATCA AGGTAGACAA GTTTCCTTAC TAACTCGTTA AGAAAGGCAG GATTTTTTTT TTTTTTTAGT ATTACCCAGT GTGTGACTTT CAGGGTCTAA GCCTTATGTA AAATAAAAAG GTCTACAGTC AGACTTCCCA CCTTCATTAA TACCTGAGAA ATTAATGAAA TAGAGAATAC AAATAAAGAA AAATCTATCA AGTGTGGGCA CTAGATTTTG TCTCCTTTTC TCCTGAACTA AACCACGTAA ATGGAATCTC CAGGTCCCCA GAGACTGGCA GATATTCCTT AAGCAAAACC GTTTCAATGT CCTTGCTTAC CTTTCTGAAT TCATATGTTC CATTATTTGT GGTCTTTAAG GATTTCTCTT TTACTTTTTG CCAGGCCAGC AATATATTTA ATAATCTGTT GTTTAAAAAA TATTTACACA ATTATAGGTT TTTTTAAATC AAAAGTCTCA TTATGATTCC TAAGTCTGCC ATATTGCTAA

SEQ ID	Sequence
2004	TAAGTTCAAT TATAATATGT ATAGGAATAA GGTACCTCAA TATGTAAAAA ATCATCAAAT GAACTGGGCA GTGAAAATCA ACTGGCTTTA ACTGTTCATC ATATTTGAGT CATTTCTCTC AAACTCAAAC ATACTAAAAC TTCTTCAGCA AATCCATCAG TATTTGGTTT TCTTTTATAT GCTGATAAAA TCATAGATAA TCTTACAATT GACATCCTCC AAAAGATTCA AAGCTGATTC GAACCTTGGA GTTCAGGTTC CTGGCTTCTC TGTCTACTGG GGGTCAGGAT ACAGGAAGCA CAAGGAGGAG GGGAGAAGAT TGTGTGGGCA AAGGGGCAGG GAAGGGGCCA CCACTCACCA CCACTGCAGG ACGAGGCGCT GAGTAAGGGA CGGGGCTGCT CCCAGCAGAA TCCACAAAGT AGCTCATTCT GCTCTCAGCA CCTGTGTGAG AGAAGGCGTT GGCTGAGCCT CTGGATGCTC ACAGGTTTGT GGATTAGAAT **M** CACAAGGAAG ACACGAACCT TAGAACTAAA AGTCTCCTTA GGAGCCAACC AGTTCACTTC TTTGCATGGC AGGGAAAGCA ATGGAAATTC AGAAAGATCA GTGACTAACC CCCAGCACCG GTAAGAGCAG ACCTCAGACA GAACCAGTTC CCTGGTTGCA AGGTAACATG GATAACAGAC CATGTCTACA CACTGCAGAC AGCAAGCAGT AAACCAGTGC ACAAGAGGCA CATTTTTGTA GGGTTTCTGA GCAGGAACCA GTTCTTGTGT GTCTCCCCCA CCCACAACCA GGCCTGGCAG ATAAGTAGGC ATACAATACA CAGTTGGGGT GTAAATTAAT TGATAAAGGA ATAAACATAG AAAGGATTGG AGAAAGGAAG GATGGAAAAA GCTCTCCTGA AGAGGTATGT CACCCAGTAA CCCAAGAAAC AGATAAACAG AGAGAAACCC TGCAAAAGGG ATTGAGCATT ATTGATCTTG AAAAAAGGAG AAGGGCTATT

SEQ ID	Sequence
2005	GACCTAGAAG GATGCTTATG AAATGCTAAG TGGAAAAAAA GTGTGTTGCA ATATGGGTCA TAAGAAATGG TGTCTTTTCT TTTCTAAAGA GAGAATAGGC TGGGTGCAGT GGCTCACTCC TGTAATCCCT ACAATTTGGG AGGCCAAAGC AGGAAGATCA CTTGAGGCCA GGAGTTCGAG ACCAACCTGG GCAACATAGT GAGACCTCTG TATCCATAAA AAATTTTTAA AAATTAGCCA GATGTGGTGG CACGTGCCTG TAGTCACAGC TACTCTGAGA CTGAGGTGGA AGGATCACTT GAACCCAAGG AATTTGAGGC TGCAGTGAAC CGTGATCACA CCACTGCACT TCAACCTGGG TGACAGAGCA AGACCGTGTC TCAAAAAAAA GAGAAAGAAA AAACTATATA TGTGTGTGTA TCTGCAGAAA TCAGGTTAGA AATACACACA TTACACACAC ACATACATAT GTGTGTGTAT ATATATATAA TTTATTTAAT **R** CTAACGTTAT TGGTAGGTTC TTTAAACATT TTTTGAAACA AATGTGGAAA TTAAAAAATA ACATGGGCTG GTGGGGAATG TTAATGAGGG GGAGGCTGTG CACGTGGGGG CAGGGAGAAC ATGGGAACAC TATGTACTTT CCACTCCATT TTGATGTAAA CCTAAAACTG CTCTAATAAA TACTAAGTTA TTAAAAGCAA CCGTGAGGCC AGGCGCAGTG GCTGATGCCT GTAATCCCAG CACTTTGGGA GGCCAAGGCA GGTGCATCAC TTGAGGTCAG GAGTTCCAGA CCATCCTGGC CAACATAGTG AAACCCCATC TCTACAAAAA ATACAAAAAT TAGCTGGACG TGGTGGTACA CGCCTGTAAT CCCAGCTCCT CGGGAGGCTG AGGCAGGAGA ATCGCTTGAA CCCGGAAGGC ACAGGTTGCA GTGAGCCGAG ATCGCGCCAC GGCACTCCAG CCTGGGTGAC AGAGAGACTC CATTTCAAAA CTAACTAGCT

SEQ ID	Sequence
2006	ACTGCTAGAT CTGACATACA GAGAAGAGCA ATTACAGGGC TCTTCAAAGA TGCAGGTGCT GCCTTCACAA ACCTATTTTG CAAGGCATAT ATCAAGGGTA TTAAATATAT TAGCTGGGCG TGATCAGGCA TGATGGCACA TACCTGTAGT CCCAGCTACT TGGGAGGCTG AGGCATGAGA ATCGCTTGAA CCCGGGAGAC AGAGGCTGCA GTGAGCCAAG ATTGCACCAC TGCAATCCAG CCTGGGTGAC AGAGTGACTC TGTCTCCAAA AAAATAAGTA AATAAATAAA AAGAAGTTCT TAAGAGAGAA GGAAAATGAT ATAGGTTTGA AACTCAGATC TACATGAACA ATGGAAGAGC GTTACAGAGA TAACAGGTGA AGGTAAAACA AAACCCAAAG GGTATAATGG GTTTCCCTTC CCTTCTCTCT TTCTACGAAT GCAGTGAAAG GTGAGTTGTA ATCATTTCTA ATGATTTGTG CACATTCTTA TAAATATTAA **M** TTAATTCATA CACATGGGTA AACATATATA TATTCCTAGA TTATTATTGT TTATATGACA ATTTTTAATT CTAGTGAAAT AAAGATGTTA ATTTTAATCT ATAAAACTAC AAATTACCTA AAATTATTTT TGTCCCTTTT CTACATAAAC TTGTTAGAAA AAAATTATGT GCTCTTCATT TAACAGAAAT TTGAAATCAA GAGAACTGAT AATGCTCTTA TTTTCCGTAG AAGGTTTTGG ATTGACCAGT TTGCGTCAGG GAAAATATTT TTGTGCTTTT CACCTTCCTC AAAGCTGACA GATAGTTAAC TCTCTCCTTT CTTCCTTGGC ATGCAGGTTT CCTCCATGTT TTAGGTGGGC CTAGAGATGT AAAGTCATGG CCTTTTTCAA AAGCTACAAG CTGAGCCAAG CATGGTGGCT CATGGCTGTA ATCCCAGCAC TTTTGGAGGC TGAGGTGAGT GGAACACCTG AGGTTGGGAG TTCCAGACCA GCCTAGGAAA

SEQ ID	Sequence
2007	ACAAATGGGG AGGGCCTGTG TCCTCTACAA AGGAGTCCCC GTAGAGGAAC CCCTTCCACA GGGCACCCCT TCCACAGGGA GGGGCTGGGC CAGCAGCCGT GCGCAGTGGG ATTCCCGTGT CTGGGGGCTT CAGTCTTCTC AGGGGACACA CGCCCAAGAG GCAGGGAGCT TGGGTGGGGG CTGCACAGCT GTGGGCTTCT GTTCTGGGCT GCTGCTGCCT AGTGCTGCGG CTTCTGAAGT GTTACCCAGC CTCAGAGTTC AGCCCTCATC TGTAAAGTAG GTTTAAGAAA ACCGACTCCA GGTGAAGAAA ATGGAGCAAT ATGCACTGGG CACGGCACCC ATTCCTGTTC CCAGAGACCG CGGTGGTTCT CACTGTGCGG CATGTGCCTC TCACCTCCCC TCCCTTCCAA CCACCTTTCG GGTGCTGAGC CGCGTCGAAG GGACTTTTTG TCTCCTACCT CAGAGGCTCT CCCAAGCCAG CCCTGGCCCC ACTGTCGGGC **W** CAGCTCAGCA CGCAGGCGCC GGGACCTTAC CTGTCTGGCT GCCGACAGTC AGGTTCTGCT GCAGAAGCAC GTTCTCTATG CAGCAGCCAA TGTTCACGCT GGGGGTCCGT GCGATCCTCA GCACGCTGAC CACGTCATAC AAGCCCCGCA TGTTCAAGAA GACGGTGTCA TTCTGCAGAG CCTGGTCCAG CAGGCTGTTG TCCGTCTTAT TGATCCAGTA CACGTTGGGC CTGGGGTAGC CGTTTATGGA TGTACACGTG AAGGTGAGCT CATCCTGGGA GGGGCTGTGG GGGGCGCTGA CGACGGGCAC GCTGAAGTTT GCTGCAGGGG AGGGAAACAG ATTGTGAGAG ATGCCAGACC CTGCTGGTCA AGAAACAGAG GGTACACGGT GCCAAGGCTG GGTCAGAGGG GAGGCGGCCC ATTGTGCCCC GACATGGGTG ACAGGCCAGG ACCAGGGCTG TGGTCCGAGC AGCAGGCTCC GCCCTGTCCT GCCCAAGAGT

SEQ ID	Sequence
2008	CAAAGAAGGT TTTATCTTCT TTTGTGTAAT CCACCAAAGA GATGTCACTG ACGTTCACCA TTAGCTTGTC CCCTTCTTGC AAGGAGAACA TGGCTCCGAG GTAGATGGGC TGGAACCAGT TGCTACCTAC TTCGCATACA GACTTGGTCC CCATGAGGAG CTGGGTTGGC TCAGGGTAGC TGTCTGTTAC CTTGGTGATG ACCACAGTGA TGGAGTCTGG CTTGTTTGGT CGGCCTGCTT GTCTGATTTC ACTGCACTCA GAGGTCATCC CACGGAATGT GACCTGGGAG TAAATGAAGT AGTCTCCCGA CTCTGGGATC AGCAGGAATT TGTTGGTATA GTTCATTCGG TTCTTGGTGA AGGCCAGGCC TAGTTCATGT TCCCAGTGCA GAGCTGGGAA CTGATTTTTA AAGTGCTGTG TGGGAGTTTG TCTCACAACT GGAAAGACAA GAAAGAGGAT TAATTTTCTC ATTGGGAAAC TGTAGACTTT GCTTAAAAAG **H** GTCTCATATC ATTTTCAAAA TAGACTAAAG TGATCGAATA TACCTAACAG CTAAAAACTG CTTTGGGGAG GAATGAATGA AGAATATGTG ACTGGACATA CACATTTGTT CAAAGAGAAT AACATCTTGG ACTAGTGACC TGGGGCAAAT TACTTTGCCT TTCTGAGACT GAGTGGTCTG ACCTGAAAAT TTTTAATTTT ACCTGAGACC TATGATCCTG GAGAACAATG AAGGTTAAGG AATCCCCCTA TTCTTCTGTG TTTAGGAAAA TGGCTTGCTG CAAGAATTAT CCTTTCCCAA ATGACTCAGA TAAAACTCAT CGATGCCTCT CTTGTTTACG TATGACAAGG CCAGGCACCA GACCCTTCAA ATTCCCATTC TTTGCCCCAT AAGTGATTGG CTGAACTGTT TTATCCCCAT TCATCAATTG GAACAAAACA CTTGTCTTAC AGGCATGAGG TAAGTGATAG AAACTTGGCA TCTCCCTGGT CCTAATCCTC

SEQ ID	Sequence
2009	GGTCATGGTG GCTCACGCCT GTAATCCCAG CACTTTGGGA GGCTGAGGAA GGAGGATCAC TTGAGGTGAG GAGCTTGAGA CCAGCCTGGC CAACATGGTG AAACCCCATC TCTACTAAAA ATACAAAAAT TAGCCGGGCG TGGTGGTGCA CACCTGTAAT CCCAGCTACT CGGGAGGGTG AGGCAGGAGA ATTGCTTGAA CCTGGGAAGT GGTGGTTGCA GTGAGCCGAG ATCTCACCAC TGCACTCCAG GCTGGGCAAC ACAGCAAGAC TCTGTCTAAA AAAAAAAAAA AAAAGAAAGA AAAAAAGAGT TATATTATTT ACGACTCTTT TAGCTTCACT TTCTTATAAG ATTGTTGTGA GAAGTGAGTA AGACACATGC AAAGTGGTAA ACTGCCTGGC TGTCATAAAA GTCTTGGCTA CTATCACGGC TGGGAGGCAA AGGAGATTCA GAGAAGGGCA GAATGACTGC ATAAGGTGAT CTGCCTGTAA CTCGTGTTTC **Y** TCCTTTCTAG TATAAAGAGA TAAAGGACTT CAAGGTCTTA AACTGGTGAG GGAGTATTAC AGCCTTTGTA TGGAAAGGTT TGACTTTGTG TCTCTGCTTA AACCCCCATT GTGTTGCCCC TACCAATTAT TGTGCTGCCC CCTTGTGGTT AACTGTGCTA AGACCTTTCT TTTGCTCTTC TCCCATTACA TTTCCCACCC TTCCCCACTC CCTTTTAGAC CCCTCCTCTT AGCTCCCAGT TTCCCAAACT GTGTGCCAAG GTGCCCAGAG CACCTCAGGC TTGAACTTGT GTTTTGAGTT GGTTCATGGT TTCAATATTA GATACCTACA CCCGTTTCTA CAATGTCATG TCTTTGTAAA GATGTATTTT CAGAGGTTGC TCCGATAAAA AGCAACTACT ACATGAAAAT GAATGTAGAA CAGGAAATGA CAGTGTGGTA TTGTCCAATT TGATTCTAAG GTTTGATAAG TTCTACAGTG CTCTACACTA AGTTGTAAGG

SEQ ID	Sequence
20010	TGAGCAGGTG CAGCCCACGC TGTCAGGAAT GCCCTGAGAG CCTGGCAACA CTCCCGGGAC TCAAGAAGGC AGGTGGGATA AGAGCTACAA GAGAGGTGCT AATGGTACCA CTGTTATCAT CAAAGAGGGT AGAGTAGATT TCCCCTCACT GCGCATCTGG GACACCTTAC TGGAGGAGGT GGCATTTGAG CTCGTTTTGA TGAGATAGCA TATATTTTAA TCAAATCATG TGTACCTGAA TCAGGTAACT TATATTTTGA TATTATGAAT CAGGTAACTT ATATTTTGAT ATTATGATCC CTCCAGGAAA ATAAAAACTA GAAGATGGTA ATAGCTCACA TTTATGGAAG GCGACCTATA CAGCAAGCTT TTCACATCAT GTCCTACGTA TCTCATGAGG ATGCTGAGAT GCTCAGGGGC TCTGAAACAT ACCCGAGGGT TCACAGTGAG AGGGTGGCAG AGTTGGAATT TGAATCCTGG TAGGTTTGTT CCCAAAGAGA **M** CCTGGCATAT TGGATTATAG GGGCTATTCC TGCCTGACAG ATCGGACAGG TAGTGGAAGG AGAAATGCAG CTCAGAGCCC CATTTAGGAG GCTGGTTGAC TGCATCATAA GACACCCTCT GCTGAGGCTT GAAATGCATT GTTCAAAACA GTTTACAGCC AATTTTGGTT TGCCTCTGAT AGAAGGAGCT GAACACAATT TTGATTATTT GCTTTAATTC AAATCAGGTT AACAAAATCA GTATATTAGT GCAATTTAAG GACCTTTTTC CCCCTTTATT ACATAAGCTA GTGGACTTCC CATCTGATGT ATGAAATGTC ACTTTGTCTT TAATTCTTGA CGTTCACAAA CACTGGTGCT ACTGGAAAAG GAGTGGGAGT GAGCGTATGT GTGTGTGTGT GTGTGTGTGC ATGTGCATGT ATGTATATAC ACATATATAT GAGAGTGAAA ACCAAACTGA GGTTTCAGAT GGACTTTAGA AGGATTGAGC AGGTTTTGAA

SEQ ID	Sequence
20011	AAAGATCTCC AGATTGCTTG TCCCGCAAAT TCCTAGCATC CTCCTGTACT ATTGGATGGA CTGTTAGGAA GTTGACTTGT ATTACAAATG CATACTGATA ATTTTTTTTT AAAGTTGAAA TGTTGATGTG ACTACCTGAA AAGAGATCTT TGGCTGGGTA CAGTGGCTCA TGCCTGTAGT CCCAGCACTT TGTGGGGTCA AGGCAGGCAG ATCACTTGAG GTCAGGAGTT CGAGACCAGC CTGGCCAACA TGGTGAAACC CTGTCTCTAC CTAAAATATT TTTAAAAATT AGCTGAGTGT TATGGTGCAC ATCTGTAATC CCAGCTACTC AGGAGGCTGA GGCAGGAGAA TCCCTTGAAC CCAGGAGGGG GAGGCTGCAG TAAGCCGAGA TCGTGCCACA GTTGCACTCC AGCCTGGGTG ACAGAGCAAG ACTACATCTC AAAAAAAAAA GAGAGAGAGA TCTTGGGAAT CAGATAGGTG CAATTCCTAC CACCATTAAA **K** TCAGAGTAAA ACTGAAGTAT ATTTATTAGT CATTTCTACC TCTTATATAC AAATATGTCT GGCAGTTGTG ACTTGATTTT GTTTCTTTTC TCCTAAGAAA CTCTTTTACT CACTCGCTAG TATCATTAAG AGGTATGAAT CAACATCGAA ATTACCAGAC TTTTAAAATA GCCCTCTTTT TTTAAAAAAA AGTTGACGTT CTATTTTTGT TTAAATATCC CTTTTGATGT GCTAACTAGG TTAGTCTATC ACCTTTAATG AAAACTTGAA TTTCTAAAGG TGCATTTCTA AAGCCAAGAA AACAAGTAGG TTATGACAAA CAAACAAACA GTGGAAGTGA TGCTATGCAT CAACTGTTCT CCAGAGAAGT ATCAATAAAT TGCTTGTAGT TATACAAATG CAGATGCATA CATTAGAGAT TTCCAAAATA CAAAATAATT AAGCTTGATG AAGACTGATA TTATATATGG CAAAGGGAAA TATTTAGGCA GTGTCATCTT
20012	TTCTTTCTTATTTATTTGTACATTATCTGTTTGTATCCTTGAATTT TCTCTGGGATGTTATAAAAGAAAAATATTACAAGCATAATTTCT GACACAATGTTTTATAACTGTTTTCAAAAGCAATCTATTTCTCTC TTAATTTCTATAGAACCCATTTTAGTCATTCCTATGATGAATGA AAAAAAACTCACAATTAGTTGTCAGTTTCAGAAAGGAGTCTCA GAAGCATCTTAGAACCACCTAGGCGGTCTTATAGGCGTCACAG AAAAATATTCCACCTTACTTATTCTTATCTTCTTCAAACTGACTC CAAATATAATAAGCAGGCTTAAGTTATATAAGGTTCCTTAAAA GTTGTTCTCAAAAACAATTAAATGCAGACTGTCCTCAGTAAAAC TTGCATTGGCCCAGTCCATTTTACCAAGTTTGCTCCTTCTTACAT GTACGACTGCCCCTGTGACAAGTTTAAGCCTACGTTAATTAATC ATCTTTCCATAACA**N**GAGACATATTCATCCAACCCTGAGAGGG ATAAGGGGTAACAGGCAAGATATATTCAAATTGTGACATTTAA GGTCAACTTGACTTTAAAACTCATATACTGCTCAGTTTTCATAT ACGTGGCTGAAAACAAGTCATCACAGAGAACTGGTCACACTGT TAGAGGACCAAAATAGTAAAATATGAACAATTCTTCCATATTTA ATGATATTAAATATAACAGGTCCTATGTCTATGCAATTGAAGTC AACATGTCACTAATTAGGGCTTCCTTTGTTATCAAACTTGCTGA GAAGATAGAACAGTGAGGAAAAAATAGCAGGAATTGAGCTGT ACAGAATTAAAGACATTCTTATGAACCTTAAGACTTAAGGTCA GTCACACTCATATGACATTTGGACTATTAGACAACTCTTCTGAC CTCAAATTTTGCTCTTACCAGTTGGTGATAATCCTTTGGTAAGA GAGCATGTTAAAAGTAACCAAATCAGATAAGGACTA

SEQ ID	Sequence
20013	TTCTGAGCAC TCACATTTTA ATGCTGGGAA TTTTATGCTG AGGTTCAGTG CTTTTCAGGG AGCCATGAAC CCCCTGCAAT GACTTGCAGA CTGTAGGTAT TACATGTAAA ACTTGTGTGA GTAATTTCCT GAAGAAGGGG TTTCATTCTT CAGATCCTCA AAAAGATCTA TGATCCGGCC AGGCGCGGTG GCTCATGCCT GTAATCCCAG CACTTTGGGA GACCAAGGCG GGCATATCAG GAGGTCAGGA GATCAATACC ATCCTCGCTA ACACAGTGAA ATCCCATCTC TACTAAAAAT ACAAAAAATT AGCTGGGTGT GGTGGCGCAT GCCTGTAATC CCAGCTACTC GAGAGGCCGA GGCAGGACAA CAGCTTGAAC CCAGGAGGCG GAGGTTGCAG TGAGCCAACA GAGTGAAACT CTGTCTCAAA AAAAAAAAAA ATATATATAT ATATATATGA TCCTAAAAAG ACATTGATAT TAAAGAGTAA TGATGGGGAA **R** GACCACCAAG TGATCATTTA TAAGATGCTG CGAGAATTGC TAAAGTTGAG GGATGGATTC TGCATTCCAG GAGAACAAAG GAGGTAGATC CCGATTAACT GAGTAGCAGG ATATTGAGGG AAGCTTCTTG TAATGATTCA GCTGAGTCTT ACACAATGAA TGAGACTTGG ATAGATGAAC ATGCATTAGG AGACATCAGT TCTGGTCAGA GGAAACAGCA AATGCAAAGG CCCAGAGCCA TAAGAGATTC AGATGCACTA AAGAAATATC CCATCATTTA GGATGGTCGG CATATACACA GAGGGCCTAT AAGGAAGGAG AAGAAACTGA GGTTGTAGAA GCTGGTAGGG ACTGCATGCT GAAAGGCATT GTAAATCTTA GACTAAAATC TGTGGGAGAC TTTGAACAAC CTAAAGATTT TAAGCAGAGT GATGCAATGC ATTTGTCTTT TGAATGCAAA TATTGCTGGG GCGGGTCTTT TGTGTTATCA GCTAATGATT

SEQ ID	Sequence
20014	TGTAAACTTA TTAGTGCCTC TGCACACCAT ATAATTAAGA TCAAATTCTC CAAGGGTTTA AAATAGGGAC TGCTGCTATT GTGCTGCTGA CAGCGCTAAG GAACAGATAT TTGCCTTTTT TACATAGACG GCTCTGCCCC GCTTTTGCTG AAATTCCCAC TCTCACAGGG CTGGGAGCCC AGCAGGGTTT ACCTGGACCA ATGAGGGGGG CTCACTCTGC TGGGAAATTT GCTTTTATAG ATGGCACCAC CAACGCTGAA AACATGGAAG TGGAGGCAAA CATTCCAGAG CATCTACTGT CGCATCCCCT AGAAGGGGAC TGTGGTCAAG GCAGATCAGT AGACAGAAGG CTGGAAGGGA AATGAGCCCC AAGGAAGAGG CTCAGATCCA GAGCCTGTGT CTTGGTGAGA CTCCAACAGA AGTGCCTCGA GGCTGGTGCT TCAGAAGGAA GTGGGTGTAC AGCTGTGTAA GTGATCTGGG TCATGAATAA ACAAATGAAC **M** CAGGAATGCA TGCACCATGA GAGCCTGGAG GGGACTATAA GACAGACAAC GGGTGATCTG GGCACAGGTA TCAACTGCTG AACGCCCAGT GTGTGCGTGG AGGAGGAAGG GGGTCAGAAA GGCAAGGAGG ATGTACCAGT ATGGTAGAGA CGAGCAACTG TGGGCAAGGG GTGCTCAGGA TGCATGGGGG TGTGGAGAGA AGGGGAGAGC AAGAAAGGCT TCCAGGGGTG AGGAGCCAAG GAGGTCCTGA AGACAGCTAG GAGTTAGCAG GCAGAGGAAG GGGATGGGCA TCCCAGGGAG AAGGAACGGC AAGAACAAAG CAGCACAGCC GTGGAGAGCC TGTCAGTGAG CGGAGAGCCC GTCAGTGAGC AGCTCGCCTG GGTTCCAGGG AACAGGGCCA GAATTTTTGG CAGGATAGAC TCAAAGGCCT GAGGTGAACC TGCAAACAAA GGTAAAAACA CTAACTGGTT TTAAGCAGGA GAGAAATATG ATCAGATTT

SEQ ID	Sequence
20015	TCACTGCAAC CTCCACCTCC CAGGTTCAAG CGATTCTCCT GCCTCGGCCT CCCGAGTAGC TGGGATTACT GGCATGCACA TCATGCCTGG CAAATTTTTG TATTTTTAGT AAAGACAGGG TTTCACTATG TTAGCTAGGC TGGTCTTGAA CTTCTGACCT CAAGTGAACC GCCCACCTCG GCCTCCCAAA GTGCTGGGAT TACAGGCATG AGCCACCGTG CCTGGCCAGG GGATGATCTC TTTCTAGAAA TTCATATCCT TCAATTCTGG AAATGTTTCT CATGATAGTT CTTTGATAAC TGACCCTCCT TCCTTCACTG TATTTCTCTT TCTGGGACTT TTACTAGTCA GTGTATTTCT GGGTTGGTCT CTCTCTTTTC TCTTTTATTG GCAACCCTGA TCTAAGGAAC TAAGGTATAG AGGTGGTTGA GTCCTGACCA GAGCCGTGAG GGTCTAGATT TATGTAAATG ATGGAGCCAT ACACGTTACT TTATTTATAG **Y** AAGATATTGT AAAGATTTTG AAATGTCATT TATATGAAAT GTCAAGATTA TTAAATTCGT AGTTCACTGT AACCTCAAAC TCCTGGGCTC AAGCAATCCT CCCACCTCAG CCTCCAAAGT AGCTGGGACT ACAGGCACAT CCCACCATGC CCAGCTAATT TTTGTATTTT TTGTAGAGAC GGGGTTTCAC CATGTTGCCT AGCCTTGTCT CGAACTCCTG GACTCAAGCA ATCCTCCTGC CTTGACCTCC CAAAGTGTGG GGATTACAGG CACTGAGCCA CTGCACCTGG TCAATGCATT TTTAAATATG GTCTAAGGGT ATCAGCAAGT TGCAGATTTG ATAACAGCTG GGTCTTTTCA TTTAGTAACC ACCCTTTTTT CCTCCTCTGT ACTCTCACAC AATATTAAAA TACCTCCTAT TAAATCTCTA TTATCCTCTT CTCTTCCTGT TGCATTTTTC TCCCACAACT TAAGGCTCAA GTCTAAGCAG TGAAAACATA

SEQ ID	Sequence
20016	ATAAATTAAA ATAACAGATA ACATGGGCTG TTTTTGACAG GAATATATTT TAGCTTCTGA TAATTAGCTT TAGTAATCAT TAGCTTAGTT AATGAAAAAT AAAATACTTA TAATATTAAA AATATGAGAA GCTAAACTAT GAGCAACTAA CAAATCAAAA CCACGTTCTT CTGAATTCCT GACTCCCCCG CAAATAGTTC CAAATCACTA TAGTATTCAC ATAGCCCTAT AATAACCTTT GTGGATAAAC AGTGAATTCC ATGTTCAATG TAAAATAACA CAGAAATTTA GAGTTTTAAT TGCAATGTCC TATGTAAACT TTAAAAGTTT CCAAAGCAAT TTTCATAAAT GGGATTCCAT TTTCCACAGC CAAAATACTA TACTGACACT GACCCTCATG AACTGTTACC TATGCATTTG TGTGCCATTT ACTTTTAATT ACAAAATTTC TCCCCTTGAT TAAATTTATT GTATGCCTTG CAATATATCA AAATGATAGA **W** TAAATGTATA AATAAATTAT TATTTATAAC AAAATTGAAG CTTGTCCTTG GAATCATTTT CTTGTAGTTC CATGTAGCTA AAATGGGGCT TTGATTTCAA CCTTGCCCCT GATGAGCTGT GTGATGAAAT CTTAGGCAAG TTACTCAACC TAAGCCTCAG TTTCCTCATC TGCAAATCAG GGAAAATAAT ACATGCTTTA GACTATTATT TTGAGAATTA AATGAAATCA TGTATACAAA TTGTCAAACA GGGCACAGCA TACTCAGTAC CTTATCATTG TTTAGTGTTG TTATTTTGTA TCTACAGTGT TTTTGGAAAA TAGCATGATT AATCAATTGA CTGGAAGACA CACAGTCTAA CAGACAATAT ATAGACCATT TATATTGGCC ATGAAAGTGT CCATAATGGC TGACTTAACT GGCTTTAATG TGTAAAATAT GGTGACTCCC ATGGTTTTTA AGATATGGCT TAAAGTAGAT ATCAATTTCT TTACATTGGT

SEQ ID	Sequence
20017	GACCTAGAAG GATGCTTATG AAATGCTAAG TGGAAAAAAA GTGTGTTGCA ATATGGGTCA TAAGAAATGG TGTCTTTTCT TTTCTAAAGA GAGAATAGGC TGGGTGCAGT GGCTCACTCC TGTAATCCCT ACAATTTGGG AGGCCAAAGC AGGAAGATCA CTTGAGGCCA GGAGTTCGAG ACCAACCTGG GCAACATAGT GAGACCTCTG TATCCATAAA AAATTTTTAA AAATTAGCCA GATGTGGTGG CACGTGCCTG TAGTCACAGC TACTCTGAGA CTGAGGTGGA AGGATCACTT GAACCCAAGG AATTTGAGGC TGCAGTGAAC CGTGATCACA CCACTGCACT TCAACCTGGG TGACAGAGCA AGACCGTGTC TCAAAAAAAA GAGAAAGAAA AAACTATATA TGTGTGTGTA TCTGCAGAAA TCAGGTTAGA AATACACACA TTACACACAC ACATACATAT GTGTGTGTAT ATATATATAA TTTATTTAAT **R** CTAACGTTAT TGGTAGGTTC TTTAAACATT TTTTGAAACA AATGTGGAAA TTAAAAAATA ACATGGGCTG GTGGGGAATG TTAATGAGGG GGAGGCTGTG CACGTGGGGG CAGGGAGAAC ATGGGAACAC TATGTACTTT CCACTCCATT TTGATGTAAA CCTAAAACTG CTCTAATAAA TACTAAGTTA TTAAAAGCAA CCGTGAGGCC AGGCGCAGTG GCTGATGCCT GTAATCCCAG CACTTTGGGA GGCCAAGGCA GGTGCATCAC TTGAGGTCAG GAGTTCCAGA CCATCCTGGC CAACATAGTG AAACCCCATC TCTACAAAAA ATACAAAAAT TAGCTGGACG TGGTGGTACA CGCCTGTAAT CCCAGCTCCT CGGGAGGCTG AGGCAGGAGA ATCGCTTGAA CCCGGAAGGC ACAGGTTGCA GTGAGCCGAG ATCGCGCCAC GGCACTCCAG CCTGGGTGAC AGAGAGACTC CATTTCAAAA CTAACTAGCT

SEQ ID	Sequence
20018	ACTGCTAGAT CTGACATACA GAGAAGAGCA ATTACAGGGC TCTTCAAAGA TGCAGGTGCT GCCTTCACAA ACCTATTTTG CAAGGCATAT ATCAAGGGTA TTAAATATAT TAGCTGGGCG TGATCAGGCA TGATGGCACA TACCTGTAGT CCCAGCTACT TGGGAGGCTG AGGCATGAGA ATCGCTTGAA CCCGGGAGAC AGAGGCTGCA GTGAGCCAAG ATTGCACCAC TGCAATCCAG CCTGGGTGAC AGAGTGACTC TGTCTCCAAA AAAATAAGTA AATAAATAAA AAGAAGTTCT TAAGAGAGAA GGAAAATGAT ATAGGTTTGA AACTCAGATC TACATGAACA ATGGAAGAGC GTTACAGAGA TAACAGGTGA AGGTAAAACA AAACCCAAAG GGTATAATGG GTTTCCCTTC CCTTCTCTCT TTCTACGAAT GCAGTGAAAG GTGAGTTGTA ATCATTTCTA ATGATTTGTG CACATTCTTA TAAATATTAA **M** TTAATTCATA CACATGGGTA AACATATATA TATTCCTAGA TTATTATTGT TTATATGACA ATTTTTAATT CTAGTGAAAT AAAGATGTTA ATTTTAATCT ATAAAACTAC AAATTACCTA AAATTATTTT TGTCCCTTTT CTACATAAAC TTGTTAGAAA AAAATTATGT GCTCTTCATT TAACAGAAAT TTGAAATCAA GAGAACTGAT AATGCTCTTA TTTTCCGTAG AAGGTTTTGG ATTGACCAGT TTGCGTCAGG GAAAATATTT TTGTGCTTTT CACCTTCCTC AAAGCTGACA GATAGTTAAC TCTCTCCTTT CTTCCTTGGC ATGCAGGTTT CCTCCATGTT TTAGGTGGGC CTAGAGATGT AAAGTCATGG CCTTTTTCAA AAGCTACAAG CTGAGCCAAG CATGGTGGCT CATGGCTGTA ATCCCAGCAC TTTTGGAGGC TGAGGTGAGT GGAACACCTG AGGTTGGGAG TTCCAGACCA GCCTAGGAAA

SEQ ID	Sequence
20019	GGCAATTCCA GTGAAATAAT TGTTTGTTTG TTTGTTGAGA CAGGGTCTCC TTCTGTCGTC CAGGCTGGAG TTCAGTGGTA TGATCTTGGC CCACTGCAAC CTCCACCTCC TGGGCTCAAG CCATCCTCCC ACCTCAGCCT CCCGAGTAGC CGGGACTACA GGTGCACACC ACCACGCCCG GCTAATTTTT GTATTTTTTG TAGAGGCGGG GTTTCCCAGC GTTGCCCAGG CTGGTCTTGA ACCCCTGAGC TCAAGTGATC TGCCCACCTT GGCCTCCCAA AGTGCTGGGA TTACAGGTGT GAGCCACCGC GCCCGGCCTG AAACAATCGT TTCTAAATAT TGGTGTGGGC CACACAGTCA TGTTTGGACC TACTTGTGGC CTTTTACAGA CCCCAGGCCA AGGCTTTGGG AACTTGGCTG TCAGCCTCCT GTGCCTTCTG CACCCCCACC CCATTTCTGC TTTCTGGAAC CCCCGATCCT GTCCTGTTCT GTGGTGATTC **R** GGTGTGCTTG GGCTCTAGGA GAAGATGTGT GAAGAATCGG CATCCTTTGA CCTGACTCCC CATGACCTGG CTTCAGGACT GGACGTCATA GACCAGGTGC TGGAGGAGCA GACCAAGGCA GCGCAGCAGG GTGAGCCCCA CCCGGAGTTC AGCGCGGACT CCCCCAGCCC AGGTGCGTTC ATAGCCAGAC TGCTTGGTCC TGAGGCCTGC GCTGCTGCAG GGTGAGCCCC ACCCGGAGTT CAGCACGGAC TCCCCCAGCC CAGGTGCGTT CATAGCCAGG CTGCTTGGTC CTGAGGCCCG TGCTACTGCA GTGGGCAGCC TGCCCTGTGG CTGTGTGTGG TCGGCCTGGG CACCATCTAT TCAGGCTGGC ACTGCAGGGC ATCCGCTTCT CTCAGAGGCT TCTTGGGTGT GAATTCTTCA GGGTCCTGTA GCCTGTGGAA GGGCTGGTAT TGTTCAGTAG TTCTGGTATT TTCCAAAGAC CTATGTCTTC TCCCAGCCAG

SEQ ID	Sequence
20020	GTTGGTGGAT TTGGCCTGCA CGGATTCTGT GTGGCCTCTT CCTTCCCCTG TTGGTGGATT TGGCCTGCAC GGATTCTGTG TGGCCTCTTC CTTCCCCTGT TGGTGGATTT GGCCTGCACG GATTCTGTGT GGCCTCTTCC TTCCCCTGTT GGTGGATTTG GCCTGCACGG ATTCTGTGTG GCCTCTTCCT TCCCCTGTTG GTGGATTTGG CCTGCACGGA TTCTGTGTGG CCTCTTCCTT CCCCTGTTGG TGGATTTGGC CTGCACGGAT TCTGTGTGGC CTCTTCCTTC CCATGTTGGT GGATTTGGCC TGCATGGATT CTGTGTGGCC TCTTCCTTTC CATGTTGGTG TCCTTTTTTC CATGCCAGGA ATCCTGGTTC TCAAGGGCGG GGTTGTTGGC ACGAGCGTGA TGCAGACTGC CTTTGCTGCC TTTCTCTTGC CCAGGGCTGA ACATGGAGCT GGAAGACATT GCAAAGCTGA AGAGTAAGTG TTGCCCTCCC **Y** GCCTCCTTGC AGCTGGGTGG GGCCTCCTCC TTGCGAGGAG GTGGGTGACA CCTCCTCGAC CCACAGTGAT CCTGCTGCGC CTGGAGGGGG CCATCGATGC TGTTGAGCTG CCTGGAGACG ACAGCGGTGT CACCAAGCCA GGGAGGTGAG AGGCGGGGAG CCAGCCCCTT CACTGCAGGC CCAGCCTAGA GCTAGAAACG GGCCATGGTG CAGTCCTGGG CTGTCACATC ACGAGTGAGG CCTGTTTTCA GGCCTGTTTT CCCTTTTTGA GACCTGGGAG GAGCACCTGC TTTGCATGAT CTGGTTGCTG AGATGTTGAG AGGAGCAGCA CACACTCCCA CGGGACAGCA CACAGCCCCC CACGGAACGG CACACACACC CATGGAACAG CACACACACT CCCACGAACA GCACACACAC TCCCACGAAC AGCACACACA CTCCCACGGA ACAGCACACA CACCCACGGA ACGGCACACA CACCCACGGA ACAGCACACA

SEQ ID	Sequence
20021	AAAAAAAATC CACATCCTAA CTCCTGGAAC CTATGAATAT GTTAGATTAC ATGGCAAAAA GGACTTAAGG CTGTGGATGG CATTAAGGTT GCTAATTAGT TGCCCTTAAA GTAGGGAGAC TATCCTGGAC TGTGGAAGTG AGCCCTGGAT TATGAATGTG ATAGGGAAGC AGAAGCATAG AGAAACTATG TTACCAGGTT TGAAGGTGCA GGAAGGAGCT ATTAACCAAG GAATATGGGC AGCTCTAGAA GCTGGAAAAG CAATGGAATA ATTCCTTCCT AGAGCCTCCA GAAAGGCACA CAGCCCTGCC ACACCTTGAT CTTAGACCAA GGAAACCTGT GTCAGACTTC TATCCTACAA AACTGTAAGA TAGAATTGCG GGTTGTTTAG GGTGCTATTT AGGGTAACTT GTGACAGCAG CAACAGAAAA GTAATGCACT TTCTCAACTT TCCTCTCTCC CTTCTCCCCC AGAACCAAAC ACTGCTGGCT CTGGGCTCTC **R** CAGAACACTG TCCTTACAGT ATTTAATGCT CTTGATACTA TCTGGGGCCT GGCCACGTGC ATCCCATCCT TCCCTTAGCT TCTCCAGGAG CATTGTGGCT TGGTGTCACG ACCTATCTGA AAGCCTTAAC CCTGCCACCA CCCACTTTCT GCTGGAAGGA CAGGCACTGT GAAGTGAAAG GACCCACAGC CCATGAACTG GAAGGAACAG GAAGGGCAGG AGAAAGAAGA AATAAGAGGA GAGCAGCAGG GGGATGCAGG GAGGAGGAGG ATAAAGGGGT TACCAGAGGA GAGGAGGTGA GAAAACAGAG GGAAGGAATG AAGGAGGAAG ACAGGGTCAA AGAAGAGGAG AAGGAAGGAA GGGCGCTGGA GGAGGACACA GAAGCTAGGG TGGCAACGAA GAGGAGAAGG GAGAATGAAG AGAAAGGACC TTGTTCTGCC CCCACCCATC TCCCACCTGA ACACCCTCTC CTCCCTCCTC CCTGAGATCT CCCCCAGCCT

SEQ ID	Sequence
20022	AGGAAATTTC ATAGAAAAGG AAGGGAAACA GTGACACTCT CCAGTTTTGG CCTGAGCATA TAAAATTATT TGCCTCTGAA GCCCTGAGAT CCTAGGCCAA AATAAAACAA AACAAATAAA ATTAAACATC ACGATAACTT CAAAGCCTTC GTTTCTACAT AAGCAGGAAC TGAGGAGGAA ACTGAAGCAT TGGGCTGCCT AGGTATATGA TCATTGCAAT GTCTCTAGGT GGATGGATGA GTGCCTGGGG AGCAGCATAG ACTGATCTCT TGCTTCTACT TCTAAATCAT GGACTTCCCC TATCATCTAC CTAACAATGT TGGACCCTGC AATTTCAACC TGTGAATTTT GTGATACTTA TTATATGCAG TTTTCAAGCT CTCTTTAGTT TGCTTTTTCT TAGGTGGAGA AAAGACTCAT TCAAGTTGAT GTTGATAGTG GATATCACCC CATCAGATAC TATGATCATA AGATTAGAGC TTGGAGAGCC CCAAAGAGTA **Y** CTGGTCTTCT TTTTCAAGCT GAGGATACAG AAAGCCCAGA AAAAAACATG ATTTGCTGAA GGTTACCTAC ATAGTGAGTA AATGCATGAG AATGAGAAGC CAGGTATTTT GCTTTCTGTG ATCACTCTTA TCAGAGGAAA TTCTTATGGT TGCACTTATG ACAGCTGCAT TAAGAGTCTG TACAATGGAA AGCTTTGGAG GAGCTGTTAA ACATATGGAG TCTAAGGAAA TGAGAGTCAG AGAGACGGCT TCAACTTATC CCTTATCTAT AACTTGGCAG TAGAGCTTTC AAGAGCTCCA ACCGCCAAAG CTATGGTTTG CTTTCTGAAT TGCTGAAACC ACAGTGAAAA AGGAGAAATA ACAGGAGTGT ACAGATTTTT CTGTGTTCTT TGGCTTTCAC ATTTATCTGG TCCAATAAAT TCAACAGGTA TTTCACTGCA AGTTGAAGTT GAATGATAAT GTACAACTAT GAGGTATATT TTCTCAGCCA TTTCTCTGAA

SEQ ID	Sequence
20023	CTCCACTGTA GCTCAAGTGT CAATGCTTAA TACTGCTTGA TTTTCCTGAA TGATTTCTCT ATCCCCCAAA GTAAAATGTG TAATTTCCCT TTTTCCGACT CCAATGTTCC TGCACTTACT GCCAACATAC CACTTTAAAA TACTCTAACA TCTGATTTTT TTATTTCCCA TTACATATCT ATTACATATC TCTTGAAGAC AAGAAATCAT TTGTATTTTT ATATCTTGTT TTCAATATTT AAATGACACA TGCTATTTCC ATTCCCAAAT TAATTGATAA ATACATGAAT AAATAAAATA GCTGTGCCAT ATAGTTATCC TTGATATCAC TCTAGATGAG GAAACTGAGG CTGGAAAGAT TAAACAGCTT AAGTAATATT AACAAAGCAA ATAACTCTTG GGACCTCCTT GCTCTGTGTA TGTCAAAGCT CATGCTCTCT TTCAACTCCA TTACATCTCT TTGAATCAGA TAGTAAGATG AAACCTCTTC TAGGAAGTAA **R** GACTTCCTGG CCCCAATCAA TTCTTTTTAC TTGCCACCTG CTTGTGAATA TTAATATTGC TTTCGCTGGA TTTTAAAAAG TAGACTCCTA GGTAAACAGC AAACAAGAGA GGCAGAGGCC AGAATGCTCA GAAAAAAGGA TACAAACTGG CGCAATAAGG ATTATATGGT CTGAAGCAGA GGTATGTGGA AGCTGAGGTG GGAAAGTGAT GGTAAAGCAA ACCAGACCCA AGGATATTGG TTTATCTTAT GGCAATACTT AACCCATGGA ATGAGAACAT TTGTATGAAT TATCCATGCC ATTGTTTTCC TCCATATAAG ATATCATATT TCCCATACGT GGTTTGGAGA GACTTCCTGG AGTAGATCGA TTCCAAGTGT ATCTTGAATG GTAGGGAAAA TATGGCTTAG TGTTTGGAAA AAGGGATCTA ATTTGCAGAC TTCAAGGCCA GTGAGATTGA AGGAGCTGAT TCAAATAAAA AATAGGCATA CTTGAAGCAA

SEQ ID	Sequence
20024	TTAGCTTCTG CTTGAGCATT TCTACTCACT GGAGTTCATT ACTTTCTGAA ACTGTTTCCT GTTGAACAGC TTTAATGGTT AGAAATTTCT TTGTTATACT GATCCCAGGC ATGCATCACG GTGATTTCTA ATAATTGACA AAATTATTCC CCAGTTTTCT TAATCTCTTC TCTACCTGAC CTGGTTCATA GTAATATATT TATATTCCTC AATATGCATT CTACTATAGC AATATTTATT TTTTCATTCT CATTGGAGAA TTGTGGATAA TGTATTGACT TCAGAAAATA TACATGTGTA ATCAGTATAC AGGTAGACTA CTGTGAGGGC CACCTTAGAG GGCTGTTTTT GGAAGCTCAG GATCCAATAA ATCTAACACC CAAGACCCAT GATTAGCTCT TCATGGGTAG TTGAGGTCTT TCAGGGGGGT TTATTTTTGG TTAGTTACCT ATCTTAATCT TTTTGGTTCA TATCTCTTAT GGGGAGAGAG GTAGGGAGGG **R** CATGGAAAAT ATCCTATCAA ACCTCCATTT ATAATTGTGC TCACTATCTT ATAAATAAGA CAAGTAAATT TTTCTAAAAC TTCGGAAGTT TTCTTGATAA TTATATAGTC ATTTAAGGAT TAATGAATTC TCTAAAGTTT AGCCAGTTAT CCATATTAAT GGTAGCTAAA AATTGAGAAT GCCACAAAAA TTTCAGACAT CTGACTTTTT AAAAATTAGA ATTTTTTGGC AGGGTGTGGT GGCCTGTAAT CCCAGCACCT TGGGAGGCCG AGGCAGGCAG ATCACTTGAA GTCAGGAGTT CCAGACCAGC CTGGCCAACA TGGTGAAACT TTGCTCTACT AAAAAATACA AAAATTAGCT GGGCCTGATG GTGCACACTT ATAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATTGC TTCAATTTGG GAGGCAGAGG TTGCAGTGAG CCAAGATGGT GCTACTGCAC TCCAGCCTGG GTGACTTGTG ACTGGGCAAC
20025	TTTTCCATCAGGCTCAGAAAGCAGAGTGACATAAAAGCTGGGT ATGTGCTAAGGAGGAGGGGGAGGGAAAGTCTCCAAATAAATCA TTTAACTCACAGAGTTTAAGACTGGAAGATTCTCCTGGGCCTTG TAAGCTATAAAAAAAAAGCAGATCTCTGTCAAGAGGCCTTTTCTC TAAAGCAGTTCTGACTCAGCCTATTTGCCCTTGGAA GATGCTGCAGCACCTAAGACATCCACAGGCCATCAGTCAACAC GTGATCTCCTCTCTAGCTATGCTCCCTCTAGAAATGCAGGATCT TTTGCCCCATCCTAAACTCAGAAAAGGGGTTTCATGTGCAGAAC ATGGTGGAGAATCCTAGGTCTCTGACTCACAAAAGGATCACCTT GGGCCTGAGCTTCCTCATCTATGAAATGGGGATGG GAATTCATGCCTTGCTGTATAATTGCAAGGATTCTATGGAGTAA TAAAGGTAAGCGTCTGGCATGGTTTCTGTACATCTC**S**GGTGCTC CTGGTACTGGCTGTCACACAGGTCAATAAATATCATTTCCTCCT AATCTTTCCACATGCATAGTTATTGGAAAGCTGGGTGGGCAGCA GGCTATAATTTTTATTTTGCCCAAAAAGGCAGGACCTTATTTTG TTTATAGAAGGCAGAACCTCTTTGTTCTGCTTGAAACAAACAAA CAAACAAAAAACCTCTCCAAAGGCTCTTTTCATCCTCTGCTAAA TTGGACAATCCAGTCGGTCCCTCTGGAGTGGACTCAGTTGATTG CCTACCCAGCACCCATTTCTCCCCAACTCCCTACCTCCTTTTTAT TTCTCCTGCTTTATAGAACTCTGATTTCATACAGATATATTCATG TTCCTCCCTGGCCATGTGCCTCAAGGAAGGTAATCCCACTCCAG CTCCAGGGGGTTTTCTGATTGGTCTAAGACTTGGTTCTCAATCT CAGAGCTATTGATATTTTGGGTTGGATTTTTTTTTATTTTTTATTT TTATT

SEQ ID	Sequence
20026	CTATCTGGTGGAATTTGAAATATTTGTGTGATCCAGGCACCTAT CTTTAAAAAGGATGGAGTACTTGACCTTCCATCCTTGTCCCATG GCCCTTCTTCCTTTGCTTGTTCAGTCAAGCCAAATCCCACCACGT CTCTATCATTGTAAAACTTTTCAGGGAGAAAACCTCAATGGAAC CAGGGAAAGCATACCTACCAGGTCTTTTACTTTTACTTTTTTTTT TTAAGGTTGAGTTCCACACACTGTTGGTGGCACCTAAAAAACCA CTGCCACCAGTTGAAAAGTTAATTATGGATTACCCCTTGAAATA AAATACAAGTTTTATTAGAAGTGGAGGGATAAATCAAAACAGC TGGAGGGGGAATGCCATGAAACTGCTATGACGAAGCCCATGAT GTTCTACTTAGAGTAAACATTCTTTTTATTTTATTTTTTTTAAGT CCTGGGTCTGCTGTGTAGAAAGTCATCATCGCTTTCATGTGGGA CAAAAGAGGATTTGGNAAGGGAATTTCCTTAAATCTGTGCATT GAAAATGCAGCTTATGGGAGCCTAAAGAAAATACGTTTTGCTTT TTCTTACAGTGGGTGCCTCTTAATTGTGACTTTTATAAACCCCTT CTGTAGCTATCATAACCATCCAATTATCTAACTTCATTTTCGTAT GATTAAAAGAGCCTCTCTTGCCGAACATATGACAATTATTAGAA CGTTTCTAAAATCTTTTTTTCTAGTGATATGAAACTCCTGTAGAT AAAATAAGTCTTGATTTATACAATCCTCAAGTACATGTGAATGT TATGTCTATAAATAAATACTCCATAGTAGATGCAAAATCCCTTT ATAAGTAACAATACATTGGCATATTCATTGACCAAAAAGCCTTG TGATGTTAATGTTAACAAAATTAAACTTCAGCCATTTCATTCAA CTAGTAATTCCTGAGTTCTAAGGACTAGGCACTATGCTAGGCAG GGAAGCTATATATGTATGTGTGTCTGTGCC
20027	ACCATCCATGGTGAGCGGCTCTAACTTTCAATCTGGCCAGATCA TTTTCCCCTTGTATTAAAATTGTCCTGGAAAACCATTAGGTTGA TTTTCAATCATCACAGCTAATACATTCCTTGTTGCAAATGCCAA GTATTCTGCACTTGCTTCAGTTTTTCAGATCTTCTCTCTCATATT CAGTACCTGGGGTGAAATCCATGCCTAGTAAAACAGCCCTTTTG TATCCAGGCCAGGATGCATCTCTGAGACTTGAATGCTTTTGCTT TCTCTCCTGTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGGTTTTG TTTTGTTTTGTTTCTCTTCTCTGCCTGATCAATACTTTCCCATCTG AAGAAGCAAAACATTCTCTCTCTTCTGTTTCCCTTGCTGCTGATT CTGGCTCAAGGGGATGGGGGCAGGAGTGGAGGAAAGAGGGTC AGAGTCTATATTTAACCACAAAGATAATTCCTCCTTGACAGCAG CTCCAGAGAGANTTTGACATTTGAGGGGACTGAGTAGCAAGAG TAATTTGCATTTATCTGGCTATAGAAACAGAAGAGATTGGGAG CAACAAGTGATCTGTGGAGGTAAAAATGAGTCAGGGGTTTGGA AGAGGGAATATAGGGCAGGTGAAGAAGAAGAAATTATTTGCCA ACAATGATGGAAGGATAAAGAACAAGACTCCTGAAACTATTTC CTTAAATGTCACACTAAAGCAACTCCAAGAGGATTGTAATAGC TTTGGAGTGGGACAAGTGGCACAGATGGGAAGGCTGACATGTC CCGGCTGCTTAAATACTCTGAATTCTAGATCTGCATTTATCAAA ATTTAATGTACACCCGAATTGCCCTGGATCTTGAATAAAATGCA TATATTAATTCAGTAGGTTGGGGTGGGCCCCAAGATTTTGTATT TTTAGCAAGCTTCCAAATGAAGCTGATGTTGGTCCTGGGACCAC ACTTTGATTAGCAAAGCTCTGCTAGAGCGTTTTGG

SEQ ID	Sequence
20028	ATATTCTTTC CTGTCTGCTG CCTTGTAAGA CGTGACTTTC GCTTTCTGCC ATGATTGTGA GGCCTCCGTA GCCATGTGGA ACTGTGAGTC CATTAAACTT CTTTTTGTTT ATAAATTACT CAGTCTCATG TATGTCTTTA TCAGCAGCAT AAAAACAGAC TAACATAACC CCCCTTTCTT CCTACCCCTG TGATTTGGGT GGATATTAAA ATTTTGCAAG CCGCCACTCT AGAGAAGTAC CACTCAAACC ATGGTCTGCA GACTACCAGC ATTAGCAAGG CCTGGGAGTT TGTGAGAGAT GCAGATTCTT GGTGCCCATC CAAACCTACA GAAGCAGAAT CTCTGGTGGC AGGAACCAGC AATCTGTGCT TTCAACAAGC TCTCTGAGTG CTTCTTCTGA ATGTTAAAGT ATAAGAACCT CTGCTGCACA GGGAGACCTC ACTTTCATTA TTCTCATTTC ACAGATGAGA AAAATGAGTC AGTAGGAGGA AAAGTGATTG **N** CTCAAGTGCT TAATAAGTGT CTAAGCTAGG ATTTGACCCT AGGGCTTGTG AATCTGGAGC CCATAGACTC AACTCCTGTG CTATACTGCC TCTGTGTCTT TGGTCTGTGT TCTCTTCTTT TTTTTTTTTT CTTACCACCC TCCAAAATTC TTATTTATTT ATTTTCTATC ACCGTACTTA CTGGTGGAGT GGAAGTCCCT TGGAAGTGGG GGACGTGTCT GATTTGTGCA TGGCTATTTT GCGATTTGCC ATTGCTGGAA TATTTAGCAA GCATCAATGA GTCCTGGAGG GCTTTTAAAC CATAGATGAT CAGGGCCCCT GCTTGGTCTA GGATGGAGCC TGCAATTTTG CATTTGTGAC AAGCTCCCAC GGATGCTGGT GCTCACTTGG CATAGCAAGG GGTTATGCTA TTTTTCAAAG GCAAGAGAAG TGTGCATGTA CTTGAGAGGA GAAGGGGTCG GTCACCATTT ACTTTGTGCC TCTTGCTACC CTTCGTTGCC

SEQ ID	Sequence
20029	TAAGTTCAAT TATAATATGT ATAGGAATAA GGTACCTCAA TATGTAAAAA ATCATCAAAT GAACTGGGCA GTGAAAATCA ACTGGCTTTA ACTGTTCATC ATATTTGAGT CATTTCTCTC AAACTCAAAC ATACTAAAAC TTCTTCAGCA AATCCATCAG TATTTGGTTT TCTTTTATAT GCTGATAAAA TCATAGATAA TCTTACAATT GACATCCTCC AAAAGATTCA AAGCTGATTC GAACCTTGGA GTTCAGGTTC CTGGCTTCTC TGTCTACTGG GGGTCAGGAT ACAGGAAGCA CAAGGAGGAG GGGAGAAGAT TGTGTGGGCA AAGGGGCAGG GAAGGGGCCA CCACTCACCA CCACTGCAGG ACGAGGCGCT GAGTAAGGGA CGGGGCTGCT CCCAGCAGAA TCCACAAAGT AGCTCATTCT GCTCTCAGCA CCTGTGTGAG AGAAGGCGTT GGCTGAGCCT CTGGATGCTC ACAGGTTTGT GGATTAGAAT **M** CACAAGGAAG ACACGAACCT TAGAACTAAA AGTCTCCTTA GGAGCCAACC AGTTCACTTC TTTGCATGGC AGGGAAAGCA ATGGAAATTC AGAAAGATCA GTGACTAACC CCCAGCACCG GTAAGAGCAG ACCTCAGACA GAACCAGTTC CCTGGTTGCA AGGTAACATG GATAACAGAC CATGTCTACA CACTGCAGAC AGCAAGCAGT AAACCAGTGC ACAAGAGGCA CATTTTTGTA GGGTTTCTGA GCAGGAACCA GTTCTTGTGT GTCTCCCCCA CCCACAACCA GGCCTGGCAG ATAAGTAGGC ATACAATACA CAGTTGGGGT GTAAATTAAT TGATAAAGGA ATAAACATAG AAAGGATTGG AGAAAGGAAG GATGGAAAAA GCTCTCCTGA AGAGGTATGT CACCCAGTAA CCCAAGAAAC AGATAAACAG AGAGAAACCC TGCAAAAGGG ATTGAGCATT ATTGATCTTG AAAAAAGGAG AAGGGCTATT

SEQ ID	Sequence
20030	CACGCCGCAC AGCTGCCACC GCCGGCCCTG GCCCGGGAGA GGGGGGTCTC TGGGGATCTT AGCAGGCCAT GGTGGGGGTG TCTTGGGGCC AGCCTGAACT GAAAGACCAT CACAGCTTGC AAGCCACCTC CCTGCTCTGT TGCTGGCTCT CCTTGAAGAC AAGTGTTTTT CAATTAACCA AAGCGGTGCA TGGCAATGTG ATAGGGGAAT GAAACACAGC AACAGAATCA ATGCCCCACG CTGGGCAATA GCCGACTTTC TGTTCGCTCC CATCCCTTCC TTCCCTCCCC GCCTCCTTCC CCTGCTCCTT CCATTCCACA AACATTTATT GAGCACCCGC TGTGTGCCAG CCACTGTTCT AGGCCCTGAA GACACAGAAG TGAACAAAAA AAAAGAGTCC CTGTGCACAT CCTGGAGGGA CTTTCCCCGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTCT ATACAGTGTA TGGAGACAGT GGATAATAAA AGCTGTTTAT **S** AGGCACTTTC TCTGAGCTGT TCCATGTGCT TCACTTATAC TCATTCAGCT AATCCTCAGG ACACCCCCGT GAAGTCAGTG ATATTAGTCA CAGAGGCCCA GAGAAGTGAA GTGACTTGCC CAAGGTCACA CAGCCAGCAA GAGGCCAAGC CCGGATTGAA CCCCAGCCGC CTGGCTCTGG AGCCTGCAGC ATAACCACAG CAGGGAACTG CCACCGGAGA CAGACATCGA CAGCCACTAG GAGATGTTAA CCAACAGGCT TGTCTTCACG GCACGGCCCC CGCTTCACCA GCTGCACTGT TTGATGAGCT TTGCAGGTCC CAGATCTTAT AAGCTCATGG TGATTGATCC AAATGATGCA GAGGTCGGCC TAAAGTTAGA AGTGGGCCCC TCTCTGCCCC AAGACAGCCC TTCACCCCAA TTCCATTCCC ACAGTTTGGG CATCCACCCA GGCTGCCAAG CCAAGCGGGG GCTGCCCGGG TTAGCAGGGA CCTGGCCATG

SEQ ID	Sequence
20031	GGCAGCAAAT TCCCCTCGTG ACTCCAATGC CCCTGCCATC TTGGGTCTGG GAGCCTTTGC ACCCTGCACG CCACAGGCTC GCCACCTCCT CCCGCCAGCC CCCAGGATGC CTTCCCCACG TGGGGGCCCT TAGTGGCCGG GACCACTTTG GTAGCAGTGC TTACCCCAGC CCCCCAAACC ATCAGTTTCT GGGGCCAGCT CCCCATGAAG CAAGAGCCCC AGGAGCAGGG ACATCTCCTT CTCTGATGTC CCTGCACCTC CAAGGTCTGG GAGACGCTCA TCCCTCTTCT CTGTGGCCTC TGCCTGGGAA AGCTTGGGGG CTTTGTAAGT CAAAGGTTGG TCTTGTGGGA ACCTCCCAGT GGGCTGTCCC TGAGCCCTGG AGCCACAGAA ACCCCTGCCC CACCCACGAT GGCTGTCATC TGAGTCTGCA TGGAGGTGTG TCTGTGCCAA GTGAGCACAC ATGCACCAAG GCGGCCCCTG GCCACCAGGG GCTCTTGAAG **Y** CTGCAGGCGG CCCTTCCTCT CTCTCCCACT CCCCCTGTTG GGGCCACCAT TCTGGCTGGC AAGATGGCTG TGATGGCCTC CAGCAGGCCC CCTGCCTCCA CCCTTAGCCC CTTCAAGCAT TTCCCCAGAG CCACCATCTA AACGACAGCT GTGAGAACTC CTCTGTGCCC CCATTTGTCT CCCACAGTGC CCATATTCAT CACCAGCCCA CAAGGCCCCT CCTGTCTATG GAGGCCTCCT CAGGACATCT GGGGGCTTCC TGGGCCAGGG TGGGGGGTGC CTGCTCCAGG CTGTTTCTGG CTTGTCCCCT CCCTGGGTGC TGCCTAAGCA GCGGCCTCTG TGTCCTTTCC TTGGACCCTC AGCACCCCTG CATCTAACCT ACCCCCACCC CGAGCTTGCC TCAAGACCCA GCATGGACAG GGCCGCCTAC CTGAAGGTGT GGGTGGCGGA GGGCTAAGAC ATTTGGGAGG GCTATGACAT TCCGGGACCT TTAAATTCTT

SEQ ID	Sequence
20032	ATATATTGAT CAGTTGATGA AAATGTTGTG ACCAGGGCTC TCAGGAACTT AACCATATGT TTCCCTGGAG TGATGGTTCA GAATTTGTTA ATTCAGTGTC CCAAGTGAGT TTATAGAATA ACCACCACGA ATAATGAGAA GCAACGGCAC AAACTTTGTG TACACAGGCA TTTTTTGAGA GAGAGAGAGA GCTATAATAT TTATCAAATT CTCAAGGGGG TAACTGAAAA ATGTTCAACC ATTACTTCAG AACTTCTATT ATGAGACAAA TAGTGCTGGT CCTCTTGAGA AACCAAGGGA GTGGGCTCAG CTCAGTGACT GTCTGGATCA GCCCAGAAAC AATGTAGGCT GCCATCTTGA TCTGTGCTTT TCCCCAGGGA CATGAGCAAG GGCACTTCTA GGCCAAGCAA AATCAATCGT GTTTCATAGA TTTGGATTTA GAGGGCGCTC TAAACCAGCT CAGAGGAATG GTATGTTTTA GAATCCTAGG GAAATTGAGT **W** CTCCAATCAT CACTTCAGTC AGCTAGGAAA GATACACTTT TGGCAGGGTG CGGTGGCTCA CGCCTGTAAT CCCAGCACTT TGGGAGGTCG ATCACAAGGT CCGGAGTTCA AGACCAGCCT GGCCAATATG GTGAAACCCT GTCTCTACTA AAAAATACAA AAATTAGCCA GGTGTAGTGG CATGTGCTTG TAGTCCCAGC TACTTGGGAG GCTGAGGCAG GAGAGTCGCT GGAACCAGGG AGGCGGAGTT GCAGTGAGCC GAGATTGTGC CACACTCCAG CCTGGGCAAC AGAGCGAGAC TCTGTCTCAA AAAAATAAAT AAATAAAAAA GATATCCTTT TAATAAAGAA AAAAAAACAA CACATAAAAC TTAAGAGTGT AATAATAGCT GCTGTTCATT GAATGCTTAC CAGGAACTAG TATGATCATA AGGAACTCTT ACAATCACCC TGAGAGGGAG GGCATGGCAA GCCCTAATTA ATGGATGAAG AAACTAAGGC

SEQ ID	Sequence
20033	GGTCATGGTG GCTCACGCCT GTAATCCCAG CACTTTGGGA GGCTGAGGAA GGAGGATCAC TTGAGGTGAG GAGCTTGAGA CCAGCCTGGC CAACATGGTG AAACCCCATC TCTACTAAAA ATACAAAAAT TAGCCGGGCG TGGTGGTGCA CACCTGTAAT CCCAGCTACT CGGGAGGGTG AGGCAGGAGA ATTGCTTGAA CCTGGGAAGT GGTGGTTGCA GTGAGCCGAG ATCTCACCAC TGCACTCCAG GCTGGGCAAC ACAGCAAGAC TCTGTCTAAA AAAAAAAAAA AAAAGAAAGA AAAAAAGAGT TATATTATTT ACGACTCTTT TAGCTTCACT TTCTTATAAG ATTGTTGTGA GAAGTGAGTA AGACACATGC AAAGTGGTAA ACTGCCTGGC TGTCATAAAA GTCTTGGCTA CTATCACGGC TGGGAGGCAA AGGAGATTCA GAGAAGGGCA GAATGACTGC ATAAGGTGAT CTGCCTGTAA CTCGTGTTTC **Y** TCCTTTCTAG TATAAAGAGA TAAAGGACTT CAAGGTCTTA AACTGGTGAG GGAGTATTAC AGCCTTTGTA TGGAAAGGTT TGACTTTGTG TCTCTGCTTA AACCCCCATT GTGTTGCCCC TACCAATTAT TGTGCTGCCC CCTTGTGGTT AACTGTGCTA AGACCTTTCT TTTGCTCTTC TCCCATTACA TTTCCCACCC TTCCCCACTC CCTTTTAGAC CCCTCCTCTT AGCTCCCAGT TTCCCAAACT GTGTGCCAAG GTGCCCAGAG CACCTCAGGC TTGAACTTGT GTTTTGAGTT GGTTCATGGT TTCAATATTA GATACCTACA CCCGTTTCTA CAATGTCATG TCTTTGTAAA GATGTATTTT CAGAGGTTGC TCCGATAAAA AGCAACTACT ACATGAAAAT GAATGTAGAA CAGGAAATGA CAGTGTGGTA TTGTCCAATT TGATTCTAAG GTTTGATAAG TTCTACAGTG CTCTACACTA AGTTGTAAGG

SEQ ID	Sequence
20034	TTAGCTTCTG CTTGAGCATT TCTACTCACT GGAGTTCATT ACTTTCTGAA ACTGTTTCCT GTTGAACAGC TTTAATGGTT AGAAATTTCT TTGTTATACT GATCCCAGGC ATGCATCACG GTGATTTCTA ATAATTGACA AAATTATTCC CCAGTTTTCT TAATCTCTTC TCTACCTGAC CTGGTTCATA GTAATATATT TATATTCCTC AATATGCATT CTACTATAGC AATATTTATT TTTTCATTCT CATTGGAGAA TTGTGGATAA TGTATTGACT TCAGAAAATA TACATGTGTA ATCAGTATAC AGGTAGACTA CTGTGAGGGC CACCTTAGAG GGCTGTTTTT GGAAGCTCAG GATCCAATAA ATCTAACACC CAAGACCCAT GATTAGCTCT TCATGGGTAG TTGAGGTCTT TCAGGGGGGT TTATTTTTGG TTAGTTACCT ATCTTAATCT TTTTGGTTCA TATCTCTTAT GGGGAGAGAG GTAGGGAGGG **R** CATGGAAAAT ATCCTATCAA ACCTCCATTT ATAATTGTGC TCACTATCTT ATAAATAAGA CAAGTAAATT TTTCTAAAAC TTCGGAAGTT TTCTTGATAA TTATATAGTC ATTTAAGGAT TAATGAATTC TCTAAAGTTT AGCCAGTTAT CCATATTAAT GGTAGCTAAA AATTGAGAAT GCCACAAAAA TTTCAGACAT CTGACTTTTT AAAAATTAGA ATTTTTTGGC AGGGTGTGGT GGCCTGTAAT CCCAGCACCT TGGGAGGCCG AGGCAGGCAG ATCACTTGAA GTCAGGAGTT CCAGACCAGC CTGGCCAACA TGGTGAAACT TTGCTCTACT AAAAAATACA AAAATTAGCT GGGCCTGATG GTGCACACTT ATAATCCCAG CTACTTGGGA GGCTGAGGCA GGAGAATTGC TTCAATTTGG GAGGCAGAGG TTGCAGTGAG CCAAGATGGT GCTACTGCAC TCCAGCCTGG GTGACTTGTG ACTGGGCAAC

SEQ ID	Sequence
20035	CCTCTAGAAT CCTTATTGCT GTTCCCACAT TCTGATCATA AATTTGGATA AATTCACTGC TACTCAGGCT TCAAGCTGAT ATAATGAATA GAGGGAAAAT AGGCACCCAA AGTCAATAAG AAGCACAGGT GATGATGCCC CTGTGATTTG TGGGATTGTA AAAATACATT GTCTTCTGTT TTCCCTTTTT GCCCAAATCC AAATTTAGAA GAGAACATTC TGGGAATGTA TACGTAAGAA CTGCAACATG AAGGAACAAA CAATAACCAT GATAAAGCAA GCAGGCAAAC AAAAAACAGC CCTGTGACTA TAACCACAAA GCTGGGCAGC ATATAATTCT AATTTAATAG TAGCTGGAAA AGGCTTCTCT CTACTCTATA GTCATGGCCC CCATGCTCAA CATGGAACTC CTATATTTTA GCTTTTAAGT CATCATAAAA TATTAAGGGG CCCATATTCT TTGACTCCCT AGGTTTCCAG AATTACTTGG ATTTTCTGAG S ACATTTTCAT TTCTTAGTGA CACATGCAAT GTCAATAGAT TTTGGAAAAG TATTTCTCAT GTTCCCTATT TACCTACAAA ATTCTTCTAT GCATCTTTTC TCCAAGAAAG ATTTAAGGAT GAAGAAATTA CTATGATACA TTAAGAAAGG CCAAAGGAAG TATACTCTAA TATATACCAC ATTATGTACT TAGGCTAAAA AACGTTTCAT TCCTTTGTGA TATTTTCTTC CTTCTGTGTA AGCAATTTGT CATATTTTCT AAAACCATGT TTTTAAGATT TTTCTTGGCT ACTCTTTAAA CTTATTTACT TCTGAAGTAT GAAAAACACA GTTCTCTTAG TTTGAGTGCA ATGTGCACAT ACATTAGGGA AAGAACAGCC TATTCAATAA ATAATTCTGG GAAAACTGAA TATCAACAAG CAGAAAAATG AAGCCAGACC CCTCTCACCA TATGCAAAAA TCAACTCAAA ATGAATTAAA GACTTAAAGC AAGACCCAAA
20036	TTCTTTCTTATTTATTTGTACATTATCTGTTTGTATCCTTGAATTT TCTCTGGGATGTTATAAAAGAAAAATATTACAAGCATAATTTCT GACACAATGTTTTATAACTGTTTTCAAAAGCAATCTATTTCTCTC TTAATTTCTATAGAACCCATTTTAGTCATTCCTATGATGAATGA AAAAAAACTCACAATTAGTTGTCAGTTTCAGAAAGGAGTCTCA GAAGCATCTTAGAACCACCTAGGCGGTCTTATAGGCGTCACAG AAAAATATTCCACCTTACTTATTCTTATCTTCTTCAAACTGACTC CAAATATAATAAGCAGGCTTAAGTTATATAAGGTTCCTTAAAA GTTGTTCTCAAAAACAATTAAATGCAGACTGTCCTCAGTAAAAC TTGCATTGGCCCAGTCCATTTTACCAAGTTTGCTCCTTCTTACAT GTACGACTGCCCCTGTGACAAGTTTAAGCCTACGTTAATTAATC ATCTTTCCATAACANTGAGACATATTCATCCAACCCTGAGAGGG ATAAGGGGTAACAGGCAAGATATATTCAAATTGTGACATTTAA GGTCAACTTGACTTTAAAACTCATATACTGCTCAGTTTTCATAT ACGTGGCTGAAAACAAGTCATCACAGAGAACTGGTCACACTGT TAGAGGACCAAAATAGTAAAATATGAACAATTCTTCCATATTTA ATGATATTAAATATAACAGGTCCTATGTCTATGCAATTGAAGTC AACATGTCACTAATTAGGGCTTCCTTTGTTATCAAACTTGCTGA GAAGATAGAACAGTGAGGAAAAAATAGCAGGAATTGAGCTGT ACAGAATTAAAGACATTCTTATGAACCTTAAGACTTAAGGTCA GTCACACTCATATGACATTTGGACTATTAGACAACTCTTCTGAC CTCAAATTTTGCTCTTACCAGTTGGTGATAATCCTTTGGTAAGA GAGCATGTTAAAAGTAACCAAATCAGATAAGGACTA

SEQ ID	Sequence
20037	TTCTGAGCAC TCACATTTTA ATGCTGGGAA TTTTATGCTG AGGTTCAGTG CTTTTCAGGG AGCCATGAAC CCCCTGCAAT GACTTGCAGA CTGTAGGTAT TACATGTAAA ACTTGTGTGA GTAATTTCCT GAAGAAGGGG TTTCATTCTT CAGATCCTCA AAAAGATCTA TGATCCGGCC AGGCGCGGTG GCTCATGCCT GTAATCCCAG CACTTTGGGA GACCAAGGCG GGCATATCAG GAGGTCAGGA GATCAATACC ATCCTCGCTA ACACAGTGAA ATCCCATCTC TACTAAAAAT ACAAAAAATT AGCTGGGTGT GGTGGCGCAT GCCTGTAATC CCAGCTACTC GAGAGGCCGA GGCAGGACAA CAGCTTGAAC CCAGGAGGCG GAGGTTGCAG TGAGCCAACA GAGTGAAACT CTGTCTCAAA AAAAAAAAAA ATATATATAT ATATATATGA TCCTAAAAAG ACATTGATAT TAAAGAGTAA TGATGGGGAA **R** GACCACCAAG TGATCATTTA TAAGATGCTG CGAGAATTGC TAAAGTTGAG GGATGGATTC TGCATTCCAG GAGAACAAAG GAGGTAGATC CCGATTAACT GAGTAGCAGG ATATTGAGGG AAGCTTCTTG TAATGATTCA GCTGAGTCTT ACACAATGAA TGAGACTTGG ATAGATGAAC ATGCATTAGG AGACATCAGT TCTGGTCAGA GGAAACAGCA AATGCAAAGG CCCAGAGCCA TAAGAGATTC AGATGCACTA AAGAAATATC CCATCATTTA GGATGGTCGG CATATACACA GAGGGCCTAT AAGGAAGGAG AAGAAACTGA GGTTGTAGAA GCTGGTAGGG ACTGCATGCT GAAAGGCATT GTAAATCTTA GACTAAAATC TGTGGGAGAC TTTGAACAAC CTAAAGATTT TAAGCAGAGT GATGCAATGC ATTTGTCTTT TGAATGCAAA TATTGCTGGG GCGGGTCTTT TGTGTTATCA GCTAATGATT

SEQ ID	Sequence
20038	ATATTCTTTC CTGTCTGCTG CCTTGTAAGA CGTGACTTTC GCTTTCTGCC ATGATTGTGA GGCCTCCGTA GCCATGTGGA ACTGTGAGTC CATTAAACTT CTTTTTGTTT ATAAATTACT CAGTCTCATG TATGTCTTTA TCAGCAGCAT AAAAACAGAC TAACATAACC CCCCTTTCTT CCTACCCCTG TGATTTGGGT GGATATTAAA ATTTTGCAAG CCGCCACTCT AGAGAAGTAC CACTCAAACC ATGGTCTGCA GACTACCAGC ATTAGCAAGG CCTGGGAGTT TGTGAGAGAT GCAGATTCTT GGTGCCCATC CAAACCTACA GAAGCAGAAT CTCTGGTGGC AGGAACCAGC AATCTGTGCT TTCAACAAGC TCTCTGAGTG CTTCTTCTGA ATGTTAAAGT ATAAGAACCT CTGCTGCACA GGGAGACCTC ACTTTCATTA TTCTCATTTC ACAGATGAGA AAAATGAGTC AGTAGGAGGA AAAGTGATTG **N** CTCAAGTGCT TAATAAGTGT CTAAGCTAGG ATTTGACCCT AGGGCTTGTG AATCTGGAGC CCATAGACTC AACTCCTGTG CTATACTGCC TCTGTGTCTT TGGTCTGTGT TCTCTTCTTT TTTTTTTTTT CTTACCACCC TCCAAAATTC TTATTTATTT ATTTTCTATC ACCGTACTTA CTGGTGGAGT GGAAGTCCCT TGGAAGTGGG GGACGTGTCT GATTTGTGCA TGGCTATTTT GCGATTTGCC ATTGCTGGAA TATTTAGCAA GCATCAATGA GTCCTGGAGG GCTTTTAAAC CATAGATGAT CAGGGCCCCT GCTTGGTCTA GGATGGAGCC TGCAATTTTG CATTTGTGAC AAGCTCCCAC GGATGCTGGT GCTCACTTGG CATAGCAAGG GGTTATGCTA TTTTTCAAAG GCAAGAGAAG TGTGCATGTA CTTGAGAGGA GAAGGGGTCG GTCACCATTT ACTTTGTGCC TCTTGCTACC CTTCGTTGCC

SEQ ID	Sequence
20039	AAAGCTCAGT CCCAGATCCT CGGCCATGCT CCTGCTGCTC CTGGAGGCAC CTCTGACTCC TGGGCAGAGA GAGCCCCCAT TAAATAGAAG ACCAGCTCTC ACAGTGGGTG ACTTAATCAC TCAGTCTCCT CCTTCCCTTT TCCTCTCCCC TCCCCTCTTC AAGAGCACAC TGTGGCCCTA CCCTGCTAGA GAATGCACCG CCTACAACAG AAACCAAGTT TGGTTTGAGG AAAAAAAAAA AAAAAAAAAA AAGAAGAAGA AGGAGAAGAA GAAAGCTTTC CCAAGCATAT TTATATACAG TATGCTCATG TGCTCCTTCC TTCGTTTACA GAAGGAAGTT AGGAAAGTCC CTGAAGGAGG AGAGAAAGAA TTCATCAAGT CAGTGGGTGG GGCAAATTAA AATATACCTG TTCCCTGCAC TGGAGGCTTA CCAGCTGTGC CAGTCTGGGG AGTGTGCTTC TGGAAGTGAA AGTGAGGGAT GAGAGGTGTG TGGTTTGCAG **R** TTGGGAAACG GAAATCACAT TTGCATCAGC TCTTTGCAAA GTGCTGCCTA GCCCTCTGTC ATTTTGAACC TCATAGAAAT TCATTCTCAG TGTACAGATG GGAATAGCAA AGTTCTAAAA GGTGAAGGCA CTTGTCCTAG GTCATCCAAG GATGAAGACA GAGGAGCTAG GAAGATGACC TAGTTCTAAA TCACGGCTTG GAGTTGTAAC CTCTAGCACA TGACTGCCCA TGAAAGGAAA GTATTTCCAG TCTGCATTGA CCATTGTTTA ATCAGAGTAT GAGGCCACAG ATCGAGGTGA CTGTCTGTGA GGGTAGAACA TTAACCACTA CTCCCTGATT AGTCTAAAGT TAATTGATCA TGTGATGTGC TTTGCCTGCA GTTGGGTGTG GGGGCCACAA CATGTAATAA AAGATTATAT TTATTAAGTG CTTACTTTGT GCCAATCACT GCTCTAAGTT AAATACATCA ATAAAATTAT TCAATCCTGA GATAAATTTT

SEQ ID	Sequence
20040	CTCAGCA CTTTGGGAGG CTTAGGCAGG AGCATCGCTT GTGTCCAGGA GCTTGAATCT AGCCTGGGCA ACACAGTGAG GCCCCATCGC TACAAATAAT CAAAATTAGC CAGGCGAGGT GCATGTGCCT GTAGTCCCAG ATACTCAGGA GGCTGAGGCA GGAGAATTGC TGTCCTCCTG CACCAGAAGC CTCCAGTTGC TTTGTGTCTC AGTGGCTCAC CCTATTCTGG ACACTTTGCA TAAACAGAGT CCCACAGGCT TGTCCTCAGG TGTCTGGCTC TGTCACTCGC ATAATGGCCT TGAGGTTCTC CACGCCGCAG CGTGCGTCAG GACAGCGGCC TCCTTCCTTT TTCAGGCTAA TTCTCCCCTG CACGCATGGA TCACGTTTGG TGCATCCGTC CACCCACGAG GAACACTCGG GTGGTTCCTA CCTTCTGGCT GCCATGAACA TTCACGGACA GGCATTTGTT TGAGTCCCTG TTCTGAATCC TCTGGCCTAT ATC **S** CTAGGAGAGA ACTGCTGGGT CCTGCAGTGC TTCCACGCTG AGCTTTTCGA GGAACTGCCA CAACGTTCCC CATGGCAGCT GCGCCCTTCT GCTTTTCCGC CACGATGCAC AAAGCTAACA ATGCCTCTGG TCTCTGTGTG CAGTGCCCTT CAGAGAGCCG TCCTCACCGG CAAACAAGCA GCGGCATCCC CCTGGGAGCT TGTTCTGAAT GCCCGGCGCG TCTCCAAACA CACTTGGAGA AACCACCTGG ACGGTGCTCA ACCTTGAACC TCTGAAGCTT TTAGACACTG TCCCGATGCC AGGTGCCAGC CCAGAGCTTC AGGTGCAATG GGTCTGGGCA TGGGGGCTTT CATAGGCTGC CCAGATGACC CCACTGTGTG GCCGGGGTTG AGACGACAGC CCTGGGAGAA GCTTCTGCTG CCACCTGGGC TGCTCTGCGG GGAGTATGCT GGC

SEQ ID	Sequence
20041	AGACACACTT CGTGACCTCA CTAGGATTTG CTTTACAAGA TAAGATTTTC CTGGCAAGCA TTGAAGTTAG TGCCCAGATT CAAAACAGCA AACTTAAAAC TATTATCTTC ATGCTTGCTA TAATCAGGTG TACCGCCCAA CTTCCCATCC CTACCTCCCC TTCCCTAGTA ATCCAGAGGT ACTCAAGGTC ACTACTGGCT ACTTAAGGTT TACATCCACT CCCAAGGAAA CACCAGCAAC CAAAAGAATA CTTCCCAGAT GGAAAACCCG TCATTTGACC TTGGAATGCT CTGCCTCCCA TAATGACCAA AATAAGGTCC GGCCAGAGGG GCTTACGTTT TTTGGTAAGG AACAACACAT TGTTTTAGAG AGATAATCTG ACATAACTCT GCTAAGCTCT GAGTGTCTAT GCATGGTACC ACAGCAAACA CCCTATGTCC CAAATGGAAA CTAGCAGGGT GAAAAAATTG TTCATCTAAG ATGACATTAA TCTCTGTATG **H** CTCCTTGGTA CAGTTCTTTT CCACAACATG CAGCTTAAGA TTCAACAATT TTTTCATTGT GTTTTGTGTT TCCTGAAGCA TTCCTCCAGC TACCTGAAGC TCTCACTGAT TAAAATAGAC CTCCTTTACT AAAAGGGGTA AACTGAGGCA CAGAAGAACA AAGCAATGTG CCTTATAGTT CAGAATAGGT AAACAAAAAT TGGACATCTA TTATTTTCAA ATCTCTTTAG ATTAAAAGAA AAAAAAATGT ATTTCTCAAA GTCCAAAGTC AACCTTCTCC AAAGGGAAAC TGCATGTCTG TCTAGTAACC TATAGGATCA TTCACACTTT TTTTTCCTTG AGAAGGAACT AACTTGCCAG CCTACCAACA ATTTTGCCAG TGCCTTGGCA TCAGGCATAT CTGCACAACC TTTCCAGAGC CTATATCATA GTGATCTGTT CAAGCTGCTC AAAGCTCAGT AATCATACTA ATCTGTGCAT AGTGACCAGT GCTACCTGCT
20042	GCTCCCCCAAAGATATTTACATCCTACCCTGTGAATATGCTACC TTACATGGAAAAAGGGGCTTTAAAAATATGATTGAGTTGAGAA TCTTGAGATGGAAAGTTATCCAGTATTATCTGAGTGGGCCCAAT GTCCTCACAAGGGTCCTTATAAAGTGAGAAATAAGAGGATCAA AGTAAGTAGTAGGTGATGTGACAGCAGAAGCAAGAGGTTGGAG TGATTTAAGGAAGTGGGAGATCAGGAAGTGTTAAGCACAAAGT TAACTTATACCTTTAAAAAAAAAAGGAAAATTAAAGACAACAAG CAGATATATACATTATATAAATAAACACAAGAACTTGTTAAACT TGTGAAACACAGGACTACCCAAGACAAATGTTTCCCTTTCCATT TCTACTCTAGGCTATATGAGGAATCTATT TTTCTCTTTTTCTTAGAACTCTTACTCTGCAGGATCAAAATGTCA AGCAGTGACCACATAAGTGGGAAGTAGATCAAGAC**N**TGCTTAT AATTACATTCTTGTGGTTGGTATAAAATTCTGTACCACAGCCAT TCCTTAGAAGCCAGCTCATGGGATCAAACAGACAAGCAAGCTC ACTTCTCAAGCCCACGATGTTACGTATTAGTCCATATTGGTGAG TTCCTTTGTGCCCAAACTTAGCTGCCGCACACTACAGTGATAGG AAACTGCCAACAGTTTTTTGTCAAACCCACTACAGTGGATCCCA CAATGGGCTGAGACCTCGTCTAGAGTCATCAGGTTTTCCAGGAT GTGCAGATGGCCTGGAAACTTGGCCAAGAGGTAGGGATCAGCA CTCTTTAGTAAGCTGTATATCCACCAAATGCTGTGACACAAGGA ATGGGCCTCAAAATGTTTCAGGCCAGCACAGCTTTGTCTTTGCA AGTCATTTTTCAGTGGCAGTTAAATATTGTGGCAAAGCCAAGGT ACAGACTCACGTGCATTAAAATATGCTTATGAGTAATAATACCA TAAGTATTTCC

SEQ ID	Sequence
20043	GGGGTCAGGTTGCTGGTCCCAGCCTTGCACCCTGAGCTAGGAC ACCAGTTCCCCTGACCCTGTTCTTCCCTCCTGGCTGCAGGCACC CCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCCAGGCACCT TCTCAGCCAGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCG CAACTGCACGGCCCTGGGCCTGGCCCTCAATGTGCCA GGCTCTTCCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTT CCCCCTCAGCACCAGGGTACCAGGTGAGCCAGAGGCCTGAGGG GGCAGCACACTGCAGGCCAGGCCCACTTGTGCCCTCACTCCTGC CCCTGCACGTGCATCTAGCCTGAGGCATGCCAGCTGGCTCTGGG AAGGGGCCACAGTGGATTTGAGGGGTCAGGGGTCC CTCCACTAGATCCCCACCAAGTCTGCCCTCTCAGGGGTGGCTGA GAATTTGGATCTGAGCCAGGGCACAGCCTCCCCTGGNGAGCTC TGGGAAAGTGGGCAGCAATCTCCTAACTGCCCGAGGGGAAGGT GGCTGGCTCCTCTGACACGGGGAAACCGAGGCCTGATGGTAAC TCTCCTAACTGCCTGAGAGGAAGGTGGCTGCCTCCTCTGACATG GGGAAACCGAGGCCCAATGTTAACCACTGTTGAGAAGTCACAG GGGGAAGTGACCCCCTTAACATCAAGTCAGGTCCGGTCCATCT GCAGGTCCCAACTCGCCCCTTCCGATGGCCCAGGAGCCCCAAG CCCTTGCCTGGGCCCCCTTGCCTCTTGCAGCCAAGGTCCGAGTG GCCGCTCCTGCCCCCTAGGCCTTTGCTCCAGCTCTCTGACCGAA GGCTCCTGCCCCTTCTCCAGTCCCCATCGTTGCACTGCCCTCTCC AGCACGGCTCACTGCACAGGGATTTCTCTCTCCTGCAAACCCCC CGAGTGGGGCCCAGAAAGCAGGGTACCTGGCAGCCCCCGCCAG TGTGTGTGGGTGAAA

SEQ ID	Sequence
20044	CACAAACCAT ATAAGACATT ATTGTTCCCA TTTTACAGGT GGAAATCTGA AGCTCTGAGA GGTGGAATGA GTTGCCTGAA TTTACCAGAA TGTGGGATTT ACCAGAATGT TTACCAGAAC GAATTTACCA GTCAGGCTTT GAGGCCAGAT CTGTCTGATC CAAAATCAGT GCTCTTTCTG AAATGCTGAT GCAAAAGGAA GTCATCAGAA CTCTATAGAC CAACCCTGCA CATTTGTTAC CTTCTCCAGA AGTGCTTTCG TTGCTGATAT ACCAGACGTC TTTTGTTAAA ATTAATCTAC TACCATCACC GTATGGGGAA TAACTCTGGC TAGCCTAAGA AAAGCAACCT TACATAGGTA AAAATAATTG CACCCCTTCC ATCTGCCAAA AGAGTTCTAT TGTCGGTTTC CCAGGCAATA TATGTGCTTT GGGAAATATT GCCATTAGAC AATCTGAGTG TGGTTGCAGT AAAGTATTCT AGAATGACTG GAATACCCAG **M** AAACTGGGTA AGAATCATGT GTTCTGCTGT CAGCAGACCT TGTCTGGGCC TGGCAAACTC TGCCTCTGGG GTTAGCAAAA CTCCCTTACG CTCCCCTCTT TCAAACAAGA GTGATTATCA GTTGTCAAAG TTGTTACTTC TGCAGAGAAG GAAAAGTGGT TCTGGACACT GTCCACAGAT TGTTTCCTCC TCTGGGGCAA GAGGATTGGG AGAGGGGTAT GCACATGCTT TTCTCAATTT GTGGTTTTTG CTTGGGTTTG TGGTTTAAAT CCCTAATTTT GGCAATCATC TCTGCCACAG ACCATCCAAT CCATGCAGGT GGGTTCATTC CATACTCTGT GAAATATATT TTGATGTTAG AGGGGTGGGA ATGTCTGATT TATTGTTTCA TCCTCGTCTC TGGGGAGGGG AAGCAAAGCT AGTAGTAGTT TTTTTTCAA GGGCAATCTC AGGCCATTCT AGAATGCTTC ATTGCAGCCA CACTCTGATT GCCTAATGGC

SEQ ID	Sequence
20045	GTGGGAGGAT CACTTGAGGC CAGGAGCTTA AGGCTAGCCT GGGCAACATA GCGAGACCCC ATCTCTACAA AAAATAAAAA ATTAGCTGGG CATGGTGGTA TGTGCCTGTG GTCCTAGCTA CTTGGGAGGC TGAGGTAGGG GCATTGAGCC TAGGAGTTCA AGGCTGCAGT GAGCTATAAT CACACCACTG CACTCCAGCC TGGGTAACAG AGTGAGACCC TGTCTCAAAA AAAAGAAAGA AAAAGAAAAA GAAAAGGGGT ATTTATTGAA CACCTACTAT GTTTCAGGCA CTGTGCTAGA TCCTAAGTGA ATATCAGCAC ATGAACAAGA CAAAGGCGAA AAGTTACCAA ACAAGTCTAA GTTGATTTCG GTATATGCAT CTTCCTGACT TCTGGTCCCG TGCTTTGACC ACAACCCTTC ACCACTAGAC CAGACTTCCC CAAATAAACA ACTACTTCTG CATGCTGGGG ATGGGCTGTG TGCGGCAGCA TTTACGTAGG **Y** GGTACAGACA GCAGCCTTTC ACTTAATGTT GCAATAACAC CAGGCTAAAC AATGTGCACT GACTTCAAAA GTGTGGGGTC AGGTCTCCTT CAAGTGCCAC AGGGAGAGTG CAAAGTAGGA AAAGTCTATC GGATGAGGAA ACACTGTAGA GGGAAAGTGA ATTTTTTTTC AATTTGGGTT AAAATTCAGA TGTGGAATTC TACCCTCCTT TTCACTTTTG GATCCCCAGA TAGGAGGAAC TCAGCACATA GATAATCATG AACTACACAC ATTTTGGTTT TATATGCTCA GACTTGTCCA GAGCATGAAA TCCCTGCCCT GTTGGAAGGC AGCGCCGTGC TCACGGAGGC ACACAAGCAC CTGTCTCAAA GTCACCCTGA CCTGCAGATC TGCAAATGGC AAAAATAATT TCACATGTTT GTTCTGATTT GTCTTCATTT TTAGGCTACC TTGTGTGAGC TCCACTTTTT AGAATGTGAT TTTGCAGTCC TGAAATGGAT

SEQ ID	Sequence
20046	GACAGGAGCT GGGCAGCAGC AGGAAGACGG GGGGCACCCC TCCTGGCGTC CTGGCCGCCG GGACACCCCT CTCCGGGAGA GGACACTCGG TGCCCCTCCG TGAAGCCGGT AACCTCGGCT GCGCCACCTC CCCCACCCGC GCGCCCGCGC CGGGAAAGCC AGCGTGGCCC CAGTCTCCGA ATTTCTCGGA ATGAACAACA GCAAATTGAA TCCAGGGCTC CGGCGGGGGC CGCCTTTGCT GGCCACTGGT TCTGCAGCCT GGCGAGACTG CGCTTAGTCC CCGCCTGGAG TGCCTCCCGA AGGCCTGGCT GGAAGCTAGA CTCAGTCCCT TTGTAGTAGC AGCGGTGGAG CAGGGACCAG CGTCTTGGAC GGGTGACCCA GACTCAATTC CGACTTTGGC CGAGGGCATG TTTGACACTG GGTGTGAAAT CTAGACAGTT CCCGCGGTCA TAGAGATGGG GCAGCAGCAT TCAGGCAGGG CTCAGAACTG TCCGGGTCCC **R** TCAGTGTTGG GGCGGAAGAG GAAGAGTGTC AACTGAGCCA GCATTTATT TATTTTATTG TTGTTTGAGA CAGGGTGTCG CTCTGTCGCC CAGGCTGGAG TGCAGTGGGC AGCATCTCAG CTACTGCAGC CTCCGCCTCC CGTGCTCAAG CGATCCTCCC ACGTCAGCCT CCCAAGAAGG TGGTATTATT GGCCACGCCT GGCCAATTTT TGTATTTTTT GTAGAGAGGA GGTCTCACTG TGTTGCCCAG GCTGTTCTTG TACTCCTGAG CTCCAGCAAT CCACCCGCCT TGGCCTCTGA AAGCGCTGGG ATTACAGGCT TGAGGCACCG TGCCCAGCTG AGCCAGGCTT TTAAAACCGG TTCTGTCCCT ACCCAGAGAG CTTCTTACCT GGCGGCCTCC TTAACCTCTG ACACCAGCTG ACCACGCTTA TGAGCCAAAC ATAAAAACCA AAAGAAACCC AGGCTTGGTG GCTCACGCCT GTAATCCCAG CACTTTGGGA
20047	tatccac cagccttggc ctcccaaagt gctaggatta caggcatgag ccaccacgca tggcctgtct tttcttcttg gtcattttcg ctaaaggttt gtcaattttg ttgatctttt ttgttgctga tctctattgt tttcccattc tgtttcattt atttccattt taacctttgt ttccttttt ctgctggttt gggtttaatt tgctcttttt ttcccctaat tttTCAAGGT ATACAGTTAA GTTATTGATT TGAGATCTCT TTTTTCTTtt cttttttttt ttttttttt ttttttggtt gctgttgaga tggagtctcc ctctgtcacc cagactggag tgcagtggca tgatctcagc tcactgcagc ctccgccgcc caggcgattc tcctgcctca gcctcctgag tagACGTTTC CCGGCCAagg tgtttctttt tgaatgtaag catttacagc tacagatttc cctctaaaca ctgctttcac tgc **D** ttccataaga ttgtttttg ttgttgtttt gttgtttgag acacagtctc actctgttgc cgtttggaga gcagcgatgc gatcatagct ctgtagcctt gagctcctgg actcaatcag tcctcctgcc tcagcctccc aagtagctgg gactacaggt gtacaccact gcacctaact aatttctttt ataagttttt gcagaggcca ggcacagtgg ctcacacctg taatcccagc actttgggag gccaaggtgg gtggatcacc taaggtcagg agttcgagac cagcctggcc gacagggaga aaccccatct ctactaaaaa tacaaaaatt agctgggcgt ggtggcaggt gcctgtaatc ccagctactc aggaggctga ggcaggagaa tcgcttgaac ctgggaggca gaggttgcag tgagccagga tcacaccatt gcactccagc ctgggtaaca aaagcaaaac tccatctcaa gaaaagaaaa

SEQ ID	Sequence
20048	CATCTGGCTACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGT GAGCCACCAAGCCCAGCCTAACGTTACATTTCTTTCTTTCTTTTT CTTTCCTTTTTTTTTTTTTTGAGACAGACTCTCACTCTGCTGCCC AGGCTGGAGTGCAGTGGCATGATCTTGTCTCACTACAACCTCTG TCTCCCAGGTTCAAGCAATTCTCGTGCCTCAGCCTCCCCAGTAG CTAGGATTACAGGCACCCACCACCACCCCCAGCTAACTTTTTAT ATTATTAGTAGAGACAGGGTTTCACCATGTTGGCTGGGCTGGTC TTGAACTCCTGACCTGAAGTGATCCACCCTCCTCAGGCTTCCAA AGTGCTGGGATTACAGGCATGAGCCATGGTGCCCGGCTATATTT CTAAGTTTATTTTGCTTCATATACCAGGAACCGTAGTTTGTTTCA CATGTGGTCTTGAAAATAGTTTGTTCTGTTCTGATTATAAGTAA CATGTGTTTATTGNTTTTTTTTAAAAAAGGGTAAATATCCAGGT GCAGTGGCATGTGCTTGTAGTCCCAGCTACTCAGGAGGCTGAG GCCGGAGGAAGCTTTTGAGCCCAGGCATTTGAGACTGTAGTGA GCTGTGATTGTTCCACTGCATTCTAACCTGGGTGATAGAGCAAG ACCCTGTCTCAAAAATAAAATACAATTAAATTAAATTTAAAAAT TAAAAAATTGATAAATATAGAAAAAATGTGAAAACCAAAGGG GAACGCCTCCCACTACCAGAGATCATTTCTATTTTCATTCTGGA GAATTTCCTTCTAGTTTTTTTTTAAAACGCATAAATATGGGAAA TACACAATTATGGGAAATATACAACTTCCCATAATGAGTTAACA CACCATTTACGATTTTGTGTCCTGCTAGTCTGTCATTATGTCATT AGCGTTTATCCCTTGCATAAAATGCTTCTCAGATTACTAAATGG CAACATACTATAATATTGAACTTTGTGGATATC
20050 >sp|O95150|TNF15_HUMAN Tumor necrosis factor ligand superfamily member 15 OS=Homo sapiens OX=9606 GN=TNFSF15 PE=1 SV=2	MAEDLGLSFGETASVEMLPEHGSCRPKARSSSARWALTCCLVLLP FLAGLTTYLLVSQLRAQGEACVQFQALKGQEFAPSHQQVYAPLRA DGDKPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNY TNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSITVVIT KVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKL MVNVSDISLVDYTKEDKTFFGAFLL

SEQ ID	Sequence
20051 >sp|O95150-2|TNF15_HUMAN Isoform 2 of Tumor necrosis factor ligand superfamily member 15 OS=Homo sapiens OX=9606 GN=TNFSF15	MQLTKGRLHFSHPLSHTKHISPFVTDAPLRADGDKPRAHLTVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL
20052 >sp|O95150-3|TNF15_HUMAN Isoform 3 of Tumor necrosis factor ligand superfamily member 15 OS=Homo sapiens OX=9606 GN=TNFSF15	MRRFLSKVYSFPMRKLILFLVFPVVRQTPTQHFKNQFPALHWEHELGLAFTKNRMNYTNKFLLIPESGDYFIYSQVTFRGMTSECSEIRQAGRPNKPDSITVVITKVTDSYPEPTQLLMGTKSVCEVGSNWFQPIYLGAMFSLQEGDKLMVNVSDISLVDYTKEDKTFFGAFLL
20053 tumor necrosis factor receptor superfamily member 8 isoform 3 (NP_001268359.2)	MFCSTSAVNSCARCFFHSVCPAGMIVKFPGTAQKNTVCEPASPGVSPACASPENCKEPSSGTIPQAKPTPVSPATSSASTMPVRGGTRLAQEAASKLTRAPDSPSSVGRPSSDPGLSPTQPCPEGSGDCRKQCEPDYYLDEAGRCTACVSCSRDDLVEKTPCAWNSSRTCECRPGMICATSATNSCARCVPYPICAAETVTKPQDMAEKDTTFEAPPLGTQPDCNPTPENGEAPASTSPTQSLLVDSQASKTLPIPTSAPVALSSTGKPVLDAGPVLFWVILVLVVVVGSSAFLLCHRRACRKRIRQKLHLCYPVQTSQPKLELVDSRPRRSSTLRSGASVTEPVAEERGLMSQPLMETCHSVGAAYLESLPLQDASPAGGPSSPRDLPEPRVSTEHTNNKIEKIYIMKADTVIVGTVKAELPEGRGLAGPAEPELEEELEADHTPHYPEQETEPPLGSCSDVMLSVEEEGKEDPLPTAASGK

SEQ ID	Sequence
20054 tumor necrosis factor receptor superfamily member 8 isoform 1 precursor (NP_001234.3)	MRVLLAALGLLFLGALRAFPQDRPFEDTCHGNPSHYYDKAVRRC CYRCPMGLFPTQQCPQRPTDCRKQCEPDYYLDEADRCTACVTCSR DDLVEKTPCAWNSSRVCECRPGMFCSTSAVNSCARCFFHSVCPAG MIVKFPGTAQKNTVCEPASPGVSPACASPENCKEPSSGTIPQAKPTP VSPATSSASTMPVRGGTRLAQEAASKLTRAPDSPSSVGRPSSDPGL SPTQPCPEGSGDCRKQCEPDYYLDEAGRCTACVSCSRDDLVEKTP CAWNSSRTCECRPGMICATSATNSCARCVPYPICAAETVTKPQDM AEKDTTFEAPPLGTQPDCNPTPENGEAPASTSPTQSLLVDSQASKT LPIPTSAPVALSSTGKPVLDAGPVLFWVILVLVVVVGSSAFLLCHR RACRKRIRQKLHLCYPVQTSQPKLELVDSRPRRSSTQLRSGASVTE PVAEERGLMSQPLMETCHSVGAAYLESLPLQDASPAGGPSSPRDLP EPRVSTEHTNNKIEKIYIMKADTVIVGTVKAELPEGRGLAGPAEPE LEEELEADHTPHYPEQETEPPLGSCSDVMLSVEEEGKEDPLPTAAS GK
20055 heavy chain variable region (CD30L)	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTDYYITWVRQAPGQA LEWMGWIYPGSGNTKYSQKFQGRFVFSVDTSASTAYLQISSLKAE DTAVYYCANYGNYWFAYWGQGTLVTVS
20056 light chain variable region (CD30L)	EIVLTQSPDSLAVSLGERATINCKASQSVDFDGDSYLNWYQQKPG QPPKVLIYAASTLQSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYC QQSNEDPWTFGGGTKVEIK

SEQ ID	Sequence
20057	TCCTTATTCCTGGCTCTTCCAGAGGCTGGTGGCTCTTAGGGCTC AGCAGGGCTGCTGCCTGGGACAGGGAGACCAGGGGACCCAGG AAGCCCTGGCTCAGAGGAACTGCATTCTGCCCGCAACAAAGAC GGAGTCAAACAAGAACTCCGGAGTTTGCAGAAGTGTTTCCCTTT AAGGAAACGCTTCTATCCTGTGCAGCAACCTAGGTTTAGGGTCC AACTGTCTCCAAAGGACCACTTGAGAAGCAAGAAGGAGCCTGG TGAGGCTGCTCCCAGTGCCCTGCGGCCAGCAGTCCACACAGCC GGAGAGCCCATCTCTGAGCTGGGCGCCCCATGGCAAAGCACCC CCTGAACTTACCAGCTCGAAGGCTGCTGAAGAGCAGGAAGAGC AGTCCAGGACTGGAAAAAACAACCAGAAAGGCAGGTGAGGCG GGGCCACCAGGGAGTTACCTGTATCTTCCAAACAGGAACAGGC TGGTTCCCATGAGCAGGAGGTAGTTANGCCCATCACAGAAATG TGAAGGCAGAGCCAGGAGCCTGCCTGCCTCTGTTCTCCATGGG AATTCGGGGTC CGGGGCCAGGACCACCACCCTCCTGCCCAGCACAGCAAGTCCG AGGGGCTGGCAGCCTCTCACCACTCTCTAGCTCTCGCGGTAACA AATCCCCAGAAACACAGTGATGCTGGCGTGAGGATGAAGGGGA GCGAGGGACGCCAGTGAGGCTGGTCTAGCCTTCCTGGGGACAG ATGCCAAGAAGTTGTAGGAAATCAGAAAAAAAAAAAAAAAAA AAAGCTTTCAGGGCACATATAGTAGGAGTGTCACTTAAAATGC TGGGGAGACGGAGAACATCAGGCGTGCCCGTGACAGGGTCAGG TGAGTGACGGGACAGCCCTGTGCGGAACGCGGATCATTTTGAA ACCAAACCTGAGCTCCTCCTGTTTCAGATCCTGCTGCAGCTGGT GCCCCTGCCTCGGGCAGCAAATTCCCCTCGTGACTCCAATGC

SEQ ID	Sequence
20058	TCTGGCTGCCGACAGTCAGGTTCTGCTGCAGAAGCACGTTCTCT ATGCAGCAGCCAATGTTCACGCTGGGGGTCCGTGCGATCCTCA GCACGCTGACCACGTCATACAAGCCCCGCATGTTCAAGAAGAC GGTGTCATTCTGCAGAGCCTGGTCCAGCAGGCTGTTGTCCGTCT TATTGATCCAGTACACGTTGGGCCTGGGGTAGCCGTTTATGGAT GTACACGTGAAGGTGAGCTCATCCTGGGAGGGGCTGTGGGGGG CGCTGACGACGGGCACGCTGAAGTTTGCTGCAGGGGAGGGAAA CAGATTGTGAGAGATGCCAGACCCTGCTGGTCAAGAAACAGAG GGTACACGGTGCCAAGGCTGGGTCAGAGGGGAGGCGGCCCATT GTGCCCCGACATGGGTGACAGGCCAGGACC AGGGCTGTGGTCCGAGCAGCAGGCTCCGCCCTGTCCTGCCCAA GAGTCATCCCCCAAGCCAGTCCCAGTAGCCAGGGACCNCTGAG CCTGTCGGGCAGTGACTGGCACCCACAGACCCCCCACTCCACA GCCGTCGGCTGTGCCGGGACCCCCTCATTTGGATCTGGTCATTC TCACTGCTGACACAGGGGCTCACAGTCCATCTGAAATGGACAC AGCTGTTCTCCCCAATGAACTGCCCAGAGCTCCTTGGTTGCCTC TTATTTTTCTCTTAAATTTTGTTCTCATTTAGTGCTTTATAGAGTT CCCTTCAAATTTCACTTTTAAAACTCTAGTTTGGATGTGGTGGCT CACGCCTGTAATCACAGCACTTTGGGAGGGTGAGGCAGGAGGA TCGCTTGTGTCCAGGAGTTTGAGACCAGCCTGGGCAACATAGTG AGACCCCATTTCTACAAATAATCAAAATTAGCCAGGCGAGGTG GCATGTGCCTGTAGTCCCAGATACTCAGGAGGCTGAAGCAGGA GAATTGCTTGAGCTCAGGAGGTCAAGGCTGCAGCGTGATCACG CTACTGCACTCCAG

SEQ ID	Sequence
20059	AGAATTTCTCAGCAATTACATTATATTGCTGCTCACTTGCAGTA GGAAAGCTGTCACAAATGTGGCAGACACAGGGTAGCTTTACTG TTTGTGCAGCTACGTAAATGCCTGTGGGAAAATCTTTTTTTTTG AGATGGAGTCTTGCTCCGTCACCCAGGCTGGGGTGCAATGGCG TGATCTCAGCTCACTGCAACCCCCGACTCTGGGGTTCACGCCAT TCTCCTGCCTCACCCTCCCAAGTAGCTGGGATTACAGGTGCCCG CCACCATGCCCAGCTAATTTTTTGTATTTTTAGTAGAGATCGGG CTTCACTATGTTGGCCAGCCTGGTCTCGAACTCCTGACCTCAGG TGATCCACCCGCCTTGGCCTCCCAAAGTCCTGGGATTACAGGAG TGAGCCACTGCACCTGGCACCTGCAGGAAAATCTGTGTGTGTCC CCTGCCCCCAAAGCCCTCTGGGCTGGAAGGCTTGGCAAGGTTTC AGGTTTGTGCTGCGGTGCNTCGTCCTTATTCCTGGCTCTTCCAG AGGCTGGTGGCTCTTAGGGCTCAGCAGGGCTGCTGCCTGGGAC AGGGAGACCAGGGGACCCAGGAAGCCCTGGCTCAGAGGAACT GCATTCTGCCCGCAACAAAGACGGAGTCAAACAAGAACTCCGG AGTTTGCAGAAGTGTTTCCCTTTAAGGAAACGCTTCTATCCTGT GCAGCAACCTAGGTTTAGGGTCCAACTGTCTCCAAAGGACCAC TTGAGAAGCAAGAAGGAGCCTGGTGAGGCTGCTCCCAGTGCCC TGCGGCCAGCAGTCCACACAGCCGGAGAGCCCATCTCTGAGCT GGGCGCCCCATGGCAAAGCACCCCCTGAACTTACCAGCTCGAA GGCTGCTGAAGAGCAGGAAGAGCAGTCCAGGACTGGAAAAAA CAACCAGAAAGGCAGGTGAGGCGGGGCCACCAGGGAGTTACCT GTATCTTCCAAACAGGAACAGGCTGGTTCCCATGAGCAGGAGG TAG

Example 19: Validation of an 8-SNP Model for TL1A Companion Diagnositics

[0510] The machine learning workflow identified several SNP model combinations for the development of the TL1A companion diagnostic (TL1A CDx). Previous analyses had identified 3-SNP combination models composed of variants associated with *TNFSF15 (rs6478109), ICOSLG(rs7278257, rs2070557), ETS1 (rs7935393),* and *RBFOX1 (rs9806914)* genes as well as variant *rs1892231*. Next, 8-SNP models were investigated to identify novel combinations with improved positive predictive value (PPV), as well as negative predictive value (NPV).

[0511] 8-SNP models were identified using the methods described above via a Cedars Sinai Crohn's Disease cohort. These additional SNP models (Models_1-Model_495) consisted of 8-SNP combinations of the following SNPs: *TNFSF15 (rs6478109), ICOSLG (rs56124762), ETS1 (rs7935393), RBFOX1 (rs9806914), C14orf177 (rs1892231), CTNND2 (rs16901748), CLEC16A (rs12934476), RTEL1-TNFRSF6B (rs2297437), (LINC01031) rs1326860, PTPN2 (rs12457255), RGS7 (rs2815844), JAK2 (rs10974900), XKR6 (rs2409750), RBM17 (rs1541020), ENOX1 (rs4942248), and PRDM1 (rs7759385)*. **Table 25**

provides, in accordance with the embodiments disclosed herein, the 8-SNP model combinations.

Table 25. 8-SNP Models

Model_1	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs2297437
Model_2	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs1326860
Model_3	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs12457255
Model_4	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs2815844
Model_5	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs10974900
Model_6	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs2409750
Model_7	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs1541020
Model_8	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs4942248
Model_9	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs9806914,rs7759385
Model_10	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs1326860
Model_11	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs12457255
Model_12	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs2815844
Model_13	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs10974900
Model_14	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs2409750
Model_15	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs1541020
Model_16	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs4942248
Model_17	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2297437,rs7759385
Model_18	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs12457255
Model_19	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs2815844
Model_20	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs10974900
Model_21	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs2409750
Model_22	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs1541020

Model_23	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs4942248
Model_24	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs1326860,rs7759385
Model_25	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs12457255,rs2815844
Model_26	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs12457255,rs10974900
Model_27	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs12457255,rs2409750
Model_28	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs12457255,rs1541020
Model_29	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs12457255,rs4942248
Model_30	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs12457255,rs7759385
Model_31	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2815844,rs10974900
Model_32	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2815844,rs2409750
Model_33	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2815844,rs1541020
Model_34	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2815844,rs4942248
Model_35	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs2815844,rs7759385
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Model_37	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs7935393,rs10974900,rs1541020
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Model_47	rs6478109,rs56124762,rs1892231,rs16901748,rs12934476,rs9806914,rs2297437,rs12457255
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Model_495	rs6478109,rs56124762,rs1892231,rs16901748,rs2409750,rs1541020,rs4942248,rs7759385

Example 20: A SNP Genotyping Assay

[0512] This assay is used to identify the 8 SNPs in the 8 SNP models of Example 19. DNA from a sample derived from a subject is combined with primers specific to each SNP, PCR reagents, a wildtype probe and a mutant probe. Wildtype probes are tagged with Hex at the 5' end and quencher dye at the 3' end. Mutant probes are tagged with FAM at the 5' end and a quencher at the 3' end.

[0513] For each SNP to be tested, 4 standard reactions are run: no template, homozygous wildtype, hetozygous, and homozygous mutant. Standard reactions use templates comprising a gblock comprising all 8 WT or mutant SNP sequences. For the heterozygous standard reaction the template comprises both the WT gblock and the mutant gblock.

[0514] Samples are run in duplicate. The reactions are run and analyzed using QuantStudioDx software to detect the genotypes of each sample. Genotypes are identified as homozygous wildtype, heterozygous, or homozygous mutant for each SNP and sample tested.

Example 22: A Phase 2, Multi-Center, Double-Blind, Placebo-Controlled Study to Evaluate the CDx for Treatment with an Anti-TL1A Antibody in Subjects with Moderately to Severely Active Ulcerative Colitis.

[0515] To validate the efficacy of the CDx treatment with anti-TL1A antibodies in ulcerative colitis (UC), a phase 2 clinical trial is conducted. The detailed design of the clinical trial protocol is provided in the protocol synopsis of Table 26 below and shown in FIGS. 11A-11B.

TABLE 26. PROTOCOL SYNOPSIS

TITLE:	A Phase 2, Multi-Center, Double-Blind, Placebo-Controlled Study to Evaluatethe CDx for Treatment with an Anti-TL1A Antibody in Subjects with Moderately to Severely Active Ulcerative Colitis
PROJECT PHASE:	Phase 2
OBJECTIVE:	**Primary:** • To assess the safety and tolerability of A219 following 12-weeks of induction therapy • To compare the efficacy of A219 vs placebo for induction of clinical remission at Week 12 **Secondary:** All objectives below refer to comparison of A219-treated subjects vs placebo-treated subjects in Cohort 1. For the objectives where the companion diagnostic (CDx) status is a variable, a comparison of subjects in both Cohort 1 and Cohort 2 will be conducted. • To compare the efficacy of A219 vs placebo for induction of endoscopic improvement at Week 12 • To compare the efficacy of A219 vs placebo for induction of clinical response at Week 12 • To compare the efficacy of A219 vs placebo in CDx positive (CDx+) subjects (Cohort 1 + Cohort 2) for induction of clinical remission at Week 12 • To compare the efficacy of A219 vs placebo for induction of histologic remission at Week 12 • To compare the efficacy of A219 vs placebo for induction of histologic-endoscopic mucosal improvement at Week 12 • To compare the efficacy of A219 vs placebo in CDx+ subjects (Cohort 1 + Cohort 2) for induction of endoscopic improvement at Week 12 • To compare the efficacy of A219 vs placebo in CDx+ subjects (Cohort 1 + Cohort 2) for induction of clinical response at Week 12 • To compare the efficacy of A219 vs placebo in CDx+ subjects (Cohort 1 + Cohort 2) for induction of histologic remission at Week 12 • To compare the efficacy of A219 vs placebo in CDx+ subjects (Cohort 1 + Cohort 2) for induction of histologic-endoscopic mucosal improvement at Week 12

	• To compare the efficacy of A219 in CDx+ (Cohort 1 + Cohort 2) vs CDx negative (CDx-) subjects for induction of clinical remission at Week 12 • To compare the efficacy of A219 vs placebo for induction of mucosal healing at Week 12 • To compare the efficacy of A219 vs placebo in CDx+ subjects (Cohort 1 + Cohort 2) for induction of mucosal healing at Week 12 • To compare the efficacy of A219 vs placebo for change in Inflammatory Bowel Disease Questionnaire (IBDQ) at Week 12 • To compare the efficacy of A219 vs placebo in CDx+ subjects (Cohort 1 + Cohort 2) for change in IBDQ at Week 12 • To compare the efficacy of A219 vs. placebo in subjects who are CDx+ per alternative algorithm (Cohort 1 + Cohort 2) for clinical remission at Week 12 **Exploratory:** • To assess the pharmacokinetics (PK) of A219 in subjects with ulcerative colitis (UC) over time • To assess the effects of A219 on tissue and serum pharmacodynamic (PD) markers, including total TL1A concentrations over time • To assess the effect of A219 on inflammatory biomarkers including fecal calprotectin and high sensitivity C-reactive protein (hsCRP) over time • To assess the proportion of subjects in 3-component Modified Mayo Score response, 3-component Modified Mayo Score remission, endoscopic improvement, Robarts histopathology index (RHI) histologic remission, Geboes score histologic remission, and mucosal healing at Week 50 • To assess the change in Partial Mayo Score over time • To assess the change in Geboes Index and RHI from Baseline to Week 12 and Week 50 • To assess the exposure-response relationship of A219 on PD markers over time • To assess the proportion of subjects achieving corticosteroid-free-remission at Week 50

STUDY DESIGN:	This is a multi-center, double-blind, randomized, placebo-controlled proof of concept study designed to assess the safety, tolerability, and efficacy of A219 following 12 weeks of induction therapy in subjects with UC. This study will be conducted under the aegis of a Data Monitoring Committee (DMC) and will commence following the demonstration of an acceptable safety profile of A219 at a dose of ≥ 500 mg in the multiple ascending dose study in normal healthy volunteers (Example 16).
	The study has 4 periods (Screening Period, Induction Period [IP], Open- Label Extension [OLE] Period, and Follow-Up [FU] Period). The study will have 2 Cohorts that will enroll subjects in a sequential fashion utilizing an adaptive design as described below. **Cohort 1:** Following the Screening Period, approximately 120 eligible subjects with moderately to severely active UC will enter the IP and be randomized in a 1:1 fashion to receive intravenous (IV) administration of A219 1000 mg on Week 0/Day 1, followed by 500 mg on Weeks 2, 6, and 10, or placebo at the same timepoints. Randomization will be stratified by CDx status of positive (CDx+) or negative (CDx-) and prior biologic experience (yes/no) at Week 0/Day 1. Subjects who discontinue from the study will have a follow-up period of 12 weeks after last dose. **Cohort 2:** When approximately 80% of Cohort 1 subjects (i.e., ~96 subjects) have reached Week 12 or early terminated from the study, the DMC will conduct an unblinded analysis of clinical efficacy in CDx+ subjects and will recommend whether an expansion to Cohort 2 is warranted. The planned sample size for CDx+ subjects (combining Cohort 1 and Cohort 2) will be approximately 40, in the case where Cohort 2 is initiated. For Cohort 2, eligible subjects (who must be CDx+) will enter the IP and be randomized in a 1:1 fashion to receive IV administration of A219 1000 mg on Week 0/Day 1, followed by 500 mg on Weeks 2, 6, and 10, or placebo at the same timepoints. Randomization will be stratified by prior biologic experience (yes/no) at Baseline. Subjects who discontinue from the study will have a follow-up period of 12 weeks after last dose. Subjects who complete the 12-week IP from either Cohort will have the option to enter OLE. During OLE, starting at Week 14 visit: • Subjects who have achieved deep remission (defined as in clinical remission [endoscopic subscore of 0 or 1, rectal bleeding subscore of 0, and stool frequency subscore of 0 or 1 and not greater than Baseline] and RHI < 3) will continue in the study and have therapy withdrawal. o Upon disease relapse (defined as rectal bleeding score of ≥1, and either hsCRP ≥ 5 and/or fecal calprotectin ≥ 250), subjects can receive another course of induction therapy (1000 mg IV followed by 500 mg IV 2, 6, and 10 weeks after the first infusion) followed by maintenance therapy of 250 mg IV every 4 weeks (Q4W) for a total of 50 weeks. • Responders (defined as reduction from Baseline ≥ 2 points and ≥

	30% in 3-component Modified Mayo Score, accompanied by a reduction ≥ 1 in rectal bleeding subscore or absolute rectal bleeding subscore ≤ 1) who have not achieved deep remission will be re-randomized, stratified by CDx status of CDx+ or CDx-, to either 250 mg IV Q4W or 100 mg IV Q4W, starting at Week 14 until Week 50. • Nonresponders will receive an open-label induction regimen of 1000 mg of A219 on Week 14, followed by 500 mg on Weeks 16, 20, and 24. Nonresponders who do not respond at Week 28 (per investigator discretion) should be discontinued from the study. Nonresponders who respond at Week 28 (per investigator discretion) will be re-randomized to either 250 mg IV Q4W or 100 mg IV Q4W, starting at Week 28 for a total of 50 weeks. The study may be amended by the Sponsor to extend the OLE period beyond 50 weeks based on emerging safety data. The study also includes an optional PK sub-study during the IP for subjects who consent to additional PK sampling.
SAMPLE SIZE:	The study is planned to randomize up to approximately 170 subjects, approximately 120 in Cohort 1 and up to 50 in Cohort 2. A sample size of 60 per arm in Cohort 1 will enable a statistical power of > 80% for the primary endpoint at 1-sided significance level of 0.025 using Cochran- Mantel-Haenszel (CMH), assuming clinical remission rate of 5% for placebo and 24% for A219. Additionally, the sample size will confer > 80% power to achieve statistical significance for the 1st secondary endpoint of endoscopic improvement with an overall 1-sided alpha level of 0.025, assuming the endoscopic improvement rates are 15% and 38% for placebo and A219 groups, respectively. Additionally, for analyses of the CDx population (combining CDx+ subjects from Cohort 1 and Cohort 2), a sample size of 40 per arm will provide a statistical power of ≥ 80% at a 1-sided alpha level of 0.025, according to a group sequential design with a non-binding futility interim analysis when 18 subjects per arm reach Week 12, assuming clinical remission rate of 5% for placebo and 31% for A219.
SUBJECT TYPE:	Male or female subjects ≥ 18 years of age with moderately to severely active UC.
FORMULATIONS:	A219 will be supplied in 10 mL vials each containing 500 mg A219 (60 mg/mL solution) for IV administration after reconstitution.

DOSAGE:	Subjects will be stratified by CDx+/CDx- status and prior biologic experience (yes/no) in a 1:1 ratio to: • A219 1000 mg IV on Week 0/Day 1, followed by 500 mg IV on Weeks 2, 6, and 10 • Placebo IV on Week 0/Day 1, followed by placebo IV on Weeks 2, 6, and 10 During OLE: • Deep remitters will enter the therapy withdrawal period o All subjects who develop disease relapse after therapy withdrawal will receive another course of induction therapy (1000 mg IV followed by 500 mg IV 2, 6, and 10 weeks after the first infusion) followed by maintenance therapy of 250 mg IV Q4W for a total of 50 weeks. • Responders at the end of Week 12 will be stratified by CDx status of CDx+ or CDx- and re-randomized to receive one of the following regimens: o A219 250 mg IV on Week 14 then Q4W until Week 50 o A219 100 mg IV on Week 14 then Q4W until Week 50 • Nonresponders at the end of Week 12 will receive open-label A219 1000 mg IV on Week 14, followed by A219 500 mg IV on Weeks 16, 20, and 24. Subjects who do not respond by Week 26 should be discontinued from the study. Subjects who respond by Week 26 will be stratified by CDx status of CDx+ or CDx- and re-randomized to receive one of the following regimens: o A219 250 mg IV on Week 28 then Q4W for a total of 50 weeks o A219 100 mg IV on Week 28 then Q4W for a total of 50 weeks
ROUTE OF ADMINISTRATION:	All study drug will be reconstituted in 250 mL of 0.9% normal saline (NS) and will be administered IV over 30 minutes.

STUDY ENDPOINTS:	**Primary endpoints:** • The proportion of subjects reporting adverse events (AEs), serious adverse events (SAEs), AEs leading to discontinuation, and markedly abnormal laboratory values. • The proportion of subjects in the 3-component Modified Mayo Score clinical remission (as defined by endoscopic subscore of 0 or 1, rectal bleeding subscore of 0, and stool frequency subscore of 0 or 1 and not greater than Baseline) at Week 12. The 3-component Modified Mayo Score ranges from 0-9 and includes rectal bleeding, stool frequency and endoscopic assessment domains. **Secondary endpoints:** • The proportion of subjects with endoscopic improvement, as defined by endoscopy subscore ≤ 1 with no friability) at Week 12. • The proportion of subjects in 3-component Modified Mayo Score clinical response at Week 12. The 3-component Modified Mayo Score clinical response is defined by reduction from Baseline ≥ 2 points and $\geq 30\%$ in 3-component Modified Mayo Score, accompanied by a reduction ≥ 1 in rectal bleeding subscore or absolute rectal bleeding subscore ≤ 1. • The proportion of subjects in the 3-component Modified Mayo Score clinical remission (as defined by endoscopic subscore of 0 or 1, rectal bleeding subscore of 0, and stool frequency subscore of 0 or 1 and not greater than Baseline), in CDx+ subjects (Cohort 1 + Cohort 2) treated with A219 compared to CDx+ placebo-treated subjects at Week 12. The 3-component Modified Mayo Score ranges from 0-9 and includes rectal bleeding, stool frequency, and endoscopic assessment domains. • The proportion of subjects with histologic remission (defined Geboes score ≤ 3.1) at Week 12. • The proportion of subjects with histologic-endoscopic mucosal improvement (defined as Geboes score ≤ 3.1 and endoscopy subscore ≤ 1 with no friability) at Week 12. • The proportion of subjects with endoscopic improvement, as defined by endoscopy subscore ≤ 1 with no friability, in CDx+

	subjects (Cohort 1 + Cohort 2) treated with A219 compared to CDx+ placebo-treated subjects at Week 12. • The proportion of subjects in 3-component Modified Mayo Score clinical response in CDx+ subjects treated with A219 compared to CDx+ placebo-treated subjects at Week 12. The 3-component Modified Mayo Score clinical response is defined by reduction from Baseline ≥ 2 points and ≥ 30% in 3-component Modified Mayo Score, accompanied by a reduction ≥ 1 in rectal bleeding subscore or absolute rectal bleeding subscore ≤ 1. • The proportion of subjects with histologic remission, defined as Geboes score ≤ 3.1, in CDx+ subjects (Cohort 1 + Cohort 2) treated with A219 compared to CDx+ placebo-treated subjects at Week 12. • The proportion of subjects with histologic-endoscopic mucosal improvement (defined as Geboes score ≤ 3.1 and endoscopy subscore ≤ 1 with no friability), in CDx+ subjects (Cohort 1 + Cohort 2) treated with A219 compared to CDx+ placebo-treated subjects at Week 12. • The proportion of subjects with clinical remission (defined as endoscopic subscore of 0 or 1, rectal bleeding subscore of 0, and stool frequency subscore of 0 or 1 and not greater than Baseline) in CDx+ subjects (Cohort 1 + Cohort 2) treated with A219 compared to in CDx- subjects treated with A219 at Week 12. • The proportion of subjects with mucosal healing (defined as Geboes score ≤ 2B.1 and endoscopy subscore of ≤ 1) at Week 12. • The proportion of subjects with mucosal healing (defined as Geboes score ≤ 2B.1 and endoscopy subscore of ≤ 1), in CDx+ subjects (Cohort 1 + Cohort 2) treated with A219 compared to CDx+ placebo-treated subjects at Week 12. • The proportion of subjects with IBDQ response, as defined by ≥ 16-point increase from Baseline at Week 12. • The proportion of subjects with IBDQ response, as defined by ≥ 16- point increase from Baseline, in CDx+ subjects (Cohort 1 + Cohort 2) treated with A219 compared to CDx+ placebo-treated subjects at Week 12. • The proportion of subjects in the 3-component Modified Mayo Score clinical remission (as defined by endoscopic subscore of 0 or 1, rectal bleeding subscore of 0, and stool frequency subscore of 0 or 1 and not greater than Baseline), in CDx+ subjects per alternative algorithm (Cohort 1 + Cohort 2) treated with A219 compared to CDx+ placebo-treated subjects per alternative algorithm at Week 12.

	The 3-component Modified Mayo Score ranges from 0-9 and includes rectal bleeding, stool frequency, and endoscopic assessment domains. **Exploratory endpoints:** • The pharmacokinetics of A219 in subjects with UC after multiple doses • The change from Baseline in serum and fecal inflammatory biomarkers (PD markers) • The proportion of subjects in 3-component Modified Mayo Score response, 3-component Modified Mayo Score remission, endoscopic improvement, RHI histologic remission, Geboes score histologic remission, and mucosal healing at Week 50 • The change in Partial Mayo Score (with or without PGA component) over time • The change in Geboes Index and RHI from Baseline to Week 12 and Week 50 • The exposure-response relationship of A219 on PD markers • Within subpopulation of subjects on corticosteroid at study entry, the proportion of subjects in clinical remission and off of corticosteroid at Week 50
INCLUSION CRITERIA:	Subjects are required to meet the following criteria in order to be included in the study: 1. Male or female ≥ 18 years of age. 2. Subjects must have had a documented diagnosis of UC (endoscopy + histology) to be eligible for study participation. For subjects with no documented confirmation of UC diagnosis or if previous diagnosis is not deemed conclusive, UC diagnosis must be confirmed at time of screening colonoscopy. 3. Moderately to severely active UC as defined by 3-component Modified Mayo score (3 components of rectal bleeding, stool frequency, and endoscopy) of 4 to 9, inclusive, with Modified Mayo endoscopic subscore ≥ 2 and rectal bleeding subscore ≥ 1. 4. Subjects must satisfy at least one of the following criteria:

	a) In the past, had an inadequate response to one or more of the following treatments: • Oral prednisone ≥ 40 mg/day (or equivalent) or budesonide ≥ 9 mg/day or equivalent or beclomethasone ≥ 5 mg/day for at least 2 weeks • Corticosteroid dependence as defined by failed to successfully taper to < 10 mg/day of prednisone or equivalent (i.e., had a flare of disease) within 3 months of starting therapy, or if relapse occurs within 3 months of stopping corticosteroids • Immunosuppressants (azathioprine ≥ 2 mg/kg/day or 6-mercaptopurine ≥ 1.0 mg/kg/day [or documentation of a therapeutic concentration of 6-thioguanine nucleotide]) for at least 8 weeks • An approved anti-TNF agent at an approved labeled dose for at least 8 weeks • Vedolizumab at the approved labelled dose for at least 8 weeks • An approved JAK inhibitor (e.g., tofacitinib) at an approved labelled dose for at least 8 weeks • An approved anti-IL-12/23 (e.g., ustekinumab) at an approved labelled dose for at least 8 weeks • An approved sphingosine 1-phosphate receptor (S1PR) modulator at an approved labelled dose for least 12 weeks **OR** b) Had been intolerant to one or more of the above-mentioned treatments (e.g., unable to achieve doses or treatment durations because of dose limiting side effects [e.g., leukopenia, psychosis, uncontrolled diabetes, elevated liver enzymes]). **OR** c) Currently receiving one or more of the following treatments: • Oral Prednisone □ 10 mg/day (or equivalent) for at least 3 months • Immunosuppressants [azathioprine ≥ 2 mg/kg/day or 6-mercaptopurine □ 1.0 mg/kg/day (or documentation of a therapeutic concentration of 6-thioguanine nucleotide)] for at least 8 weeks. Notes on subjects who have had prior biologic/biologic-like therapy(ies) (anti-TNF, JAK inhibitor, S1PR modulator, anti-IL-12/23, and/or vedolizumab): • The study will include a maximum of 70% subjects who have had prior biologic/biologic-like therapy(ies) experience.

	Upon reachingthe maximum number of allowed biologic/biologic-like experienced subjects (70%), subjects who have had prior biologic/biologic-like experience will no longer be allowed to enterthe study. • Subject cannot have failed (no response, insufficient response, lossof response, and/or intolerance) > 3 classes or > 4 individual biologic/biologic-like therapies (refer to exclusion criterion #26). 5. For subjects who are women of childbearing potential (WOCBP) involved in any sexual intercourse that could lead to pregnancy, the subject has used two highly effective methods of contraception for atleast 4 weeks prior to Day 1 and agrees to continue to use two highly effective methods of contraception until at least 12 weeks after the lastdose of study drug. 6. Male subjects must use, with their female partner of childbearing potential, two highly effective methods of contraception and refrain from sperm donation from screening to 12 weeks after the last dose of study drug. 7. Subject must meet drug stabilization requirements, as applicable: a) Oral corticosteroid treatment must be equivalent of ≤ 20 mg prednisone or ≤ 9 mg budesonide or beclomethasone ≤ 5 mg daily at a stable dose for at least 2 weeks prior to randomization b) Oral aminosalicylates should be at a stable dose for at least 2 weeksprior to randomization c) Azathioprine and 6-mercaptopurine should be at a stable dose for atleast 4 weeks prior to randomization 8. Able to provide written informed consent and understand and comply with the requirements of the study. 9. *For Cohort 2 only*: Subjects must be CDx+.

EXCLUSIO N CRITERIA:	Subjects with the following characteristics will be excluded from the study: **Sex and Reproductive Status** 1. WOCBP and men with female partners of childbearing potential who are unwilling or unable to use two highly effective methods of contraception to avoid pregnancy for the entire study period and for up to 12 weeks after the last dose of study drug. 2. Women who are pregnant or breastfeeding. 3. Women with a positive pregnancy test on enrollment or prior to randomization. **Target Disease Exceptions** 4. Diagnosis of Crohn's disease or indeterminate colitis. 5. UC limited to the rectum (< 15 cm from anal verge). 6. Current evidence of fulminant colitis, toxic megacolon, or bowel perforation. 7. Current or impending need for colostomy or ileostomy. 8. Previous total proctocolectomy or partial colectomy. 9. Surgical bowel resection within 3 months before screening. 10. Concomitant primary sclerosing cholangitis (PSC) **Medical History and Concurrent Diseases** 11. Past or current evidence of definite low-grade or high-grade colonic dysplasia that has not been completely removed. 12. Subjects who are scheduled or anticipate the need for surgery, aside from dermatologic procedures. 13. Subjects who have a history of clinically significant drug or alcohol abuse. 14. Concomitant illness that in the opinion of the Investigator, is likely to require systemic glucocorticosteroid therapy during the study (e.g., moderate to severe asthma). 15. Current symptoms of severe, progressive, or uncontrolled renal, hepatic, hematological, pulmonary, cardiac, neurological, ophthalmologic or cerebral disease. Concomitant medical conditions that in the opinion of the Investigator might place the subject at unacceptable risk for participation in this

	study. 16. Subjects with a history of cancer within the last 5 years (other than non-melanoma skin cell cancers cured by local resection). Existing non-melanoma skin cell cancers must be removed prior to enrollment. Subjects with carcinoma in situ or localized cervical cancer, treated with definitive surgical intervention, are allowed. 17. Subjects at risk for tuberculosis (TB). Specifically, subjects with: a) A history of active TB b) Current clinical, radiographic or laboratory evidence of active TB c) Latent TB which was not successfully treated. Subjects with a positive TB screening test indicative of latent TB will not be eligible for the study unless active TB infection has been ruled out, and an appropriate course of intervention for latent TB has been initiated at least 2 weeks prior to randomization, and no evidence of active TB on chest x-ray during Screening. 18. Subjects with any serious bacterial infection within the last 3 months, unless treated and resolved with antibiotics, or any chronic bacterial infection (such as chronic pyelonephritis, osteomyelitis and bronchiectasis). 19. Female subjects who have had a breast cancer screening that is suspicious for malignancy, and in whom the possibility of malignancy cannot be reasonably excluded following additional clinical, laboratory or other diagnostic evaluations. 20. Subjects with any active infections (excluding fungal infections of nailbeds) including, but not limited to, those that require intravenous (IV) antimicrobial treatment 4 weeks or oral antimicrobial treatment 2 weeks prior to randomization. Subjects with evidence of Human Immunodeficiency Virus (HIV), Hepatitis B or Hepatitis C infection detected during screening are also excluded, but subjects with successfully treated Hepatitis C with no recurrence for ≥ 1 year are allowed. Subjects with active documented or suspected COVID-19 infection within 4 weeks of randomization or asymptomatic SARS-CoV-2 PCR test within 2 weeks of randomization are excluded. 21. Subjects with herpes zoster reactivation or cytomegalovirus (CMV) that resolved less than 2 months prior to signing informed consent. 22. Subjects who have received any live vaccines within 3 months of the anticipated first dose of study medication or who will have need of a live vaccine at any time during the study. **Physical and Laboratory Test Findings**

	23. Positive stool Polymerase Chain Reaction (PCR) or culture for enteric pathogens. 24. Stool positive for *Clostridium difficile* (*C. difficile)* toxin. Subjects who are positive can be retested after the completion of a full course of treatment for *C. difficile* infection. 25. Any of the following lab values: a) Hemoglobin (Hgb) < 8.0 g/dL (80 g/L) b) White blood cell (WBC) < 2,500/mm^3 (2.5 x 10^9/L) c) Neutrophils < 1,000/mm^3 (1 x 10^9/L) d) Platelets < 100,000/mm^3 (100 x 10^9/L) e) Serum creatinine > 2 times upper limit of normal (ULN) f) Serum alanine aminotransferase (ALT) or aspartate aminotransferase (AST) > 2 times ULN g) Any other laboratory test results that, in the opinion of the Investigator, might place the subject at unacceptable risk for participation in this study **Prohibited Therapies and/or Medications** 26. Failed (no response, insufficient response, loss of response, and/or intolerance) > 3 classes (anti-TNF, anti-integrin, anti-IL12/23, JAK inhibitor, S1PR modulator) or > 4 individual biologic/biologic-like therapies. 27. Any marketed biologic or biologic-like within 2 weeks for tofacitinib, 8 weeks for anti-TNF agents, 10 weeks for S1PR modulators, and 12 weeks for vedolizumab and ustekinumab prior to randomization or if drug level per therapeutic dose monitoring is greater than lower limit of detection. 28. Any biologic immunomodulators not covered in exclusion criterion 27, used for UC or other conditions within 8 weeks or 5 half-lives, whichever is longer, prior to randomization or if drug level per therapeutic dose monitoring is greater than lower limit of detection. 29. Rituximab within 1 year prior to randomization.

	30. Parenteral corticosteroids within 4 weeks or rectal administration ofcorticosteroids within 2 weeks prior to randomization. 31. Rectal administration of 5-ASA within 2 weeks prior to randomization. 32. Tacrolimus, methotrexate, cyclosporine, mycophenolate mofetil (CellCept®), immunoadsorption columns (such as Prosorba columns), D Penicillamine, Leflunomide, Thalidomide, fish-oil preparations, probiotics, fecal transplantation, non-steroidal anti-inflammatory agents(NSAIDs), aspirin > 81 mg/day within 2 weeks prior to randomization. 33. Other investigational chemical agent within 30 days or other investigational biologic agent within 8 weeks or 5 half-lives (whicheveris longer) of randomization. 34. Prior exposure to A219. **Other Exclusion Criteria** 35. Prisoners or subjects who are compulsorily detained (involuntarily incarcerated) for treatment of either a psychiatric or physical (e.g., infectious disease) illness must not be enrolled into this study. 36. Legal or mental incapacitation, or inability to understand and comply with the requirements of the study.
Statistical Methods:	Statistical methods will be detailed in the Statistical Analysis Plan. The SAP will provide details about the method of analysis and specific plannedanalyses, and will be prepared and approved by Prometheus Biosciences and its designees before study database lock and unblinding of subject treatment assignments. The analysis populations are defined as follows: • Full analysis set (FAS) from Cohort 1: all subjects randomized andtreated in Cohort 1 • FAS for CDx+: all CDx+ subjects who are randomized and treated inboth Cohort 1 and Cohort 2 • Safety analysis set: all subjects treatedThe following analyses will be performed: **Efficacy:** The efficacy assessment will test for the difference between A219 and placebo groups in FAS. The primary endpoint will be analyzed and compared between A219 andplacebo treatment groups in FAS from Cohort 1. The primary endpoint, the proportion of subjects achieving clinical remission, will be tested between the 2 treatment groups at 1-sided

	significance level of 0.025 using CMH with stratification factors at randomization. If significant, the 1st secondary endpoint of proportion of subjects achieving endoscopic improvement will be tested between the 2 treatment groups at 1-sided significance level of 0.025. If significant, the 2nd, 3rd, 4th, and 5th secondary endpoints will be tested sequentially, each at 1-sided significance level of 0.025. Testing for statistical significance will stop when the first endpoint is not statistically significant at level of 0.025 and all remaining p values will be nominal. Treatment difference for primary and secondary endpoints for Cohort 1 will be estimated along with 95% CI for all subjects in FAS. The secondary endpoints in CDx+ subjects will be summarized and compared between A219 and placebo groups in FAS for CDx+, while the treatment difference will be estimated with 95% CI. Additional efficacy analysis will be detailed in SAP. **Interim Efficacy Analysis:** An interim analysis will be carried out when approximately 80% of subjects (approximately 96 subjects) in Cohort 1 have reached Week 12 or early terminated from the study. The DMC will review the unblinded efficacy and safety data and recommend on the expansion to Cohort 2. Decision rules to initiate Cohort 2 are determined according to the futility bounds of group sequential design of a sample size of 40 per arm with one interim analysis at the information fraction of 45%. Because the exact bounds will be calculated using the actual number of subjects with CDx+ included in the interim analysis, the final decision rules, along with sensitivity analysis, will be specified in the DMC SAP, prior to the interim analysis. **Adverse Events:** AEs will be coded using the most current version of Medical Dictionary for Regulatory Activities (MedDRA[1]). A by-subject AE data listing, including verbatim term, preferred term (PT), system organ class (SOC), treatment, severity, seriousness criteria, relationship to drug, and action taken, will be provided. The number of subjects experiencing treatment-emergent adverse events (TEAEs) and number of TEAEs will be summarized by treatment using frequency counts for Safety analysis set. Medical History, chest x-ray, electrocardiogram (ECG), and physical examination will be listed by subject. Changes in ECGs and physical examinations will be described in the text of the final report. **Concomitant Medications:** Concomitant medications will be coded using the most current World Health Organization (WHO) drug dictionary and listed

	by treatment. **Pharmacokinetics:** Summary statistics of A219 concentrations and anti-drug antibody (ADA) by visit and by CDx+ and CDx-.

[0516] While preferred embodiments of the present invention 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 invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

WHAT IS CLAIMED:

1. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
   wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and
   wherein the inhibitor of TL1A activity or expression is an antibody or antigen binding fragment thereof that competes for binding to human TL1A with a reference antibody comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15.
2. The method of claim 1, wherein the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.
3. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and

wherein the inhibitor of TL1A activity or expression is an antibody or antigen binding fragment thereof that competes for binding to human TL1A with a reference antibody comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15.

4. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and

wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an

LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15.

5. The method of claim 4, wherein the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.

6. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and
wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A, comprising a heavy chain variable region comprising: (a) an HCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 1; (b) an HCDR2 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 2-5; and (c) an HCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 6-9; and the light chain variable region comprises: (d) an

LCDR1 comprising an amino acid sequence set forth by SEQ ID NO: 10; (e) an LCDR2 comprising an amino acid sequence set forth by SEQ ID NO: 11; and (f) an LCDR3 comprising an amino acid sequence set forth by any one of SEQ ID NOS: 12-15.

7. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and
wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 101-135, or 310-302, and a light chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 201-206 or 303.
8. The method of claim 7, wherein the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.
9. The method of any one of claims 1-8, wherein the heavy chain variable domain comprises an amino acid sequence at least about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 101-135, or 310-302.
10. The method of any one of claims 1-8, wherein the light chain variable domain comprises an amino acid sequence at least about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 201-206 or 303.

11. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and
wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to tumor necrosis factor-like protein 1A (TL1A), comprising a heavy chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 101-135, or 310-302, and a light chain variable domain comprising an amino acid sequence at least about 90% identical to any one of SEQ ID NOS: 201-206 or 303.

12. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and
wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A that comprises: (a) a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework; and (b) a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain

variable framework region collectively comprise less than about 14 amino acid modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework.

13. The method of claim 12, wherein the at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.

14. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,
wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and
wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A that comprises: (a) a heavy chain variable framework region comprising a human IGHV1-46*02 framework or a modified human IGHV1-46*02 framework; and (b) a light chain variable framework region comprising a human IGKV3-20 framework or a modified human IGKV3-20 framework; wherein the heavy chain variable framework region and the light chain variable framework region collectively comprise less than about 14 amino acid

modifications from the human IGHV1-46*02 framework and the human IGKV3-20 framework.

15. The method of any one of claims 12-14, wherein an amino acid modification of the less than 14 amino acid modifications comprises: (a) the amino acid modification is at position 47 in the heavy chain variable region, and the amino acid at position 47 is R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (b) the amino acid modification is at position 45 in the heavy chain variable region, and the amino acid at position 45 is A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (c) the amino acid modification is at position 55 in the heavy chain variable region, and the amino acid at position 55 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; (d) the amino acid modification is at position 78 in the heavy chain variable region, and the amino acid at position 78 is A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y; (e) the amino acid modification is at position 80 in the heavy chain variable region, and the amino acid at position 80 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; (f) the amino acid modification is at position 82 in the heavy chain variable region, and the amino acid at position 82 is A, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V; (g) the amino acid modification is at position 89 in the heavy chain variable region, and the amino acid at position 89 is A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, or Y; or (h) the amino acid modification is at position 91 in the heavy chain variable region, and the amino acid at position 91 is A, R, N, D, C, Q, E, G, H, I, L, K, F, P, S, T, W, Y, or V; or a combination of two or more modifications selected from (a) to (h).

16. The method of claim 15, wherein an amino acid modification of the less than 14 amino acid modifications comprises: A47R, R45K, M55I, V78A, M80I, R82T, V89A, M91L in the heavy chain variable region, per Aho or Kabat numbering.
17. The method of claim 15, wherein an amino acid modification of the less than 14 amino acid modifications comprises: (a) a modification at amino acid position 54 in the light chain variable region; and/or (b) a modification at amino acid position 55 in the light chain variable region; per Aho or Kabat numbering.
18. The method of any one of claims 12-14, wherein an amino acid modification of the less than 14 amino acid modifications comprises: (a) the amino acid modification is at position 54 of the light chain variable region, and the amino acid at position 54 is A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V; and/or (b) the amino acid

modification is at position 55 of the light chain variable region, and the amino acid at position 55 is A, R, N, D, C, Q, E, G, H, I, K, M, F, P, S, T, W, Y, or V.

19. The method of claim 18, wherein an amino acid modification of the less than 14 amino acid modifications comprises L54P and/or L55W in the light chain variable region, per Aho or Kabat numbering.

20. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and

wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises:

a heavy chain variable region comprising SEQ ID NO: 301 X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEW X4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HC DR3]WGQGTTVTVSS, and

a light chain variable region comprising SEQ ID NO: 303 EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[L CDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKL EIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V.

21. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms that are predictive of a positive therapeutic response in the subject to a treatment with the inhibitor of TL1A activity or expression with a positive predictive value or a specificity of at least about 51%, are detected in a sample obtained from the subject, and

wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises:

a heavy chain variable region comprising SEQ ID NO: 302 X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEW X4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS, and

a light chain variable region comprising SEQ ID NO: 303 EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[L CDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKL EIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V.

22. The method of any one of claims 20-21, wherein the at least three polymorphisms comprises rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.

23. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and

wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises:

a heavy chain variable region comprising SEQ ID NO: 301 X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEW X4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYCAR[HC DR3]WGQGTTVTVSS, and

a light chain variable region comprising SEQ ID NO: 303 EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[L CDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKL EIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V.

24. A method of treating an inflammatory, a fibrotic, or a fibrostenotic disease or condition in a subject, the method comprising administering to the subject a therapeutically effective amount of an inhibitor of Tumor necrosis factor-like cytokine 1A (TL1A) activity or expression,

wherein at least three polymorphisms comprise rs16901748, rs56124762, rs6478109, rs1892231, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof, are detected in a sample obtained from the subject, and

wherein the inhibitor of TL1A activity or express is an antibody or antigen binding fragment thereof that binds to TL1A and comprises:

a heavy chain variable region comprising SEQ ID NO: 302 X1VQLVQSGAEVKKPGASVKVSCKAS[HCDR1]WVX2QX3PGQGLEW X4G[HCDR2]RX5TX6TX7DTSTSTX8YX9ELSSLRSEDTAVYYC[HCDR3]WGQGTTVTVSS, and

a light chain variable region comprising SEQ ID NO: 303 EIVLTQSPGTLSLSPGERATLSC[LCDR1]WYQQKPGQAPRX10X11IY[L CDR2]GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC[LCDR3]FGGGTKL

EIK, wherein each of X1-X11 is independently selected from A, R, N, D, C, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y, or V

25. THE METHOD OF ANY ONE OF CLAIMS 20-24, WHEREIN:

(A) X1 IS Q OR E;

(B) X2 IS R OR K

(C) X3 IS A OR R;

(D) X4 IS M OR I;

(E) X5 IS V OR A;

(F) X6 IS M OR I;

(G) X7 IS R OR T;

(H) X8 IS V OR A;

(I) X9 IS M OR L

(J) X10 IS L OR P;

(K) X11 IS L OR W; OR

(L) X1-X11 ARE ANY COMBINATION OF (A) TO (K).

26. The method of any one of claims 20-24, wherein the antibody or antigen binding fragment comprises a heavy chain CDR1 as set forth by SEQ ID NO: 1, a heavy chain CDR2 as set forth by any one of SEQ ID NOS: 2-5, a heavy chain CDR3 as set forth by any one of SEQ ID NOS: 6-9, a light chain CDR1 as set forth by SEQ ID NO: 10, a light chain CDR2 as set forth by SEQ ID NO: 11, and a light chain CDR3 as set forth by any one of SEQ ID NOS: 12-15.

27. The method of any one of claims 20-24, wherein the antibody or antigen binding fragment comprises a heavy chain framework (FR) 1 as set forth by SEQ ID NO: 304, a heavy chain FR2 as set forth by SEQ ID NO: 305 or SEQ ID NO: 313, a heavy chain FR3 as set forth by any one of SEQ ID NOS: 306, 307, 314, or 315, a heavy chain FR4 as set forth by SEQ ID NO: 308, a light chain FR1 as set forth by SEQ ID NO: 309, a light chain FR2 as set forth by SEQ ID NO: 310, a light chain FR3 as set forth by SEQ ID NO: 311, or a light chain FR4 as set forth by SEQ ID NO: 312, or a combination thereof.

28. The method of any one of claims 1-27, wherein the antibody or antigen binding fragment comprises a human IgG1 Fc region comprising (a) 297A, 297Q, 297G, or 297D, (b) 279F, 279K, or 279L, (c) 228P, (d) 235A, 235E, 235G, 235Q, 235R, or 235S, (e) 237A, 237E, 237K, 237N, or 237R, (f) 234A, 234V, or 234F, (g) 233P, (h) 328A, (i) 327Q or 327T, (j) 329A, 329G, 329Y, or 329R (k) 331S, (l) 236F or 236R,

(m) 238A, 238E, 238G, 238H, 238I, 238V, 238W, or 238Y, (n) 248A, (o) 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, or 254V, (p) 255N, (q) 256H, 256K, 256R, or 256V, (r) 264S, (s) 265H, 265K, 265S, 265Y, or 265A, (t) 267G, 267H, 267I, or 267K, (u) 268K, (v) 269N or 269Q, (w) 270A, 270G, 270M, or 270N, (x) 271T, (y) 272N, (z) 292E, 292F, 292G, or 292I, (aa) 293S, (bb) 301W, (cc) 304E, (dd) 311E, 311G, or 311S, (ee) 316F, (ff) 328V, (gg) 330R, (hh) 339E or 339L, (ii) 343I or 343V, (jj) 373A, 373G, or 373S, (kk) 376E, 376W, or 376Y, (ll) 380D, (mm) 382D or 382P, (nn) 385P, (oo) 424H, 424M, or 424V, (pp) 434I, (qq) 438G, (rr) 439E, 439H, or 439Q, (ss) 440A, 440D, 440E, 440F, 440M, 440T, or 440V, (tt) E233P, (uu) L235E, (vv) L234A and L235A, (ww) L234A, L235A, and G237A, (xx) L234A, L235A, and P329G, (yy) L234F, L235E, and P331S, (zz) L234A, L235E, and G237A, (aaa), L234A, L235E, G237A, and P331S (bbb) L234A, L235A, G237A, P238S, H268A, A330S, and P331S (IgG1 σ, (ccc) L234A, L235A, and P329A, (ddd) G236R and L328R, (eee) G237A, (fff) F241A, (ggg) V264A, (hhh) D265A, (iii) D265A and N297A, (jjj) D265A and N297G, (kkk) D270A, (lll) A330L, (mmm) P331A or P331S, or (nnn) any combination of two or more selected from (a) – (uu), per Kabat numbering.

29. The method of any one of claims 1-27, wherein the antibody or antigen binding fragment comprises a human IgG4 Fc region.

30. The method of any one of claims 1-27, wherein the antibody or antigen binding fragment comprises a Fc region comprising a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362.

31. The method of any one of claims 1-27, wherein the antibody of antigen binding fragment comprises and a fragment crystallizable (Fc) region comprising reduced antibody-dependent cell-mediated cytotoxicity (ADCC) function as compared to human IgG1 and/or reduced complement-dependent cytotoxicity (CDC) as compared to human IgG1.

32. The method of any one of claims 1-27, wherein the Fc comprises the human IgG1 comprises SEQ ID NO: 320.

33. The method of any one of claims 1-27, wherein the ADCC function of the Fc region comprising reduced ADCC is at least about 50% reduced as compared to human IgG1.

34. wherein the CDC function of the Fc region comprising reduced CDC is at least about 50% reduced as compared to human IgG1.
35. The method of any one of claims 1-27, wherein the Fc comprises (i) a human IgG4 Fc region or (ii) a human IgG4 Fc region comprising (a) S228P, (b) S228P and L235E, or (c) S228P, F234A, and L235A, per Kabat numbering.
36. The method of any one of claims 1-27, wherein the Fc comprises a human IgG2 Fc region; IgG2-IgG4 cross-subclass Fc region; IgG2-IgG3 cross-subclass Fc region; IgG2 comprising H268Q, V309L, A330S, P331S (IgG2m4); or IgG2 comprising V234A, G237A, P238S, H268A, V309L, A330S, P331S (IgG2σ).
37. The method of any one of claims 1-27, wherein the Fc comprises a human IgG1 with a substitution selected from 329A, 329G, 329Y, 331S, 236F, 236R, 238A, 238E, 238G, 238H, 238I, 238V, 238W, 238Y, 248A, 254D, 254E, 254G, 254H, 254I, 254N, 254P, 254Q, 254T, 254V, 264S, 265H, 265K, 265S, 265Y, 265A, 267G, 267H, 267I, 267K, 434I, 438G, 439E, 439H, 439Q, 440A, 440D, 440E, 440F, 440M, 440T, and 440V, per Kabat numbering.
38. The method of any one of claims 1-27, wherein the Fc comprises a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of SEQ ID NOS: 320-362.
39. The method of any one of claims 1-27, wherein the Fc comprises any one of SEQ ID NOs: 401-413 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 401-413.
40. The method of any one of claims 1-27, wherein the antibody or antigen binding fragment comprises a heavy chain comprising any one of SEQ ID NOs: 501-513 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 501-513.
41. The method of any one of claims 1-27, wherein the antibody or antigen binding fragment comprises a light chain comprising any one of SEQ ID NO: 514 or a sequence at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NO: 514.
42. The method of any one of claims 1-41, wherein the at least three polymorphisms are predictive of the positive therapeutic response with the positive predictive value and a specificity of at least about 51%.
43. The method of any one of claims 1-41, wherein the positive predictive value is greater than or equal about 60%, 65%, 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%,

83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%.

44. The method of any one of claims 1-41, wherein the positive predictive value is between about 60% - 100%, 65%-95%, 70%- 90%, 75%-85%, and 70%-80%.
45. The method of any one of claims 1-41, wherein the specificity is greater than or equal to about 60%, 65%, 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%.
46. The method of any one of claims 1-41, wherein the specificity is between about 60% - 100%, 65%-95%, 70%- 90%, 75%-85%, and 70%-80%.
47. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs56124762, and rs1892231.
48. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs56124762, and rs16901748.
49. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs1892231, and rs16901748.
50. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs56124762, rs1892231, and rs16901748.
51. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs2070558, and rs1892231.
52. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs2070558, and rs16901748.
53. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs1892231, and rs16901748.
54. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs2070558, rs1892231, and rs16901748.
55. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs2070561, and rs1892231.
56. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs2070561, and rs16901748.
57. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs1892231, and rs16901748.
58. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs2070561, rs1892231, and rs16901748.

59. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs7935393, and rs1892231.
60. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs7935393, and rs9806914.
61. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs7935393, and rs7278257.
62. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs7935393, and rs2070557.
63. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs1892231, and rs9806914.
64. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs1892231, and rs7278257.
65. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs1892231, and rs2070557.
66. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs9806914, and rs7278257.
67. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs9806914, and rs2070557.
68. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs7278257, and rs2070557.
69. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs7935393, rs1892231, and rs9806914.
70. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs7935393, rs1892231, and rs7278257.
71. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs7935393, rs1892231, and rs2070557.
72. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs7935393, rs9806914, and rs7278257.
73. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs7935393, rs9806914, and rs2070557.
74. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs7935393, rs7278257, and rs2070557.
75. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs1892231, rs9806914, and rs7278257.

76. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs1892231, rs9806914, and rs2070557.
77. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs1892231, rs7278257, and rs2070557.
78. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs9806914, rs7278257, and rs2070557.
79. The method of any one of claims 1-41, wherein the at least three polymorphisms comprise: rs6478109, rs56124762, and rs1892231.
80. The method of any one of claims 1-79, wherein the at least three polymorphisms further comprises a fourth polymorphism comprising rs16901748, rs1892231, rs56124762, rs6478109, rs2070558, rs2070561, rs11897732, rs6740739, rs17796285, rs7935393, rs12934476, rs12457255, rs2070557, rs4246905, rs10974900, rs12434976, rs2815844, rs889702, rs2409750, rs1541020, rs4942248, rs12934476, rs12457255, rs2297437, rs41309367, rs10733509, rs10750376, rs10932456, rs1326860, rs1528663, rs951279, rs9806914, rs7935393, rs1690492, rs420726, rs7759385, rs10974900, rs1326860, rs2548147, rs2815844, rs889702, rs9806914, rs7278257, or rs11221332, or a proxy polymorphism in linkage disequilibrium therewith as determined with an R^2 of at least 0.85, or a combination thereof.
81. The method of any one of claims 1-80, wherein the at least three polymorphisms are detected in the sample by subjecting the sample to an assay configured to detect a presence of at least three nucleotides corresponding to nucleic acid position 501 within at least three of SEQ ID NOS: 2001-20041, or 20057-20059.
82. The method of any one of claims 1-81, wherein the inflammatory, fibrotic, or fibrostenotic disease or condition comprises inflammatory bowel disease, Crohn's disease, obstructive Crohn's disease, ulcerative colitis, intestinal fibrosis, intestinal fibrostenosis, rheumatoid arthritis, pulmonary fibrosis, scleroderma, or primary sclerosing cholangitis.
83. The method of claim 82, wherein the Crohn's disease is ileal, ileocolonic, or colonic Crohn's disease.
84. The method of claim 82, wherein the pulmonary fibrosis comprises idiopathic pulmonary fibrosis.
85. The method of any one of claims 1-83, wherein the subject has, or is at risk for developing, a non-response or loss-of-response to a standard therapy comprising

glucocorticosteriods, anti-TNF therapy, anti-a4-b7 therapy, anti-IL12p40 therapy, or a combination thereof.

86. The method of any one of claims 1-85, further comprising determining whether the subject with an inflammatory, a fibrotic, or a fibrostenotic disease or condition is suitable for treatment with an inhibitor of TL1A activity or expression based, at least in part, on the at least three polymorphisms detected in the sample.

87. The method of any one of claims 1-86, further comprising obtaining, or having obtained, the sample from the subject.

88. The method of any one of claims 1-87, wherein the at least three polymorphisms are detected in utilizing assay comprising a quantitative polymerase chain reaction (qPCR), nucleic acid sequencing reaction, or a genotyping array.

89. The method of any one of claims 1-88, wherein the at least three polymorphisms comprise:

(i) three polymorphisms selected from Table 1;

(ii) four polymorphisms selected from Table 1;

(iii) five polymorphisms selected from Table 1;

(iv) six polymorphisms selected from Table 1;

(v) seven polymorphisms selected from Table 1;

(vi) eight polymorphisms from one or more 8-SNP models provided in Table 25

(vii) nine polymorphisms selected from Table 1; or

(viii) ten polymorphisms selected from Table 1.